

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 22:03:04 ; Search time 4463.92 Seconds  
(without alignments)  
12876.070 Million cell updates/sec

Title: US-09-750-240-5

Perfect score: 3549

Sequence: 1 atgtcatggttagtgacct.....aaggaccacaagtggtggcact 3549

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_esti:\*

9: gb\_esti:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	808.8	22.8	1039	14	BM811640
2	772	21.8	1016	14	BO881496
3	718.8	20.3	775	12	BF792125
4	593.4	16.7	676	12	BE840188
5	573.6	16.2	1225	13	BI691747
6	565.8	15.9	1043	12	BG297229

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

7	559.8	15.8	743	13	BI685206
8	549.6	15.5	796	12	BG287169
9	540.2	15.2	581	13	BG993320
10	532.4	15.0	790	13	BI255147
11	512.4	14.4	905	14	BQ231940
12	494.8	13.9	607	14	BM943080
13	485.4	13.7	487	9	AL119686
14	473.2	13.3	652	9	AA207907
15	463.4	13.1	565	12	BG872335
16	457.6	12.9	737	10	BE377119
17	449.6	12.7	685	14	BM964004
18	442.4	12.5	525	13	BM090325
19	437.8	12.3	809	9	AU169950
20	418.6	11.8	682	14	BQ180663
21	407.4	11.5	420	12	BF935972
22	400.8	11.3	447	10	BE487801
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31	381.8	10.8	548	10	AV604444
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33	370.2	10.4	584	14	BQ355201
34	363.8	10.3	425	10	AW481229
35	361.8	10.2	625	12	BF369868
36	347.2	9.8	611	12	BG004182
37	345.8	9.7	673	14	BQ370134
38	342.4	9.6	367	10	BE001572
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## ALIGNMENTS

RESULT 1	BM811640	1039 bp	mRNA	linear	EST 05-MAR-2002
LOCUS	BM811640	NIH_MGC_125	Homo sapiens	cdna clone	IMAGE:5724057
DEFINITION	AGENCOURT_6489534	5', mRNA sequence.			
ACCESSION	BM811640				
VERSION	BM811640.1	GI:19128463			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1039)				
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Invitrogen CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> plate: LLAMI2712 row: 1 column: 10 High quality sequence stop: 644. Location/Qualifiers 1..1039				





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DEFINITION 602252571f1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4345144 5',
mRNA sequence.
ACCESSION BF792125
VERSION BF792125.1 GI:12097179
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 775)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9964 row: m column: 17
High quality sequence stop: 711.
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Location/Qualifiers
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Note: this is a NIH_MGC Library."
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Matches 738; Conservative 0; Mismatches 12; Indels 2; Gaps 1;
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ACCESSION BE840188
VERSION BE840188.1 GI:10272566
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 676)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel.: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-QV0-FN0181-100
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Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
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mRNA sequence.
ACCESSION BI691747
VERSION BI691747.1 GI:15654376
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1225)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11872 row: n column: 14
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RESULT 7
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DEFINITION mRNA sequence.
ACCESSION BI685206
VERSION BI685206.1 GI:15647834
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLMI1879 row: j column: 04
High quality sequence stop: 741.
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/dev_stage="5 months"
/lab_host="DH10B"
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Site:2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT 149 a 208 c 213 g 173 t
ORIGIN

Query Match 15.88; Score 559.8; DB 13; Length 743;
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Best Local Similarity 87.7%; Pred. No. 9.8e-117;
Matches 634; Conservative 0; Mismatches 87; Indels 2; Gaps 2;
QY 2424 CTCAGCTTTCTGAGTGTCCATCGGGAACATGCTGCTGAGTCTCTTTGGCCAGCTCTGT 2483
Db 23 CTGAGCTTCCCTGAGTACTTCTGTCGGAACAGTGTCTGCTGAGTCTTCTAGCCAGCTCTGT 82
QY 2484 CTTCTCTACATCAGCAGCATCGGAAAGTTGGCCATGATCTTTGTTTGGGGTTCATCTA 2543
Db 83 CTTCTCTACATCAGCAGCATCGGAAAGTTGGCCATGATCTTTGTTTGGGGTTCACCTA 142
QY 2544 TTTGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2603
Db 143 CTTGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 202
QY 2604 TGGCGTCCATGGCTTGGCTTCTTCCAAATGAGACCTTTGATGGGCTGGAGCTGTCCAGTGC 2663
Db 203 TGGCGTCCATGGCTTGGCTTCTTCCAAATGAGACCTTTGATGGGCTGGAGCTGTCCAGTGC 262
QY 2664 AGGAGGCTGGCCCTCAAAATATATGACCCCTGTGATTTCTGCTGGTGTGGTGGCGCT 2723
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QY 2964 TGAGTTCTATGTGAGGCTGGAGGCAAAATGAGGCTGCGGAGTGCCTGGGCTGTCTCAA 3023
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RESULT 8
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LOCUS 602381888F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4499589 5',
DEFINITION mRNA sequence.
ACCESSION BG287169
VERSION BG287169.1 GI:13040741
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT
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Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: L1AM10363 row: p column: 22  
High quality sequence start: 7  
High quality sequence stop: 680.

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BASE COUNT 207 a 193 c 245 g 151 t

Query Match 15.5%; Score 549.6; DB 12; Length 796;  
Best Local Similarity 97.0%; Pred. No. 2.1e-114; Indels 5; Gaps 5;  
Matches 613; Conservative 0; Mismatches 14;

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Qy 2980 CTGAGGCAACAATGAGGGTGCAGTGCCTGCGGCTGCTCAAGGAGATCATGCTGAC 3039  
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Db 120 -TTATGAGATTATCAGCGAGGAGCGGTTCCGGCAGCTGGAAGATCAAGACGA-TGCT 177  
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Qy 3100 AGCACCTACATGGCTGCTCAGGGCTGAACGCCAGCACTACGATCAGTGGCGGCTCC 3159  
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Db 178 AGCACCTACATGGCTGCTCAGGGCTGAACGCCAGCACTACGATCAGTGGCGGCTCC 237  
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RESULT 9  
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LOCUS 581 bp mRNA linear EST 13-JUN-2001

DEFINITION MR3-HT0999-070201-003-h04 HT0999 Homo sapiens cDNA, mRNA sequence.

ACCESSION BG993320

VERSION BG993320.1 GI:14397390

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 581)

AUTHORS Dias Neto, E., Garcia Correa, R., Vertovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=Hr3&t2=MR3-HT0999-070201-003-h04&t3=2001-02-07&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 581.

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/dev\_stage="Adult"  
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Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 118 a 157 c 199 g 106 t 1 others

ORIGIN

Query Match 15.2%; Score 540.2; DB 13; Length 581;  
Best Local Similarity 98.2%; Pred. No. 2.6e-112;  
Matches 556; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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Db 17 GCCTGAGGATCAAGATCTTTGGGGAC-GTTACTACTGTGTGTCAGGGCTGCCGGAGGCC 75  
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Qy 1316 GGGCGGACCATGCCACATCTGTGTGGAGATGGGGGTAGACATGATGAGGCCATCTCGC 1375  
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Db 76 GGGCGGACCATGCCACATCTGTGTGGAGATGGGGGTAGACATGATGAGGCCATCTCGC 135  
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Qy 1376 TGGTACGTGAGTGACAGGTGTGAATGTGAACATCGCGGTGGGCATCCACACGGCGCG 1435  
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Db 136 TGGTACGTGAGTGACAGGTGTGAATGTGAACATCGCGGTGGGCATCCACACGGCGCG 195  
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Qy 1436 TGCATCGGGCGTCCCTTGGCTTGGCGAAATGCACTTCGATGTGTGTTGTTCAATGATGA 1495  
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Db 196 TGCACTCGGGGTCCTTGGGCTTGGGAAATGGCAGTTTCGATGTGTGTCCTCAATGATGTGA 255
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Db 256 CCCTGGCAACACATGAAGCAGAAAGCGGGGTGCGCGCATCCACATCACTCGGGCAA 315
Qy 1556 CACTGCAAGTACCTGAACGGGAGCTACGAAGTGGAGCCGCGGTGGGAAGCGCAACG 1615
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Qy 1616 CGTACCTCAAGGAGCAGACATGAGACTTTCCTCATCTTGGGCGCCAGCAGAAACGGA 1675
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Qy 1676 AAGAGGAGAAGGATGCTGGCCAAAGTGCAGCGGACTCGGGCCAACTCCATGGAAGGCG 1735
Db 436 AAGAGGAGAAGGATGCTGGCCAAAGTGCAGCGGACTCGGGCCAACTCCATGGAAGGCG 495
Qy 1736 TGATCGCGGATGGGTTCCCTGATGCTGCTTCTCCCGGACCAAGGACTCCAAGGCCCTTCC 1795
Db 496 TGATCGCGGATGGGTTCCCTGATGCTGCTTCTCCCGGACCAAGGACTCCAAGGCCCTTCC 555
Qy 1796 GCCAGATGGGATGATGATTCAGC 1821
Db 556 GNCAGATGGGATGATGATTCAGC 581

RESULT 10
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LOCUS 602977410F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5122130 5',
DEFINITION mRNA sequence.
ACCESSION Bi255147
VERSION Bi255147.1 GI:14808265
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaphs-femail.nih.gov
Tissue Procurement: ATCC
cDNA Library prepared by: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11298 row: d column: 03
High quality sequence stop: 634.
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Average insert size 1.4 kb. Library prepared by Life
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BASE COUNT 168 a 202 c 231 g 189 t
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Query Match 15.0%; Score 532.4; DB 13; Length 790;
Best Local Similarity 89.9%; Pred. No. 1.7e-110;
Matches 707; Conservative 0; Mismatches 61; Indels 18; Gaps 12;
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Qy 2602 CTTGGCGCTCCATGGCTTGGCTTCTTCCAAATGAGACCTTTTATGGGCTGGAGCTTCCAGCT 2661
Db 69 CTTGGCGCTC--ATGGCTTGGTCTTCCAAATGAGACCTTTTATGGGCTGGAGCTTCCAGCT 126
Qy 2662 GCAGGGAGGGTGGCCCTCAAAATATATATGACCCCTGATTTCTGCTGGTGTGTTGGCTGGCG 2721
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Qy 2722 CTGTATCTGATGCTGACAGAGTGAATGAGTCCGCTTAAACTTCTCTGGAACATA 2781
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Qy 2782 CAGGCAACAGGGGAAAGAGGAGAGTGAAGTGAATGAGTCCGCTTAAACTTCTCTGGAACATA 2841
Db 246 CAGGCAACAGGGGAAAGAGGAGAGTGAAGTGAATGAGTCCGCTTAAACTTCTCTGGAACATA 305
Qy 2842 CATAAATCTTGCCTCAAGGAGCTGGCGGCCACTTCTGCGCGGGAGCGCGCAATGAT 2901
Db 306 CATAAATCTTGCCTCAAGGAGCTGGCGGCCACTTCTGCGCGGGAGCGCGCAATGAT 364
Qy 2902 GAACTCTACTATCAGTCTGCTGAGTGTGCTGCTGTTATGTTGCTCCTCATTTGCC-AACTT 2960
Db 365 GAACTCTACTATCAGTCTGCTGAGTGTGCTGCTGTTATGTTGCTCCTCATTTGCCAAACTT 424
Qy 2961 CTCTGAGTTCTATGCTGAGCTGGAGGCAAACTGAGGGTGGCGAGTGCCTTGGCGCTGCT 3020
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Qy 3021 CAACGAGATCATCGTCACTTTT-GATGAGATTTATCAGGAGGAGCGGTTCCCGCAGC--T 3077
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Qy 3078 GGAAGAATCAAGACGATGGTACACCTACATGCTGCTCAGGCTGAGGCTGAACGCCAGCA- 3136
Db 545 GAACACGATCAAGACGATGGTACACCTACATGCTGCTCAGGCTGAGGCTGAACGCCAGCAA 604
Qy 3137 -CCTACGATC--AGGTGGCGCTCCACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3192
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Qy 3250 ATTGGGCTGAACA-TGGGCGGCTGCTGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 3308
Db 725 ATGGGCTGAACAATTGGGCGGCTGCTGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 784
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Db 785 TGACAT 790

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DEFINITION 5', mRNA sequence.
ACCESSION BQ231940
VERSION BQ231940.1 GI:20413340
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Db 307 CATAACATCTTCCCAAGGAGTGGCGCCACATCTCTGCGCGGAGCGCGCAACGAT 248
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VERSION AL119686
KEYWORDS EST.
SOURCE AL119686.1 GI:5925585
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 487)
AUTHORS Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
TITLE EST (Bloecker, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Bloecker H
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZp761N2323) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

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Matches 486; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 14
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type VI mRNA, complete cds (MOUSE);, mRNA sequence.
ACCESSION AA207907
VERSION AA207907.1 GI:1804964
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 652)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 417.
MG1:407635
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NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	
Contact: Robert Strausberg, Ph.D.	
Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a>	
Tissue Procurement: Jeffrey E. Green, M.D.	
CDNA Library Preparation: Life Technologies, Inc.	
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
DNA Sequencing by: Incyte Genomics, Inc.	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	

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http://image.lnl.gov
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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4923890"
/clone.lib="NCI_CGAP_SG2"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1
NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
133 a 141 c 174 g 117 t
BASE COUNT

```

Db	361	ACACGGACGNGTGCATTTGGCGGCTCTTGCCCTACGGAATGGCAGTTTGATGTCTGGT	420
QY	1484	CCATGATGTGACCTTGGCCAAACCACATGGAAGCAGGAAGCGGCGTGGCCGCATCCACA	1543
Db	421	CAACAGATGTGACCTTGCTTACCACATGGAAGCCGGGGCGCGCCGCATCCACA	480
QY	1544	TCACTCGGGCAACACTGCAGTACTTGACGGGGACTACGA-AGTGGAGCCAGGCCGTGGT	1602
Db	481	TCACTCGGGCTACACTGCAGTACTTTGAACGGGGACTATGACGGTGGAGCCAGGCCGTGGT	540

Qy 1603 GGCAAGCGCAACCGGTACCTCAAGG 1627  
|| | |||| ||||| |||||  
Db 541 GGTGAACGCAATCGGTACCTCAAGG 565

Search completed: February 23, 2003, 04:21:47  
Job time : 4501.92 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 22:03:04 ; Search time 394.948 Seconds  
(without alignments)  
12876.070 Million cell updates/sec

Title: US-09-750-240-1

Perfect score: 314

Sequence: 1 atgtcatgttttagtgccct.....acacggcgggaccgctgaa 314

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_nam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	199.2	63.4	618	10	BB866520
2	180	57.3	631	10	BB866451
3	60.2	19.2	1011	17	CNS02STX
4	58.8	18.7	941	13	BG916212
5	51.4	16.4	925	17	CNS0091P
6	50.4	16.1	1009	17	CNS010EW

7	43.4	13.8	846	17	CNS010RJ	AL099337 Drosophil
8	43	13.7	932	17	CNS0072Q	AL066742 Drosophil
9	43	13.7	950	14	BQ948546	BQ948546 AGENCOURT
10	42.4	13.5	778	14	BQ92531	BQ92531 AGENCOURT
11	42.4	13.5	925	17	CNS0091P	AL053013 Drosophil
12	42.4	13.5	1065	17	CNS0108S	AL098662 Drosophil
13	41.8	13.3	935	17	CNS006XK	AL066051 Drosophil
14	41.8	13.3	968	17	AG030603	AG030603 Pan trogl
15	41.4	13.2	1075	17	AG073983	AG073983 Pan trogl
16	41.2	13.1	1010	14	BQ064125	BQ064125 AGENCOURT
17	41.2	13.1	1203	17	CNS015Y4	AL106054 Drosophil
18	40.6	12.9	884	17	CNS018NP	AL109567 Drosophil
19	40.6	12.9	948	14	BQ646304	BQ646304 AGENCOURT
20	40.4	12.9	486	10	BE233788	BE233788 140263 MA
21	40.4	12.9	894	17	CNS0159I	AL105168 Drosophil
22	40.4	12.9	1612	13	BM455541	BM455541 AGENCOURT
23	40.2	12.8	1101	17	CNS0150D	AL104839 Drosophil
24	40	12.7	844	17	CNS0052P	AL056652 Drosophil
25	40	12.7	844	17	CNS0052P	AL056652 Drosophil
26	40	12.7	932	17	CNS0072Q	AL066742 Drosophil
27	40	12.7	935	17	CNS006XK	AL066051 Drosophil
28	40	12.7	1125	17	AG073746	AG073746 Pan trogl
29	39.8	12.7	906	17	AG081338	AG081338 Pan trogl
30	39.6	12.6	731	17	AG061169	AG061169 Pan trogl
31	39.6	12.6	935	17	AG073949	AG073949 Pan trogl
32	39.6	12.6	1538	17	AG030607	AG030607 Pan trogl
33	39.4	12.5	717	17	CNS0111L	AL100311 Drosophil
34	39.2	12.5	858	12	BG481980	BG481980 602527810
35	39.2	12.5	877	17	CNS028C5	AL211980 Tetradodon
36	39.2	12.5	1003	14	BQ886908	BQ886908 AGENCOURT
37	39	12.4	635	10	BB656840	BB656840 MI-P-CP1
38	38.8	12.4	447	13	BI403012	BI403012 MI-P-CP1
39	38.8	12.4	481	10	BE233791	BE233791 140269 MA
40	38.8	12.4	587	13	BI399585	BI399585 MI-P-AV1
41	38.8	12.4	588	13	BI402027	BI402027 MI-P-CP0
42	38.8	12.4	687	13	BI182737	BI182737 UNL-P-FN
43	38.8	12.4	725	13	BI181902	BI181902 UNL-P-FN
44	38.8	12.4	839	17	CNS004NB	AL054280 Drosophil
45	38.6	12.3	504	13	BI669206	BI669206 603295447

## ALIGNMENTS

RESULT 1	618 bp	linear	EST 27-NOV-2001
BB866520	musculus	RIKEN full-length enriched, colon RCB-0549	Cle-H3 cdna Mus
LOCUS	musculus	cdna clone G431005N18 5', mRNA sequence.	
DEFINITION	BB866520	1 GI:17112730	
ACCESSION	BB866520	EST.	
VERSION	BB866520	house mouse.	
KEYWORDS	EST.	house mouse.	
SOURCE	EST.	house mouse.	
ORGANISM	EST.	house mouse.	
REFERENCE	1 (bases 1 to 618)		
AUTHORS	Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Numasaka, R., Okazaki, Y., Okado, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., et al.		
TITLE	RIKEN Encyclopedia of Mouse Full-length cDNAs (AKIMURA, T., et al. 2001)		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		













NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

source

1. .925  
/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/clone\_lib="BACRI9D16"  
/clone\_lib="RPCI-98"  
/note="end : TET3"

BASE COUNT 120 a 61 c 61 g 172 t 511 others

## ORIGIN

Query Match 13.5%; Score 42.4; DB 17; Length 925;

Best Local Similarity 10.4%; Pred. No. 2.2;

Matches 31; Conservative 146; Mismatches 120; Indels 0; Gaps 0;

QY 14 GTGGCTCTGGTCCCTAAAGTGATGAACGAAACAGCTCGGGTGAACGCAATGGGC 73

Db 628 GTSCSSSSSSSTSSSTSSSTSSSTSSSTSSSSSSSSSSSTSSSTSSSTSSSTSSAGSGSWAGG 687

QY 74 AGAAGCTTTCGGCGCCGCTGGCACTCGGGCAGGTGGCTTCTCCACGCCCCCGCTATATGA 133

Db 688 GSGCTGTSSTSSSSSTSSSTSSSVSGSKSTBSGCSBSSGSSSSSSSTSSBBSCTSTSS 747

QY 134 CTGCTCTCGGGATGAGACCCACCCAGCCACCCCTCGGGGCCCCCTCGGTGCCCT 193

Db 748 SSSSSYSTSCCTCCCTCCSYSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSS 807

QY 194 GGCAGATGACGCTTCATCCGAGGGGGCGCCCAAGCAAGGCAAGCAAGCAAGCAAGCAAGCAAG 253

Db 808 CTTCTCCSYMBCTSTSSGSSSSSGKGGVTKCGCGGSSSTNMBGTSSACSSS 867

QY 254 GGCAGTGGCCCTGGGCTTCGAGATACCAAGTACCAAGTACCAAGTACCAAGTACCAAGTACCAAG 310

Db 868 SSCSSSVSSSSKSSASSSVSSSVSSSVSSSVSSSVSSSVSSSVSSSVSSSVSSSVSSSVSSSVSS 924

## RESULT 12

CNS0108S/c

LOCUS

DEFINITION

Drosophila melanogaster genome survey sequence T7 end of BAC  
BACN03J03 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

ACCESSION

AL098662

VERSION

GI:5610273

KEYWORDS

GSS.

SOURCE

ORGANISM

Drosophila melanogaster.

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

1 (bases 1 to 1065)

AUTHORS

Genoscope.

TITLE

Direct Submission

JOURNAL

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr))- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the European Drosophila Genome Project (EDGP) -

<http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC

library (DrosBAC) was made by Alain Billaud at CEPH (Centre

d'Etude du Polymorphisme Humain) with funding provided by a MRC

project grant. The DNA was prepared from embryos by Alain Bucheton

and Genevieve Payan. It has been constructed in the vector

pBel0BAC11.

Location/Qualifiers

1. .1065

/organism="Drosophila melanogaster"

## FEATURES

source

1. .1065

/organism="Drosophila melanogaster"

/db\_xref="taxon:7227"  
/clone="BACN03J03"  
/clone\_lib="DrosBAC"  
/plasmid="pBel0BAC11"  
/note="end : T7"

BASE COUNT 121 a 225 c 252 g 313 t 154 others

## ORIGIN

Query Match

Best Local Similarity 13.5%; Score 42.4; DB 17; Length 1065;

Matches 73; Conservative 58; Mismatches 107; Indels 0; Gaps 0;

QY 75 GAAGCGTTTCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACGCCCGCTATATGAG 134

Db 1028 GRCCSRGCGSAGGKMYCAGACCGGGGRCGCTCCSAGASACMCSCSCCACACS 969

QY 135 CTGCTCCGGGATGACAGACCCACCCACCCCTCGGGGCCCCCTCGGTGCCCTG 194

Db 968 AARGVCCSMCYCSCSCCCCGCCACGCGSCCMGTMBCMAGCGSSCCSSSCSCAMSGG 909

QY 195 GCAGGATGACGCTTCATCCGAGGGGCGCCCAAGCAAGGCAAGCAAGTGGGGCTGCG 254

Db 908 MGAGSSSSSSSSSSSSSSSGSSSSSARGCGCAKGGGGGGKGGKGGCGGGGAGGGG 849

QY 255 GGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTACCAACGACACCGCGGGACCGCTG 312

Db 848 GGGGRRGCCCGGGAACMGWACMVAAGGTGACMCCSCSMVSSCMSSSCMCGG 791

## RESULT 13

CNS006XK

LOCUS

DEFINITION

Drosophila melanogaster genome survey sequence T7 end of BAC #  
BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

ACCESSION

AL066051

VERSION

GI:4945019

KEYWORDS

GSS.

SOURCE

ORGANISM

Drosophila melanogaster.

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

1 (bases 1 to 935)

AUTHORS

Genoscope.

TITLE

Direct Submission

JOURNAL

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr))- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoedawa and

Aaron Mamoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

EcoRI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain y2; cn bw sp, the same strain used for the BDGP's

pl and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

Location/Qualifiers

1. .935

/organism="Drosophila melanogaster"

/db\_xref="taxon:7227"

/clone\_lib="BACR14N09"

/clone\_lib="RPCI-98"

/note="end : T7"

## BASE COUNT

257 a 170 c 162 g 96 t 250 others

## ORIGIN

Q4, 83 CGCGGCGCCGTGGCAGCTCGGGCAGGTGGCTTCTGCACGCCCCGGCTATATGAGCTGGCCTCC 142

Qy 138 CCTCCGGATGCAGAGCACCCAGCCCTCGGGGGCCCCCTCGGTGGCCCTCGCA 197

Db 649 GGCCCCGGCGG 708





GenCore version 5.1.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 22:29:24 ; Search time 53.5045 Seconds  
(without alignments)  
9128.329 Million cell updates/sec

Title: US-09-750-240-1  
Perfect score: 314  
Sequence: 1 atgtcatgttttagtgccct.....acacggcgaggaccgtgaa 314

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2850587 seqs, 77717511 residues  
Total number of hits satisfying chosen parameters: 5701174

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*  
1: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq.\*  
2: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	295.2	94.0	1386	1	PCT-US02-36759-83
2	199.2	63.4	5826	6	US-10-144-771-5921
3	39.8	12.7	36303	6	US-10-152-724-24
4	39.8	12.7	36303	6	US-10-152-724A-24
5	38.2	12.2	1878	5	US-09-724-676-33617
6	38.2	12.2	1878	5	US-09-724-676A-33617
7	38.2	12.2	3174	6	US-10-218-140-5849
8	38.2	12.2	3182	5	US-09-724-676-33618
9	38.2	12.2	3182	5	US-09-724-676A-33618
10	36.6	11.7	1542	1	PCT-US02-38526-349
11	36.6	11.7	2216	1	PCT-US02-38526-347
12	36.4	11.6	485	5	US-09-585-645A-59
13	36	11.5	22118	6	US-10-287-313-16
14	35.8	11.4	1824	5	US-09-724-676-45770
15	35.8	11.4	1824	5	US-09-724-676A-45770
16	35.2	11.2	2883	6	US-10-125-923A-157
17	35.2	11.2	2883	6	US-10-205-892-157
18	35.2	11.2	2883	6	US-10-174-575-157
19	35.2	11.2	2883	6	US-10-174-575A-157
20	35.2	11.2	2883	6	US-10-015-610A-23
21	35.2	11.2	2883	6	US-10-226-254A-23
22	35.2	11.2	2883	6	US-10-187-755-157
23	35.2	11.2	2883	6	US-10-187-749-157
24	35.2	11.2	2883	6	US-10-017-253A-23
25	35.2	11.2	2883	6	US-10-199-672-157
26	35.2	11.2	2883	6	US-10-194-486-157

Sequence 3, Appli  
Sequence 3, Appli  
Sequence 65, Appl  
Sequence 21648, A  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 652, App  
Sequence 23402, A  
Sequence 319, App  
Sequence 179, App  
Sequence 66, Appl  
Sequence 17257, A  
Sequence 26872, A  
Sequence 143, App  
Sequence 14604, A  
Sequence 14604, A  
Sequence 14611, A  
Sequence 14611, A  
Sequence 14602, A

ALIGNMENTS

RESULT 1  
PCT-US02-36759-83  
; Sequence 83, Application PC/TUS0236759  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: DUGGAN, Brendan M.  
; APPLICANT: YANG, Junming  
; APPLICANT: GIETZEN, Kimberly J.  
; APPLICANT: LEE, Soo Yeun  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: AZIMZAI, Yalda  
; APPLICANT: WALIA, Narinder K.  
; APPLICANT: WARREN, Bridget A.  
; APPLICANT: BARROSO, Ines  
; APPLICANT: BECHA, Shanya D.  
; APPLICANT: YUE, Henry  
; APPLICANT: LEHR-MASON, Patricia M.  
; APPLICANT: THANGASELOU, Kavitha  
; APPLICANT: LEE, Sally  
; APPLICANT: EMERLING, Brooke M.  
; APPLICANT: KABLE, Amy E.  
; APPLICANT: KHARE, Reena  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: GANDHI, Ameena R.  
; APPLICANT: TRAN, Uyen K.  
; APPLICANT: RICHARDSON, Thomas W.  
; APPLICANT: MARQUIS, Joseph P.  
; APPLICANT: LAL, Preeti G.  
; APPLICANT: FORSYTHE, Ian J.  
; APPLICANT: LEE, Ernestine A.  
; APPLICANT: SWARNAKAR, Anita.  
; APPLICANT: KALLICK, Deborah A.  
; APPLICANT: GRIFFIN, Jennifer A.  
; APPLICANT: ELLIOTT, Vicki S.  
; APPLICANT: GORVAD, Ann E.  
; APPLICANT: HAFALIA, April J.A.  
; APPLICANT: ISON, Craig H.  
; APPLICANT: JIN, Pei  
; APPLICANT: JIANG, Xin  
; APPLICANT: JACKSON, Alan  
; APPLICANT: BHATIA, Umesh  
; APPLICANT: BURRILL, John D.  
; APPLICANT: BLAKE, Julie J.  
; APPLICANT: HO, Ann  
; APPLICANT: ZHENG, Wenjin  
; APPLICANT: GAO, Jing  
; TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS  
; FILE REFERENCE: PF-1279 PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/36759

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; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 60/333,097
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,274
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/340,542
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/342,166
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/347,580
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/348,687
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PERL Program
; SEQ ID NO 83
; LENGTH: 1386
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7506194CB1
PCT-US02-36759-83

Query Match      94.0%; Score 295.2; DB 1; Length 1386;
Best Local Similarity 97.1%; Pred. No. 1.5e-65;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTGTAGTGGCTCTCTGTCCTAAAGTGGATGAACGAAACACGCTGGGGT 60
Db 1 ATGTCATGTTTGTAGTGGCTCTCTGTCCTAAAGTGGATGAACGAAACACGCTGGGGT 155
QY 61 GAACCAATGGCAGAAAGCTTCGGGGCGCGTGGGCACTCGGGCAGGCTTCTGCAGC 120
Db 156 GAACCAATGGCAGAAAGC---CCACGCCACGCGAATCGAGCCAGTGGCTTCTGCAGC 212
QY 121 CCCCGCTATATGAGTGCCTCCGGGATGCAGACCCAGCCAGCCACCCCTCGGGGCC 180
Db 213 CCGTCTACATGAGTGCCTCAAGATGCGGAGCCACCCAGCCCACTCTCGAGCTCAC 272
QY 181 CCGTCTGCCCCCTGCGCAGGATGACGCTTCATCCGAGGGGCGGCCANGAGGCAAG 240
Db 273 ACTCGTGCCTCGCAGGATGAAGCTTCATCAGGAGGGCGGCCCGGCGGAGGTGTG 332
QY 241 GAACCTGGGGCTGGGGCAGTGGCCCTGGGCTTCGAGATACCGAAGTGACAAC 293
Db 333 GAGCTGGGGCTCGGCTCAGTGGGCTTGGGCTTGGAGACACTGAGGTGACCAC 385

RESULT 3
US-10-152-724-24/C
; Sequence 24, Application US/10152724
; GENERAL INFORMATION:
; APPLICANT: LITTLE, Melissa
; APPLICANT: HOLMES, Gregory
; APPLICANT: KOLLE, Gabriel
; APPLICANT: YAMADA, Toshiya
; APPLICANT: GEORGAS, Kylie
; APPLICANT: WILKINSON, Lorine
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptide
; FILE REFERENCE: P22378
; CURRENT APPLICATION NUMBER: US/10/152,724
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: Australian App No PQ 4348
; PRIOR FILING DATE: 1999-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 36303
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-152-724-24

Query Match      12.7%; Score 39.8; DB 6; Length 36303;
Best Local Similarity 55.4%; Pred. No. 1.3;
Matches 77; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 78 GCGTTGCGGGCGCGCTGGGCACTCGGGCAGGTGGCTTCTGCACGCGCCCGCTATATGAGCTG 137
Db 34505 GAGTGGGGCGCGCGGGAGTGGGGAGGCTCCCTACCCCTCGCCCGACCGGCAG 34446
QY 138 CCTCCGGGATGCAGACCCAGCCAGCCAGCCCTCGGGGCCCTCGGTGCGCCCTGGCA 197
Db 34445 CCTACGCGCGCAGCTCTCTCCCTCGGCTTCTCGGCGGAGTCCCGGCGGAGTCCCGGCC 34386
QY 198 GGATGACGCTTCATCCGG 216
Db 34385 TCTCGCTCTCTCCCGG 34367

RESULT 4
US-10-152-724A-24/C
; Sequence 24, Application US/10152724A
; GENERAL INFORMATION:
; APPLICANT: LITTLE, Melissa
; APPLICANT: HOLMES, Gregory
; APPLICANT: KOLLE, Gabriel
; APPLICANT: YAMADA, Toshiya
; APPLICANT: GEORGAS, Kylie
; APPLICANT: WILKINSON, Lorine
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptide
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; FILE REFERENCE: P2378
; CURRENT APPLICATION NUMBER: US/10/152,724A
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: Australian App No PQ 4348
; PRIOR FILING DATE: 1999-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 36303
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-152-724A-24

Query Match      12.7%; Score 39.8; DB 6; Length 36303;
Best Local Similarity 55.4%; Pred. No. 1.3;
Matches 77; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 78 GCGTTCGCGGGCGGTGGCACTCGGGCAGGTGGCTTCTGCAGCGCCCGCTATATGAGCTG 137
Db 34505 GAGTGGCGGGCGCGGGGAGTGGGGGAGGCTCCCTACCCCTGCGCCGACGGCGAG 34446

Qy 138 CTTCCGGGATGCAGAGCCACCCAGCCACCCCTGCGGGGCCCTCTCGGTGCCCTGGCA 197
Db 34445 CCCTACGGCGCAGCTCCTCTCGGCGCTCTTCCCGCGGAGCGGAGTCCCCGCC 34386

Qy 198 GGATGACGCCCTTCATCCGG 216
Db 34385 TCTCGCCTCTCTCTCCGG 34367

RESULT 5
US-09-724-676-33617/c
; Sequence 33617, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724, 676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33617
; LENGTH: 1878
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-33617

Query Match      12.2%; Score 38.2; DB 5; Length 1878;
Best Local Similarity 46.0%; Pred. No. 1.7;
Matches 127; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

Qy 13 AGTGGCCTCTCTGTCCTAAAGTGGATGAACGGAAACAGCCTGGGTGAACGCAATGGG 72
Db 1319 AGAGCCCCCAGGCCCGGAGAGCCAGAGCCGCTGGCTGGCAGAGGTGGAGGTGAGGA 1260

Qy 73 CAGAAGCGTTTCGGCGGCCCTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCCGCTATATG 132
Db 1259 CAGACAGCCCCCAGCAAAATGGCAGGTGGGCGTGGCGTGCAGGCAGACGTGCTGTG 1200

Qy 133 AGTGGCTTCGGGATGCAGAGCCACCCAGCCACCCCTCGGGGGCCCCCTCGGTGCCCC 192
Db 1199 TGCTGCCAGGGCGGGGCCCTCTGCTGCGCCCTCTGCGCAGGCTCCCGGTAGATCGGC 1140

Qy 193 TGGCAGGATGACGCTTTCATCCGAGGGCGGCCCCANGCAAGGGCAAGAACTGGGCGTG 252
Db 1139 AAGCAGATCGACTCGGCTGGCCCAAGCGCTGCAGCCGAGTGGCGTGGGGCGGCG 1080

Qy 253 CGGCGAGTGGCCCTGGGCTTTCGAAGATACCGAAGTG 288
Db 1079 CAGCGGGCGGTGCACCCAGCGGCGAGGCTG 1044

RESULT 6
US-10-218-140-5849
; Sequence 5849, Application US/10218140
; GENERAL INFORMATION:
; APPLICANT: Shinketsu, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES
; FILE REFERENCE: 15966-543 CON
; CURRENT APPLICATION NUMBER: US/10/218,140
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/127,728
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/127,636
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/127,607
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 6322
; SOFTWARE: Curator Version 1.0
; SEQ ID NO 5849
; LENGTH: 3174
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1870)..(2332)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
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; FILE REFERENCE: P2378
; CURRENT APPLICATION NUMBER: US/10/152,724A
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: Australian App No PQ 4348
; PRIOR FILING DATE: 1999-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 36303
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-152-724A-24

Query Match      12.7%; Score 39.8; DB 6; Length 36303;
Best Local Similarity 55.4%; Pred. No. 1.3;
Matches 77; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 78 GCGTTCGCGGGCGGTGGCACTCGGGCAGGTGGCTTCTGCAGCGCCCGCTATATGAGCTG 137
Db 34505 GAGTGGCGGGCGCGGGGAGTGGGGGAGGCTCCCTACCCCTGCGCCGACGGCGAG 34446

Qy 138 CTTCCGGGATGCAGAGCCACCCAGCCACCCCTGCGGGGCCCTCTCGGTGCCCTGGCA 197
Db 34445 CCCTACGGCGCAGCTCCTCTCGGCGCTCTTCCCGCGGAGCGGAGTCCCCGCC 34386

Qy 198 GGATGACGCCCTTCATCCGG 216
Db 34385 TCTCGCCTCTCTCTCCGG 34367

RESULT 5
US-09-724-676-33617/c
; Sequence 33617, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724, 676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33617
; LENGTH: 1878
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-33617

Query Match      12.2%; Score 38.2; DB 5; Length 1878;
Best Local Similarity 46.0%; Pred. No. 1.7;
Matches 127; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

Qy 13 AGTGGCCTCTCTGTCCTAAAGTGGATGAACGGAAACAGCCTGGGTGAACGCAATGGG 72
Db 1319 AGAGCCCCCAGGCCCGGAGAGCCAGAGCCGCTGGCTGGCAGAGGTGGAGGTGAGGA 1260

Qy 73 CAGAAGCGTTTCGGCGGCCCTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCCGCTATATG 132
Db 1259 CAGACAGCCCCCAGCAAAATGGCAGGTGGGCGTGGCGTGCAGGCAGACGTGCTGTG 1200

Qy 133 AGTGGCTTCGGGATGCAGAGCCACCCAGCCACCCCTCGGGGGCCCCCTCGGTGCCCC 192
Db 1199 TGCTGCCAGGGCGGGGCCCTCTGCTGCGCCCTCTGCGCAGGCTCCCGGTAGATCGGC 1140

Qy 193 TGGCAGGATGACGCTTTCATCCGAGGGCGGCCCCANGCAAGGGCAAGAACTGGGCGTG 252
Db 1139 AAGCAGATCGACTCGGCTGGCCCAAGCGCTGCAGCCGAGTGGCGTGGGGCGGCG 1080

Qy 253 CGGCGAGTGGCCCTGGGCTTTCGAAGATACCGAAGTG 288
Db 1079 CAGCGGGCGGTGCACCCAGCGGCGAGGCTG 1044

RESULT 6
US-10-218-140-5849
; Sequence 5849, Application US/10218140
; GENERAL INFORMATION:
; APPLICANT: Shinketsu, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES
; FILE REFERENCE: 15966-543 CON
; CURRENT APPLICATION NUMBER: US/10/218,140
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/127,728
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/127,636
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/127,607
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 6322
; SOFTWARE: Curator Version 1.0
; SEQ ID NO 5849
; LENGTH: 3174
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1870)..(2332)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
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FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (961)...(961)  
OTHER INFORMATION: "n" = "a", "c", "t" or "g"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1191)...(1191)  
OTHER INFORMATION: "n" = "a", "c", "t" or "g"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1193)...(1193)  
OTHER INFORMATION: "n" = "a", "c", "t" or "g"  
US-10-218-140-5849

Query Match 12.2%; Score 38.2; DB 6; Length 3174;  
Best Local Similarity 53.4%; Pred. No. 1.9;  
Matches 79; Conservative 0; Mismatches 69; Indels 0; Gaps 0;  
QY 137 GCTCGGGGATGACAGCCACCCAGCCCTCGCGGCCCCCTCGGTGCCCTGGC 196  
DB 2049 GCCCCTCCAGGCTGAGCTTCCACCCACAGCCTCCCGGTCGCCACATTGCCCTCAGC 2108  
QY 197 AGGATCACCCCTTCATCCCGAGGGGGCCCGCCAGCAAGGCAAGNACTGGGGCTCGGG 256  
DB 2109 AGGGCTTATCCAGTTCTCTGGGGTGGGGGAGGAGTCCCTGGCACAGTGCACAGGCT 2168  
QY 257 CAGTGGCCCTGGGCTTCGAAGATACCGA 284  
DB 2169 CAGGCGCCCTGGCTAGCTGGACATCCA 2196

RESULT 8  
US-09-724-676-33618/c  
; Sequence 33618, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Comugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 33618  
; LENGTH: 3182  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-33618

Query Match 12.2%; Score 38.2; DB 5; Length 3182;  
Best Local Similarity 46.0%; Pred. No. 1.9;  
Matches 127; Conservative 0; Mismatches 149; Indels 0; Gaps 0;  
QY 13 ACTGGCTCTCTGGTCCCTAAAGTGATGAACGAAACAGCCTGGGGTGAACGCAATGGG 72  
DB 2623 AGAGCCCCCAGCCCGGAGAGCAGGAGCCGTGGCTGGCACAGGTTGGAAGGTGAGGA 2564  
QY 73 CAGAAGCGTTTCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACGCCCGCGCTATATG 132  
DB 2563 CAGACAGCCCCCAGCAAAATGGCAGGTGGCGTGGCGGTGCAGGCAGACGTGCTGTCTG 2504  
QY 133 AGCTGCTCCGGGATGCAGACGCCACCCACCCCTCGGGGCCCCCTCGGTGCCGCC 192  
DB 2503 TGCTGCCAGGGGGGGCCCCCTGCTGCTGCTCTCTGCGAGGCTCTCCCGGTAGATCGGC 2444  
QY 193 TGGCAGGATGAGCCCTTCATCCGGAGGGGGCGCCCAAGCAAGGCAAGTGGGGCTG 252  
DB 2443 AAGCAGATGACTGGCCCTGGCCCAAGCCCTGCGAGGCCGAGTGGCCCTCGGGGGGGCG 2384  
QY 253 CGGGCAGTGGCGCTTTCGAAGATACCGAAGTG 288  
DB 2383 CAGCGGGGGCGGTGCACCCAGCGGCGAGCGAGCTG 2348

RESULT 9  
US-09-724-676A-33618/c  
; Sequence 33618, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Comugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 33618  
; LENGTH: 3182  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-33618

Query Match 12.2%; Score 38.2; DB 5; Length 3182;  
Best Local Similarity 46.0%; Pred. No. 1.9;  
Matches 127; Conservative 0; Mismatches 149; Indels 0; Gaps 0;  
QY 13 ACTGGCTCTCTGGTCCCTAAAGTGATGAACGAAACAGCCTGGGGTGAACGCAATGGG 72  
DB 2623 AGAGCCCCCAGCCCGGAGAGCAGGAGCCGTGGCTGGCACAGGTTGGAAGGTGAGGA 2564  
QY 73 CAGAAGCGTTTCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACGCCCGCGCTATATG 132  
DB 2563 CAGACAGCCCCCAGCAAAATGGCAGGTGGCGTGGCGGTGCAGGCAGACGTGCTGTCTG 2504  
QY 133 AGCTGCTCCGGGATGCAGACGCCACCCACCCCTCGGGGCCCCCTCGGTGCCGCC 192  
DB 2503 TGCTGCCAGGGGGGGCCCCCTGCTGCTGCTCTCTGCGAGGCTCTCCCGGTAGATCGGC 2444  
QY 193 TGGCAGGATGAGCCCTTCATCCGGAGGGGGCGCCCAAGCAAGGCAAGTGGGGCTG 252  
DB 2443 AAGCAGATGACTGGCCCTGGCCCAAGCCCTGCGAGGCCGAGTGGCCCTCGGGGGGGCG 2384  
QY 253 CGGGCAGTGGCGCTTTCGAAGATACCGAAGTG 288  
DB 2383 CAGCGGGGGCGGTGCACCCAGCGGCGAGCGAGCTG 2348

RESULT 10  
PCT-US02-38526-349/c  
; Sequence 349, Application PC/TUS0238526  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Malabika  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Zhao, Qing  
; APPLICANT: Xu, Chongjun  
; APPLICANT: Mulero, Julio J  
; APPLICANT: Boyle, Bryan J.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL POLYPEPTIDES AND POLY  
; FILE REFERENCE: HYS-B1/PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/38526  
; CURRENT FILING DATE: 2002-12-03  
; PRIOR APPLICATION NUMBER: US 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: PCT/US00/35017  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/620,312  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: PCT/US00/34263  
; PRIOR FILING DATE: 2000-12-26  
; PRIOR APPLICATION NUMBER: US 09/496,914  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: US 09/560,875  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: PCT/US01/03800





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QY 230 GCAAGGGC 237
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Db 133 CCACGGGC 126
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RESULT 13
US-10-287-313-16/c
; Sequence 16, Application US/10287313
; GENERAL INFORMATION:
; APPLICANT: Hadlaczky, Gyula
; Szalay, Aladar
; TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
; AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/287,313
; FILING DATE: 01-Nov-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/724,726
; FILING DATE: 28-NOV-2000
; APPLICATION NUMBER: 08/835,682
; FILING DATE: 10-APR-1997
; APPLICATION NUMBER: 08/695,191
; FILING DATE: 07-AUG-1996
; APPLICATION NUMBER: 08/682,080
; FILING DATE: 15-JUL-1996
; APPLICATION NUMBER: 08/629,822
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6869-402N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-450-8403
; TELEFAX: 858-587-3360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22118 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-287-313-16
Query Match 11.5%; Score 36; DB 6; Length 22118;
Best Local Similarity 48.3%; Pred. No. 11;
Matches 99; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 40 GAACGGAACAGCTGGGTGACGCGCATGGGACAGAGCTTCGGGGCGCGTGGCACT 99
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Db 13499 GAATCTGCACACACCGGGGGGTGACTGCATCGCGGCACGAGCGCGCGGTCCCGGG 13440
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*QY 100 CGGGCAGGTGGCTTCTGCACGCGCGCGCTATATAGCTGCCTCCGGGATGCAGAGCCACC 159
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Db 13439 CCGGCGCGGAGCGGGTACCGCCCGGGTCAAGGAGAAGCGGAGACGAAGACGACCG 13380
|||||
QY 160 AGCCCCACCCCTGCGGGCCCCCTCGGTGCCCCCTGGCAGGATGACGCTTCATCCGGAGG 219
|||||
Db 13379 GGGCCACGGGCCCCCGACCGCCCCCTAGCGCGCGCTGCGGCGGAGAGGCGCCACCGAGG 13320
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QY 220 GCGGCGCCGANGCAGGCGCAAGGAAC 244
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Db 13319 AGGAGGACGAGCGACGCGGGAC 13295
|||||

RESULT 14
US-09-724-676-45770/c
; Sequence 45770, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45770
; LENGTH: 1824
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1515)..(1516)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1522)..(1522)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1525)..(1525)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1528)..(1528)
; OTHER INFORMATION: n is a,c,g, or t
; US-09-724-676-45770
Query Match 11.4%; Score 35.8; DB 5; Length 1824;
Best Local Similarity 47.3%; Pred. No. 6.9;
Matches 97; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 104 CAGGTGGCTTCTGCACGCGCCCTATATAGCTGCTCCGGGATGCAGAGCCACCCAGCC 163
|||||
Db 1634 CAGGAGAGCCCCCTCACCCGGGTCTGAGGTGGCACCAGGAGGGGTGGGGCGCGCC 1575
|||||
QY 164 CCACCCCTGCGGGCCCCCTCGGTGCGCCCTTGCAGAGATGACGCTTCATCCGGAGGGGG 223
|||||
Db 1574 AGCACCAGCGGCTCTGCTCAGCCCCCTCTGCAGGAGGAGCGAGNCCNGNAAAGNN 1515
|||||
QY 224 GCCCANGCAAGGCAAGGAAGTGGGGCTGCGGCGAGTGGCCCTGGCTTCGAAGATACG 283
|||||
Db 1514 CCCCCCAAAAGGACGAGCAAGCCCTGGGCGGTGGGAGCTCACCACCGAGGAATCGCG 1455
|||||
QY 284 AAGTGACAACGACACGCGGGGACC 308
|||||
Db 1454 ATGAAGCTTCCAGAGCTTGGTGACC 1430
|||||

RESULT 15
US-09-724-676A-45770/c
; Sequence 45770, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 22:19:04 ; Search time 619.645 Seconds  
(without alignments)  
12740.746 Million cell updates/sec

Title: US-09-750-240-1  
Perfect score: 314  
Sequence: 1 atgtcatggttagtgccct.....acaccggcggaaccgctgaa 314

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2\_6/ptodata/1/pna/US06\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pna/US07\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pna/US08\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/pna/US082\_COMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pna/US083\_COMB.seq.\*
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- 9: /cgn2\_6/ptodata/1/pna/US085\_COMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pna/US086\_COMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pna/US087\_COMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pna/US088\_COMB.seq.\*
- 13: /cgn2\_6/ptodata/1/pna/US089\_COMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pna/US090\_COMB.seq.\*
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- 18: /cgn2\_6/ptodata/1/pna/US094\_COMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pna/US095A\_COMB.seq.\*
- 20: /cgn2\_6/ptodata/1/pna/US095B\_COMB.seq.\*
- 21: /cgn2\_6/ptodata/1/pna/US095C\_COMB.seq.\*
- 22: /cgn2\_6/ptodata/1/pna/US095D\_COMB.seq.\*
- 23: /cgn2\_6/ptodata/1/pna/US096A\_COMB.seq.\*
- 24: /cgn2\_6/ptodata/1/pna/US096B\_COMB.seq.\*
- 25: /cgn2\_6/ptodata/1/pna/US096C\_COMB.seq.\*
- 26: /cgn2\_6/ptodata/1/pna/US096D\_COMB.seq.\*
- 27: /cgn2\_6/ptodata/1/pna/US096E\_COMB.seq.\*
- 28: /cgn2\_6/ptodata/1/pna/US097A\_COMB.seq.\*
- 29: /cgn2\_6/ptodata/1/pna/US097B\_COMB.seq.\*
- 30: /cgn2\_6/ptodata/1/pna/US097C\_COMB.seq.\*
- 31: /cgn2\_6/ptodata/1/pna/US098A\_COMB.seq.\*
- 32: /cgn2\_6/ptodata/1/pna/US098B\_COMB.seq.\*
- 33: /cgn2\_6/ptodata/1/pna/US098C\_COMB.seq.\*
- 34: /cgn2\_6/ptodata/1/pna/US099A\_COMB.seq.\*
- 35: /cgn2\_6/ptodata/1/pna/US099B\_COMB.seq.\*
- 36: /cgn2\_6/ptodata/1/pna/US099C\_COMB.seq.\*
- 37: /cgn2\_6/ptodata/1/pna/US099D\_COMB.seq.\*
- 38: /cgn2\_6/ptodata/1/pna/US100A\_COMB.seq.\*
- 39: /cgn2\_6/ptodata/1/pna/US100B\_COMB.seq.\*
- 40: /cgn2\_6/ptodata/1/pna/US101A\_COMB.seq.\*
- 41: /cgn2\_6/ptodata/1/pna/US101B\_COMB.seq.\*
- 42: /cgn2\_6/ptodata/1/pna/US102A\_COMB.seq.\*
- 43: /cgn2\_6/ptodata/1/pna/US102B\_COMB.seq.\*

- 44: /cgn2\_6/ptodata/1/pna/US6000\_COMB.seq.\*
- 45: /cgn2\_6/ptodata/1/pna/US6001\_COMB.seq.\*
- 46: /cgn2\_6/ptodata/1/pna/US6002\_COMB.seq.\*
- 47: /cgn2\_6/ptodata/1/pna/US6003\_COMB.seq.\*
- 48: /cgn2\_6/ptodata/1/pna/US6004\_COMB.seq.\*
- 49: /cgn2\_6/ptodata/1/pna/US6005\_COMB.seq.\*
- 50: /cgn2\_6/ptodata/1/pna/US6006\_COMB.seq.\*
- 51: /cgn2\_6/ptodata/1/pna/US6007\_COMB.seq.\*
- 52: /cgn2\_6/ptodata/1/pna/US6008\_COMB.seq.\*
- 53: /cgn2\_6/ptodata/1/pna/US6009\_COMB.seq.\*
- 54: /cgn2\_6/ptodata/1/pna/US6010\_COMB.seq.\*
- 55: /cgn2\_6/ptodata/1/pna/US6011\_COMB.seq.\*
- 56: /cgn2\_6/ptodata/1/pna/US6012\_COMB.seq.\*
- 57: /cgn2\_6/ptodata/1/pna/US6013\_COMB.seq.\*
- 58: /cgn2\_6/ptodata/1/pna/US6014\_COMB.seq.\*
- 59: /cgn2\_6/ptodata/1/pna/US6015\_COMB.seq.\*
- 60: /cgn2\_6/ptodata/1/pna/US6016\_COMB.seq.\*
- 61: /cgn2\_6/ptodata/1/pna/US6017\_COMB.seq.\*
- 62: /cgn2\_6/ptodata/1/pna/US6018\_COMB.seq.\*
- 63: /cgn2\_6/ptodata/1/pna/US6019\_COMB.seq.\*
- 64: /cgn2\_6/ptodata/1/pna/US6020\_COMB.seq.\*
- 65: /cgn2\_6/ptodata/1/pna/US6021\_COMB.seq.\*
- 66: /cgn2\_6/ptodata/1/pna/US6022\_COMB.seq.\*
- 67: /cgn2\_6/ptodata/1/pna/US6023\_COMB.seq.\*
- 68: /cgn2\_6/ptodata/1/pna/US6024\_COMB.seq.\*
- 69: /cgn2\_6/ptodata/1/pna/US6025\_COMB.seq.\*
- 70: /cgn2\_6/ptodata/1/pna/US6026\_COMB.seq.\*
- 71: /cgn2\_6/ptodata/1/pna/US6027\_COMB.seq.\*
- 72: /cgn2\_6/ptodata/1/pna/US6028\_COMB.seq.\*
- 73: /cgn2\_6/ptodata/1/pna/US6029\_COMB.seq.\*
- 74: /cgn2\_6/ptodata/1/pna/US6030\_COMB.seq.\*
- 75: /cgn2\_6/ptodata/1/pna/US6031\_COMB.seq.\*
- 76: /cgn2\_6/ptodata/1/pna/US6032\_COMB.seq.\*
- 77: /cgn2\_6/ptodata/1/pna/US6033\_COMB.seq.\*
- 78: /cgn2\_6/ptodata/1/pna/US6034\_COMB.seq.\*
- 79: /cgn2\_6/ptodata/1/pna/US6035\_COMB.seq.\*
- 80: /cgn2\_6/ptodata/1/pna/US6036\_COMB.seq.\*
- 81: /cgn2\_6/ptodata/1/pna/US6037\_COMB.seq.\*
- 82: /cgn2\_6/ptodata/1/pna/US6038\_COMB.seq.\*
- 83: /cgn2\_6/ptodata/1/pna/US6039\_COMB.seq.\*
- 84: /cgn2\_6/ptodata/1/pna/US6040\_COMB.seq.\*
- 85: /cgn2\_6/ptodata/1/pna/US6041\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	313	99.7	314	18	US-09-472-667-1	Sequence 1, Appli
2	313	99.7	314	29	US-09-750-240-1	Sequence 1, Appli
3	295.2	94.0	3549	18	US-09-472-667-5	Sequence 5, Appli
4	295.2	94.0	3549	29	US-09-750-240-5	Sequence 5, Appli
5	295.2	94.0	3552	18	US-09-472-667-10	Sequence 10, Appli
6	295.2	94.0	3552	29	US-09-750-240-10	Sequence 10, Appli
7	295.2	94.0	3582	29	US-09-750-240-12	Sequence 12, Appli
8	295.2	94.0	4942	42	US-10-201-000-1	Sequence 1, Appli
9	263.2	83.8	18618	68	US-60-245-228-129	Sequence 129, App
c 10	263.2	83.8	36346	68	US-60-248-592-55	Sequence 55, Appl
c 11	199.2	63.4	5826	80	US-60-360-207-5921	Sequence 5921, Ap
12	198.2	63.1	4131	9	US-08-538-815-11	Sequence 11, Appl
13	163.4	52.0	358	18	US-09-482-933-165	Sequence 165, App
14	163.4	52.0	358	35	US-09-933-797-165	Sequence 165, App
15	148.6	47.3	562	17	US-09-397-022-2574	Sequence 2574, Ap
16	148.6	47.3	562	24	US-09-637-890-6437	Sequence 6437, Ap
17	148.6	47.3	562	25	US-09-649-164-5083	Sequence 5083, Ap
18	148.6	47.3	562	31	US-09-808-383-2574	Sequence 2574, Ap
19	94.6	30.1	220	29	US-09-728-445-487	Sequence 487, App
20	94.6	30.1	220	29	US-09-750-456-487	Sequence 487, App
21	80	25.5	3706	68	US-60-248-592-183	Sequence 183, App

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22 77.2 24.6 3356 68 US-60-245-228-549
23 46.8 14.9 768 25 US-09-649-161-9717
24 46.8 14.9 768 25 US-09-652-127-9508
25 46.8 14.9 768 25 US-09-652-128-9469
26 46.8 14.9 768 28 US-09-700-000-5264
27 46.8 14.9 773 23 US-09-606-880-4337
28 40.6 12.9 300 14 US-09-070-695A-1695
29 40.6 12.9 300 20 US-09-535-897-15171
30 39.4 12.5 500 57 US-60-135-952-3861
31 39.4 12.5 513 20 US-09-535-897-2265
32 39.2 12.5 1587 28 US-09-708-427-57395
33 39.2 12.5 2374 24 US-09-620-392-53278
34 39.2 12.5 16861 24 US-09-620-392-5927
35 39.2 12.5 50171 28 US-09-702-134-5845
36 39.2 12.5 50171 31 US-09-815-264-59552
37 39 12.4 519 28 US-09-716-953-666
38 39 12.4 632 24 US-09-634-306B-20235
39 39 12.4 632 24 US-09-634-306B-20236
40 39 12.4 632 38 US-10-027-632-20235
41 39 12.4 632 38 US-10-027-632-20236
42 39 12.4 9104 24 US-09-620-392-43222
43 39 12.4 9104 28 US-09-702-134-10239
44 39 12.4 9104 31 US-09-815-264-81305
45 39 12.4 21334 24 US-09-620-392-48146
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## ALIGNMENTS

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RESULT 1
US-09-472-667-1
; Sequence 1, Application US/09472667
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. Kirk
; APPLICANT: Insel, Paul A.
; APPLICANT: Ping, Felipe
; APPLICANT: Post, Steven R.
; APPLICANT: Gao, Meihua
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056722
; CURRENT APPLICATION NUMBER: US/09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: PCT/US99/02702
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 09/021,773
; PRIOR FILING DATE: 1998-02-11
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: PCT/US97/15610
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/058,209
; PRIOR FILING DATE: 1996-09-05
; PRIOR APPLICATION NUMBER: PCT/US96/02631
; PRIOR FILING DATE: 1996-02-27
; PRIOR APPLICATION NUMBER: US 08/396,207
; PRIOR FILING DATE: 1995-02-28
; PRIOR APPLICATION NUMBER: US 08/485,472
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 314
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
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Sequence 549, App
Sequence 9717, Ap
Sequence 9508, Ap
Sequence 9469, Ap
Sequence 5264, Ap
Sequence 4337, Ap
Sequence 1695, Ap
Sequence 15171, A
Sequence 3861, Ap
Sequence 2265, Ap
Sequence 57395, A
Sequence 53278, A
Sequence 5927, Ap
Sequence 5845, A
Sequence 59552, A
Sequence 666, App
Sequence 20235, A
Sequence 20236, A
Sequence 20235, A
Sequence 20236, A
Sequence 43222, A
Sequence 10239, A
Sequence 81305, A
Sequence 48146, A
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; LOCATION: (1)....(314)
; OTHER INFORMATION: n = A,T,C or G
US-09-472-667-1
Query Match 99.7%; Score 313; DB 18; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGTCATGTTTAGTGGCCCTCTGTTCCCTAAAGTGGATGAACGGAAACAGCCTGGGT 60
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Db 1 ATGTCATGTTTAGTGGCCCTCTGTTCCCTAAAGTGGATGAACGGAAACAGCCTGGGT 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 61 GAACGCAATGGCAGCAAGCGTTTCGGGGCCCGCTGGGCACATCGGGCAGGTGCTTTCACG 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 GAACGCAATGGCAGCAAGCGTTTCGGGGCCCGCTGGGCACATCGGGCAGGTGCTTTCACG 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 121 CCCCGCTATATGCTGCTCCGGGATGAGAGCCACCCACCCCTCGGGGCCCC 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 CCCCGCTATATGCTGCTCCGGGATGAGAGCCACCCACCCCTCGGGGCCCC 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 181 CTTCTGGTGGCCCTGGCAGGATGACGCTTTCATCCGGAGGGGGCCCGCANGAAGGCAAG 240
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Db 181 CTTCTGGTGGCCCTGGCAGGATGACGCTTTCATCCGGAGGGGGCCCGCANGAAGGCAAG 240
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Qy 241 GAACGGGGCTCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACACGACCG 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 241 GAACGGGGCTCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACACGACCG 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 301 GCGGGACCGCTGAA 314
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 301 GCGGGACCGCTGAA 314
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RESULT 2
US-09-750-240-1
; Sequence 1, Application US/09750240
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 314
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)....(314)
; OTHER INFORMATION: n = A,T,C or G
US-09-750-240-1
Query Match 99.7%; Score 313; DB 29; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 ATGTCATGTTTACTGGCTCCTGCTAAAGTGATGAACGAAACAGCCTGGGT 60
Db 1 ATGTCATGTTTACTGGCTCCTGCTAAAGTGATGAACGAAACAGCCTGGGT 60

Qy 61 GAACGCAATGGGAGAGCGTTCCGGCGCGCTGGCACTCGGGCAGTGGCTTCTGCACG 120
Db 61 GAACGCAATGGGAGAGCGTTCCGGCGCGCTGGCACTCGGGCAGTGGCTTCTGCACG 120

Qy 121 CCCGCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCCTGCGGGCCCC 180
Db 121 CCCGCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCCTGCGGGCCCC 180

Qy 181 CCTCGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGCGGCCCCANGCAAGGCAAG 240
Db 181 CCTCGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGCGGCCCCANGCAAGGCAAG 240

Qy 241 GAACTGGGGCTGGGGCAGTGGCCCTGCGCTTCCAAAGATACCGAAGTGACAAACACACCG 300
Db 241 GAACTGGGGCTGGGGCAGTGGCCCTGCGCTTCCAAAGATACCGAAGTGACAAACACACCG 300

Qy 301 GCGGACCGCTGAA 314
Db 301 GCGGACCGCTGAA 314
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## RESULT 3

```
US-09-472-667-5
; Sequence 5, Application US/09472667
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. Kirk
; APPLICANT: Insel, Paul A.
; APPLICANT: Ping, Peipei
; APPLICANT: Post, Steven R.
; APPLICANT: Gao, Meihua
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056722
; CURRENT APPLICATION NUMBER: US/09/472,667
; CURRENT FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: PCT/US99/02702
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 09/021,773
; PRIOR FILING DATE: 1998-02-11
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: PCT/US97/15610
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/058,209
; PRIOR FILING DATE: 1996-09-05
; PRIOR APPLICATION NUMBER: PCT/US96/02631
; PRIOR FILING DATE: 1996-02-27
; PRIOR APPLICATION NUMBER: US 08/396,207
; PRIOR FILING DATE: 1995-02-28
; PRIOR APPLICATION NUMBER: US 08/485,472
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-472-667-5

Query Match 94.0%; Score 295.2; DB 18; Length 3549;
Best Local Similarity 97.1%; Pred. No. 1.4e-56;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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Qy 1 ATGTCATGTTTACTGGCTCCTGCTAAAGTGATGAACGAAACAGCCTGGGT 60
Db 1 ATGTCATGTTTACTGGCTCCTGCTAAAGTGATGAACGAAACAGCCTGGGT 60

Qy 61 GAACGCAATGGGAGAGCGTTCCGGCGCGCTGGCACTCGGGCAGTGGCTTCTGCACG 120
Db 61 GAACGCAATGGGAGAGCGTTCCGGCGCGCTGGCACTCGGGCAGTGGCTTCTGCACG 120

Qy 121 CCCGCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCCTGCGGGCCCC 180
Db 121 CCCGCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCCTGCGGGCCCC 180

Qy 181 CCTCGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGCGGCCCCANGCAAGGCAAG 240
Db 181 CCTCGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGCGGCCCCANGCAAGGCAAG 240

Qy 241 GAACTGGGGCTGGGGCAGTGGCCCTGCGCTTCCAAAGATACCGAAGTGACAAACACACCG 300
Db 241 GAACTGGGGCTGGGGCAGTGGCCCTGCGCTTCCAAAGATACCGAAGTGACAAACACACCG 300

Qy 301 GCGGACCG 309
Db 301 GCGGACCG 309
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## RESULT 4

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US-09-750-240-5
; Sequence 5, Application US/09750240
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-5

Query Match 94.0%; Score 295.2; DB 29; Length 3549;
Best Local Similarity 97.1%; Pred. No. 1.4e-56;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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```
Qy 1 ATGTCATGTTTACTGGCTCCTGCTAAAGTGATGAACGAAACAGCCTGGGT 60
Db 1 ATGTCATGTTTACTGGCTCCTGCTAAAGTGATGAACGAAACAGCCTGGGT 60

Qy 61 GAACGCAATGGGAGAGCGTTCCGGCGCGCTGGCACTCGGGCAGTGGCTTCTGCACG 120
Db 61 GAACGCAATGGGAGAGCGTTCCGGCGCGCTGGCACTCGGGCAGTGGCTTCTGCACG 120

Qy 121 CCCGCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCCTGCGGGCCCC 180
Db 121 CCCGCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCCTGCGGGCCCC 180
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QY 181 CCTCGTGCCTGGCAGGATGACGCCTTCATCCCGAGGGGGGCCCCANGCAAGGCAAG 240
Db 181 CCTCGTGCCTGGCAGGATGACGCCTTCATCCCGAGGGGGGCCCCAGGCAAGGCAAG 240

QY 241 GAACCTGGGCTCGGCGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACACGACACG 300
Db 241 GAGCTGGGCTCGGCGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACACG 300

QY 301 GCGGGACCG 309
Db 301 GCGGGACG 309

RESULT 5
US-09-472-667-10
; Sequence 10, Application US/09472667
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. Kirk
; APPLICANT: Insel, Paul A.
; APPLICANT: Ping, Peipei
; APPLICANT: Post, Steven R.
; APPLICANT: Gao, Melhua
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056722
; CURRENT APPLICATION NUMBER: US/09/472,667
; CURRENT FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: PCT/US99/02702
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 09/021,773
; PRIOR FILING DATE: 1998-02-11
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: PCT/US97/15610
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/058,209
; PRIOR FILING DATE: 1996-09-05
; PRIOR APPLICATION NUMBER: PCT/US96/02631
; PRIOR FILING DATE: 1996-02-27
; PRIOR APPLICATION NUMBER: US 08/396,207
; PRIOR FILING DATE: 1995-02-28
; PRIOR APPLICATION NUMBER: US 08/485,472
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 3552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-472-667-10

Query Match 94.0%; Score 295.2; DB 18; Length 3552;
Best Local Similarity 97.1%; Pred. No. 1.4e-56;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGAATGAACGGAAAAACAGCCTGGGGT 60
Db 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGAATGAACGGAAAAACAGCCTGGGGT 60

QY 61 GAACGCAATGGCAGAAAGCGTTTCGGGGCCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120
Db 61 GAACGCAATGGCAGAAAGCGTTTCGGGGCCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120

QY 121 CCCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCGCCCTCGGGGCCCC 180
Db 121 CCCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCGCCCTCGGGGCCCC 180

QY 181 CCTCGTGCCTGGCAGGATGACGCCTTCATCCGAGGGGGGCCCCANGCAAGGCAAG 240
Db 181 CCTCGTGCCTGGCAGGATGACGCCTTCATCCGAGGGGGGCCCCAGGCAAGGCAAG 240

QY 241 GAACCTGGGCTCGGCGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACACGACACG 300
Db 241 GAACGCAATGGCAGAAAGCGTTTCGGGGCCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120

QY 121 CCCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCGCCCTCGGGGCCCC 180
Db 121 CCCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCGCCCTCGGGGCCCC 180
```

```
QY 181 CCTCGTGCCTGGCAGGATGACGCCTTCATCCCGAGGGGGGCCCCANGCAAGGCAAG 240
Db 181 CCTCGTGCCTGGCAGGATGACGCCTTCATCCCGAGGGGGGCCCCAGGCAAGGCAAG 240

QY 241 GAACCTGGGCTCGGCGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACACGACACG 300
Db 241 GAGCTGGGCTCGGCGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACACG 300

QY 301 GCGGGACCG 309
Db 301 GCGGGACG 309

RESULT 6
US-09-750-240-10
; Sequence 10, Application US/09750240
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 3552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-10

Query Match 94.0%; Score 295.2; DB 29; Length 3552;
Best Local Similarity 97.1%; Pred. No. 1.4e-56;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGAATGAACGGAAAAACAGCCTGGGGT 60
Db 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGAATGAACGGAAAAACAGCCTGGGGT 60

QY 61 GAACGCAATGGCAGAAAGCGTTTCGGGGCCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120
Db 61 GAACGCAATGGCAGAAAGCGTTTCGGGGCCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120

QY 121 CCCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCGCCCTCGGGGCCCC 180
Db 121 CCCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCGCCCTCGGGGCCCC 180

QY 181 CCTCGTGCCTGGCAGGATGACGCCTTCATCCGAGGGGGGCCCCANGCAAGGCAAG 240
Db 181 CCTCGTGCCTGGCAGGATGACGCCTTCATCCGAGGGGGGCCCCAGGCAAGGCAAG 240

QY 241 GAACCTGGGCTCGGCGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACACGACACG 300
Db 241 GAGCTGGGCTCGGCGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACACG 300

QY 301 GCGGGACCG 309
Db 301 GCGGGACG 309
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RESULT 7  
US-09-750-240-12  
; Sequence 12, Application US/09750240  
; GENERAL INFORMATION:  
; APPLICANT: Hammon, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
; TITLE OF INVENTION: FAILURE  
; FILE REFERENCE: 220002056723  
; CURRENT APPLICATION NUMBER: US/09/750,240  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/472,667  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 3582  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Modified AC-VI  
US-09-750-240-12

Query Match 94.0%; Score 295.2; DB 29; Length 3582;  
Best Local Similarity 97.1%; Pred. No. 1.4e-56;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 ATGTCATGGTTTACTGGCTCTCTGCTCCTAAAGTGATGAACGAAACAGCCTGGGGT 60  
|||||  
Db 22 ATGTCATGGTTTACTGGCTCTCTGCTCCTAAAGTGATGAACGAAACAGCCTGGGGT 81  
QY 61 GAACGCAATGGGCGAGAGCGTTTCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120  
|||||  
Db 82 GAACGCAATGGGCGAGAGCGTTTCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 141  
QY 121 CCCGCTATATGAGCTGCCTCCGGGATGCAGACCCAGCCACCCCTGCGGGCCCC 180  
|||||  
Db 142 CCCGCTATATGAGCTGCCTCCGGGATGCAGACCCAGCCACCCCTGCGGGCCCC 201  
QY 181 CCTCGGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGCGGCCCAAGCAAGGCAAG 240  
|||||  
Db 202 CCTCGGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGCGGCCCAAGCAAGGCAAG 261  
QY 241 GAATGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTACACACACACCG 300  
|||||  
Db 262 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACACACACG 321  
QY 301 GCGGGACCG 309  
| || ||  
Db 322 GCGGGACCG 330

RESULT 8  
US-10-201-000-1  
; Sequence 1, Application US/10201000  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, James E.  
; APPLICANT: COR Therapeutics, Inc.  
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLIL  
; TITLE OF INVENTION: CYCLASE  
; FILE REFERENCE: 44481-5028-01-US

; CURRENT APPLICATION NUMBER: US/10/201,000  
; CURRENT FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: US/09/474,076  
; PRIOR FILING DATE: 1999-12-12  
; PRIOR APPLICATION NUMBER: PCT/US98/13694  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/070,904  
; PRIOR FILING DATE: 1997-07-01  
; PRIOR APPLICATION NUMBER: 08/886,550  
; PRIOR FILING DATE: 1997-07-01  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4942  
; TYPE: DNA  
; ORGANISM: human type VI adenylyl cyclase  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (145)..(3648)  
US-10-201-000-1  
Query Match 94.0%; Score 295.2; DB 42; Length 4942;  
Best Local Similarity 97.1%; Pred. No. 1.4e-56;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 ATGTCATGGTTTACTGGCTCTCTGCTCCTAAAGTGATGAACGAAACAGCCTGGGGT 60  
|||||  
Db 145 ATGTCATGGTTTACTGGCTCTCTGCTCCTAAAGTGATGAACGAAACAGCCTGGGGT 204  
QY 61 GAACGCAATGGGCGAGAGCGTTTCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120  
|||||  
Db 205 GAACGCAATGGGCGAGAGCGTTTCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 264  
QY 121 CCCGCTATATGAGCTGCCTCCGGGATGCAGACCCAGCCACCCCTGCGGGCCCC 180  
|||||  
Db 265 CCCGCTATATGAGCTGCCTCCGGGATGCAGACCCAGCCACCCCTGCGGGCCCC 324  
QY 181 CCTCGGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGCGGCCCAAGCAAGGCAAG 240  
|||||  
Db 325 CCTCGGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGCGGCCCAAGCAAGGCAAG 384  
QY 241 GAATGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTACACACACACCG 300  
|||||  
Db 385 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACACACGCG 444  
QY 301 GCGGGACCG 309  
| || ||  
Db 445 GCGGGACCG 453

RESULT 9  
US-60-245-228-129/c  
; Sequence 129, Application US/60245228  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL000878  
; CURRENT APPLICATION NUMBER: US/60/245,228  
; CURRENT FILING DATE: 2000-11-03  
; NUMBER OF SEQ ID NOS: 630  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 129  
; LENGTH: 18618  
; TYPE: DNA  
; ORGANISM: HUMAN  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(18618)  
; OTHER INFORMATION: n = A,T,C or G  
US-60-245-228-129

Query Match 83.8%; Score 263.2; DB 68; Length 18618;  
Best Local Similarity 94.5%; Pred. No. 2.4e-49;  
Matches 294; Conservative 0; Mismatches 14; Indels 3; Gaps 2;

QY 1 ATGTCATGTTTGTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGT 60  
|||||  
Db 16838 ATGTCATGTTTGTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGT 16779  
|||||

QY 61 GAACCAATGGCAGAAAGGTTTCGGCGCGCTGGCACTCGGCGAGGTCTTCTGCACG 120  
|||||  
Db 16778 GAACCAATGGCAGAAAGGTTTCGGCGCGCTGGCACTCGGCGAGGTCTTCTGCACG 16719  
|||||

QY 121 CCCGCTATATGAGTGGCTCCGGATGACAGCCACCCAGCCCTCGGGCCCC 180  
Db 16718 CCCGCTATATGAGTGGCTCCGGATGACAGCCACCCAGCCCTCGG- GGCCCC 16660  
|||||

QY 181 CCTCGTGGCCCTGGCAGATGACGCTT- -CATCGGAGGGGGCCCGCCANGCAAGGGCA 238  
|||||  
Db 16659 CCTCGTGGCCCTGGCAGATGACGCTTTCATCGGAGGGGGCCCGCCANGCAAGGGCA 16600  
|||||

QY 239 AGGAACTGGGCTCGGCGAGTGGCCCTGGGCTTCAAGATACCGAAGTGACAACGACAC 298  
|||||  
Db 16599 AGGAACTGGGCTCGGCGAGTGGCCCTGGGCTTCAAGATACCGAAGTGACAACGACAC 16540  
|||||

QY 299 CGGCGGGACCG 309  
||| || ||  
Db 16539 CGGCGGGACG 16529

RESULT 10  
US-60-248-592-55/c  
; Sequence 55, Application US/60248592  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES  
; FILE REFERENCE: CL000961  
; CURRENT APPLICATION NUMBER: US/60/248,592  
; CURRENT FILING DATE: 2000-11-16  
; NUMBER OF SEQ ID NOS: 192  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 55  
; LENGTH: 36346  
; TYPE: DNA  
; ORGANISM: HUMAN  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(36346)  
; OTHER INFORMATION: n = A,T,C or G  
US-60-248-592-55

Query Match 83.8%; Score 263.2; DB 68; Length 36346;  
Best Local Similarity 94.5%; Pred. No. 2.4e-49;  
Matches 294; Conservative 0; Mismatches 14; Indels 3; Gaps 2;

QY 1 ATGTCATGTTTGTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGT 60  
|||||  
Db 16838 ATGTCATGTTTGTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGT 16779  
|||||

QY 61 GAACCAATGGCAGAAAGGTTTCGGCGCGCTGGCACTCGGCGAGGTCTTCTGCACG 120  
|||||  
Db 16778 GAACCAATGGCAGAAAGGTTTCGGCGCGCTGGCACTCGGCGAGGTCTTCTGCACG 16719  
|||||

QY 121 CCCGCTATATGAGTGGCTCCGGATGACAGCCACCCAGCCCTCGGGCCCC 180  
Db 16718 CCCGCTATATGAGTGGCTCCGGATGACAGCCACCCAGCCCTCGG- GGCCCC 16660  
|||||

QY 181 CCTCGTGGCCCTGGCAGATGACGCTT- -CATCGGAGGGGGCCCGCCANGCAAGGGCA 238  
|||||  
Db 16659 CCTCGTGGCCCTGGCAGATGACGCTTTCATCGGAGGGGGCCCGCCANGCAAGGGCA 16600  
|||||

QY 239 AGGAACTGGGCTCGGCGAGTGGCCCTGGGCTTCAAGATACCGAAGTGACAACGACAC 298  
|||||

|||||  
Db 16599 AGGAGTGGGGTGGCGGAGTGGCCCTTCCAGATACCGAGGTGACAACGACAG 16540  
|||||

QY 299 CGGCGGGACCG 309  
||| || ||  
Db 16539 CGGCGGGACG 16529

RESULT 11  
US-60-360-207-5921  
; Sequence 5921, Application US/60360207  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF  
; FILE REFERENCE: CL001321  
; CURRENT APPLICATION NUMBER: US/60/360,207  
; CURRENT FILING DATE: 2002-03-01  
; NUMBER OF SEQ ID NOS: 47235  
; SEQ ID NO 5921  
; LENGTH: 5826  
; TYPE: DNA  
; ORGANISM: HUMAN  
; OTHER INFORMATION:  
US-60-360-207-5921

Query Match 63.4%; Score 199.2; DB 80; Length 5826;  
Best Local Similarity 82.3%; Pred. No. 6e-35;  
Matches 241; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

QY 1 ATGTCATGTTTGTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGT 60  
|||||  
Db 96 ATGTCATGTTTGTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGG 155  
|||||

QY 61 GAACCAATGGCAGAAAGGTTTCGGCGCGCTGGCACTCGGCGAGGTCTTCTGCACG 120  
|||||

Db 156 GAACCAATGGCAGAAAGGTTTCGGCGCGCTGGCACTCGGCGAGGTCTTCTGCACG 212  
|||||

QY 121 CCCGCTATATGAGTGGCTCCGGATGACAGCCACCCAGCCCTCGGGCCCC 180  
|||||

Db 213 CCTCGTACATGAGTGGCTCAAGATGGGAGCCACCCAGCCCTCTGCGAGCTCAC 272  
|||||

QY 181 CCTCGTGGCCCTGGCAGATGACGCTTTCATCGGAGGGGGCCCGCCANGCAAGGCAAG 240  
|||||

Db 273 ACTCGTGGCCCTGGCAGATGAAGCTTTCATCAGGAGGGGGGGGGGGGAGGGGTGTG 332  
|||||

QY 241 GAACCTGGGGCTCGGCGAGTGGCCCTTCCAGATACCGAAGTGACAAC 293  
|||||

Db 333 GAGCTGGGGCTCGGCTAGTGGCTTGGGTTTGACGACACTGAGGTGACCAC 385  
|||||

RESULT 12  
US-08-538-815-11  
; Sequence 11, Application US/08538815  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Wei-Jen  
; APPLICANT: Gilman, Alfred G.  
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYL  
; TITLE OF INVENTION: CYCLASE AND USES THEREFOR  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/538,815  
; FILING DATE: Concurrently Herewith

Query Match	52.0%	Score 163.4;	DB 18;	Length 358;
Best Local Similarity	83.1%;	Pred. No. 6.5e-27;		
Matches 196;	Conservative	2;	Mismatches 35;	Indels 3;
Gaps 1;				

```

RESULT 15
US-09-397-022-2574
: Sequence 2574, Application US/09397022
: GENERAL INFORMATION:
: APPLICANT: Gearing, David P.
: APPLICANT: Holtzman, Douglas A.
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
: TITLE OF INVENTION: HUMAN FETAL SKIN LIBRARY
: FILE REFERENCE: MLN98-46PM
: CURRENT APPLICATION NUMBER: US/09/397,022

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; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,465
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/106,443
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/107,257
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/126,906
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 60/132,099
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5775
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2574
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(562)
; OTHER INFORMATION: n = A,T,C or G
US-09-397-022-2574
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Query Match      47.3%; Score 148.6; DB 17; Length 562;
Best Local Similarity 84.6%; Pred. No. 1.4e-23;
Matches 187; Conservative 0; Mismatches 30; Indels 4; Gaps 2;

QY   8  GGTTCAGTGGCTCCTGGTCCCTAAAGTGATGAACGGAAACAGCGCTGGGGTGAACGCA 67
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  335 GTTTCAGTGGCTCCTGGTCCCTAAAGTGATGAACGGAAACAGCGCTGGGGTGAACGCA 394

QY   68  ATGGGCAGAACGCTTCGGCGCG--CCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCG 125
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  395 ATGGGCAGAACGCTTCGGCGCG--CCGTGGCACTCGGGCGGTGGCTTCTGCACGCCCG 454

QY   126 CTATATGAGCTGCTCCGGGATGCGAGAGCCACCCAGCCACCCCTGGGGCCCCCTCG 185
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  455 CTATATGAAGTCTCCGGGATGCAAAACACCCANCCC--ACCCCTGGGGCCCCCTCG 512

QY   186 GTGCCCTGGCAGGATGAGCGCTTCATCGGAGGGGGGCC 226
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB  513 GTGCCCTGGCAGGATGAGCGCTTCATCGGAGGGGGGCC 553
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Search completed: February 23, 2003, 07:31:19  
Job time : 635.645 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 23, 2003, 02:25:49 ; Search time 16.4885 Seconds  
(without alignments)  
10695.650 Million cell updates/sec

Title: US-09-750-240-1

Perfect score: 314

Sequence: 1 atgtcatggttagtgccct.....acaccggcgagcgcgtgaa 314

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 442118 seqs, 280819700 residues

Total number of hits satisfying chosen parameters: 884236

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	313	99.7	314	10	US-09-750-240-1
2	295.2	94.0	3549	10	US-09-750-240-5
3	295.2	94.0	3552	10	US-09-750-240-10
4	295.2	94.0	3582	10	US-09-750-240-12
5	295.2	94.0	4942	9	US-10-201-000-1
6	163.4	52.0	358	9	US-09-933-797-165
7	94.6	30.1	220	10	US-09-728-445-487
8	38.6	12.3	6503	10	US-09-935-541-12
9	37.2	11.8	1438	9	US-10-081-280-5
10	37.2	11.8	1438	9	US-10-112-793-5
11	37.2	11.8	1438	9	US-10-112-193-5
12	37.2	11.8	1438	10	US-09-884-733-5
13	37.2	11.8	1438	10	US-09-993-234-5
14	36.6	11.7	3243	9	US-09-945-901-44
15	36.6	11.7	3243	9	US-10-007-747-44
16	36.6	11.7	3243	9	US-10-038-937-44
17	36.6	11.7	3698	9	US-09-945-901-43
18	36.6	11.7	3698	9	US-10-007-747-43
19	36.6	11.7	3698	9	US-10-038-937-43

c 20	36.6	11.7	4002	9	US-09-945-901-53	Sequence 53, Appl
c 21	36.6	11.7	4002	9	US-10-007-747-53	Sequence 53, Appl
c 22	36.6	11.7	4002	9	US-10-038-937-53	Sequence 53, Appl
c 23	36.6	11.7	4017	9	US-09-945-901-49	Sequence 49, Appl
c 24	36.6	11.7	4017	9	US-10-007-747-49	Sequence 49, Appl
c 25	36.6	11.7	4017	9	US-10-038-937-49	Sequence 49, Appl
c 26	36.6	11.7	4053	9	US-09-945-901-47	Sequence 47, Appl
c 27	36.6	11.7	4053	9	US-10-007-747-47	Sequence 47, Appl
c 28	36.6	11.7	4053	9	US-10-038-937-47	Sequence 47, Appl
c 29	36.6	11.7	4068	9	US-09-945-901-5	Sequence 5, Appl
c 30	36.6	11.7	4068	9	US-10-007-747-5	Sequence 5, Appl
c 31	36.6	11.7	4068	9	US-10-038-937-5	Sequence 5, Appl
c 32	36.6	11.7	4077	9	US-09-945-901-51	Sequence 51, Appl
c 33	36.6	11.7	4077	9	US-10-007-747-51	Sequence 51, Appl
c 34	36.6	11.7	4077	9	US-10-038-937-51	Sequence 45, Appl
c 35	36.6	11.7	4092	9	US-09-945-901-45	Sequence 45, Appl
c 36	36.6	11.7	4092	9	US-10-007-747-45	Sequence 45, Appl
c 37	36.6	11.7	4092	9	US-10-038-937-45	Sequence 45, Appl
c 38	36.4	11.6	485	9	US-10-004-717-59	Sequence 59, Appl
c 40	36	11.5	22118	9	US-10-125-767-16	Sequence 16, Appl
c 41	36	11.5	22118	9	US-09-815-981-5	Sequence 5, Appl
c 42	36	11.5	22118	9	US-09-836-911A-16	Sequence 16, Appl
c 43	35.6	11.3	10797	10	US-09-764-847-1577	Sequence 1577, App
c 44	35.2	11.2	2883	9	US-10-174-590-157	Sequence 157, App
c 45	35.2	11.2	2883	9	US-10-176-750-157	Sequence 157, App

## ALIGNMENTS

RESULT 1  
US-09-750-240-1  
Sequence 1, Application US/09750240  
Patent No. US20020103147A1  
GENERAL INFORMATION:  
APPLICANT: Hammon, H. K.  
APPLICANT: Insel, P. A.  
APPLICANT: Ping, P.  
APPLICANT: Post, S. R.  
APPLICANT: Gao, M.  
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART FAILURE  
FILE REFERENCE: 220002056723  
CURRENT APPLICATION NUMBER: US/09/750,240  
PRIOR FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: US 09/472,667  
PRIOR FILING DATE: 1999-12-27  
PRIOR APPLICATION NUMBER: US 09/008,097  
PRIOR FILING DATE: 1998-01-16  
PRIOR APPLICATION NUMBER: US 08/924,757  
PRIOR FILING DATE: 1997-09-05  
PRIOR APPLICATION NUMBER: US 60/048,933  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: US 08/708,661  
PRIOR FILING DATE: 1996-09-05  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 314  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(314)  
OTHER INFORMATION: n = A,T,C or G  
US-09-750-240-1

Query Match 99.7%; Score 313; DB 10; Length 314;  
Best Local Similarity 100.0%; Pred. No. 2.9e-73;  
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGTCATGTTTAGTGGCCCTGGTCCCTAAAGTGGATGACGGAACAGCCTGGGT 60

Db 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGGAAACAGCCCTGGGGT 60  
Qy 61 GAACCAATGGCAGAACGGTTCGGGGCGCGTGCACCTCGGGCAGGTGGCTTCTGCACG 120  
Db 61 GAACCAATGGCAGAACGGTTCGGGGCGCGTGCACCTCGGGCAGGTGGCTTCTGCACG 120  
Qy 121 CCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCCTGCGGGCCCC 180  
Db 121 CCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCCTGCGGGCCCC 180  
Qy 181 CCTCGTGCCCTGGCAGAGTACGCCCTTCATCCGAGGGGGCGCCANGCAAGGCAAG 240  
Db 181 CCTCGTGCCCTGGCAGAGTACGCCCTTCATCCGAGGGGGCGCCANGCAAGGCAAG 240  
Qy 241 GAACCTGGGGCTCGGGCAGTGCCTTCGAGATACCGAAGTACCAACGACACCG 300  
Db 241 GAACCTGGGGCTCGGGCAGTGCCTTCGAGATACCGAAGTACCAACGACACCG 300  
Qy 301 GCGGACCGCTGAA 314  
Db 301 GCGGACCGCTGAA 314

## RESULT 2

US-09-750-240-5  
; Sequence 5, Application US/09750240  
; Patent No. US20020103147A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammon, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
; FILE REFERENCE: 220002056723  
; CURRENT APPLICATION NUMBER: US/09750,240  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1996-09-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 3549  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-750-240-5

Query Match 94.0%; Score 295.2; DB 10; Length 3549;  
Best Local Similarity 97.1%; Pred. No. 2e-68;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGGAAACAGCCCTGGGGT 60  
Db 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGGAAACAGCCCTGGGGT 60  
Qy 61 GAACCAATGGCAGAACGGTTCGGGGCGCGTGCACCTCGGGCAGGTGGCTTCTGCACG 120  
Db 61 GAACCAATGGCAGAACGGTTCGGGGCGCGTGCACCTCGGGCAGGTGGCTTCTGCACG 120  
Qy 121 CCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCCTGCGGGCCCC 180  
Db 121 CCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCCTGCGGGCCCC 180

Qy 181 CCTCGTGCCCTGGCAGAGTACGCCCTTCATCCGAGGGGGCGCCANGCAAGGCAAG 240  
Db 181 CCTCGTGCCCTGGCAGAGTACGCCCTTCATCCGAGGGGGCGCCANGCAAGGCAAG 240  
Qy 241 GAACCTGGGGCTCGGGCAGTGCCTTCGAGATACCGAAGTACCAACGACACCG 300  
Db 241 GAGCTGGGGCTCGGGCAGTGCCTTCGAGATACCGAAGTACCAACGACACCG 300  
Qy 301 GCGGACCG 309  
Db 301 GCGGACCG 309

## RESULT 3

US-09-750-240-10  
; Sequence 10, Application US/09750240  
; Patent No. US20020103147A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammon, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
; FILE REFERENCE: 220002056723  
; CURRENT APPLICATION NUMBER: US/09750,240  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/472,667  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 3552  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-750-240-10

Query Match 94.0%; Score 295.2; DB 10; Length 3552;  
Best Local Similarity 97.1%; Pred. No. 2e-68; 9; Indels 0; Gaps 0;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGGAAACAGCCCTGGGGT 60  
Db 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGGAAACAGCCCTGGGGT 60  
Qy 61 GAACCAATGGCAGAACGGTTCGGGGCGCGTGCACCTCGGGCAGGTGGCTTCTGCACG 120  
Db 61 GAACCAATGGCAGAACGGTTCGGGGCGCGTGCACCTCGGGCAGGTGGCTTCTGCACG 120  
Qy 121 CCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCCTGCGGGCCCC 180  
Db 121 CCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCCTGCGGGCCCC 180  
Qy 181 CCTCGTGCCCTGGCAGAGTACGCCCTTCATCCGAGGGGGCGCCANGCAAGGCAAG 240  
Db 181 CCTCGTGCCCTGGCAGAGTACGCCCTTCATCCGAGGGGGCGCCANGCAAGGCAAG 240  
Qy 241 GAACCTGGGGCTCGGGCAGTGCCTTCGAGATACCGAAGTACCAACGACACCG 300  
Db 241 GAGCTGGGGCTCGGGCAGTGCCTTCGAGATACCGAAGTACCAACGACACCG 300  
Qy 301 GCGGACCG 309  
Db 301 GCGGACCG 309

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RESULT 4
US-09-750-240-12
; Sequence 12, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3582
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified AC-VI
US-09-750-240-12

Query Match          94.0%; Score 295.2; DB 10; Length 3582;
Best Local Similarity 97.1%; Pred. No. 2e-68;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ATGTCATGGTTTAGTGGCTCCTCGTCCCTAAAGTGGATGACGGAACAGCCTGGGGT 60
    |||||
Db 22 ATGTCATGGTTTAGTGGCTCCTCGTCCCTAAAGTGGATGACGGAACAGCCTGGGGT 81
    |||||

Qy 61 GAACGCAATGGCAGAGCGTTCCGGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
    |||||
Db 82 GAACGCAATGGCAGAGCGTTCCGGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 141
    |||||

Qy 121 CCCGCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCCTCGCGGGCCCC 180
    |||||
Db 142 CCCGCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCCTCGCGGGCCCC 201
    |||||

Qy 181 CCTCGTGCCCTGGCAGGATGACGCTTTCGAGGATGCGAGGAGGCGGCCCAAGGCAAG 240
    |||||
Db 181 CCTCGTGCCCTGGCAGGATGACGCTTTCGAGGATGCGAGGAGGCGGCCCAAGGCAAG 240
    |||||

Qy 202 CCTCGTGCCCTGGCAGGATGACGCTTTCGAGGATGCGAGGAGGCGGCCCAAGGCAAG 261
    |||||
Db 202 CCTCGTGCCCTGGCAGGATGACGCTTTCGAGGATGCGAGGAGGCGGCCCAAGGCAAG 261
    |||||

Qy 241 GAACCTGGGGCTGGCGGAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACACACGACCG 300
    |||||
Db 262 GAGCTGGGGCTGGCGGAGTGGCCCTGGGCTTCGAGGATGCGAGGAGGCGGCCCAAGGCAAG 321
    |||||

Qy 301 GCGGGACCG 309
    |||||
Db 322 GCGGGACCG 330
    |||||

RESULT 5
US-10-201-000-1
; Sequence 1, Application US/10201000
; Publication No. US20020187540A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
```

```
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/10/201,000
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US/09/474,076
; PRIOR FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-10-201-000-1

Query Match          94.0%; Score 295.2; DB 9; Length 4942;
Best Local Similarity 97.1%; Pred. No. 2.2e-68;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ATGTCATGGTTTAGTGGCTCCTCGTCCCTAAAGTGGATGACGGAACAGCCTGGGGT 60
    |||||
Db 145 ATGTCATGGTTTAGTGGCTCCTCGTCCCTAAAGTGGATGACGGAACAGCCTGGGGT 204
    |||||

Qy 61 GAACGCAATGGCAGAGCGTTCCGGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
    |||||
Db 205 GAACGCAATGGCAGAGCGTTCCGGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 264
    |||||

Qy 121 CCCGCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCCTCGCGGGCCCC 180
    |||||
Db 265 CCCGCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCCTCGCGGGCCCC 324
    |||||

Qy 181 CCTCGTGCCCTGGCAGGATGACGCTTTCGAGGATGCGAGGAGGCGGCCCAAGGCAAG 240
    |||||
Db 325 CCTCGTGCCCTGGCAGGATGACGCTTTCGAGGATGCGAGGAGGCGGCCCAAGGCAAG 384
    |||||

Qy 241 GAACCTGGGGCTGGCGGAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACACACGACCG 300
    |||||
Db 385 GAGCTGGGGCTGGCGGAGTGGCCCTGGGCTTCGAGGATGCGAGGAGGCGGCCCAAGGCAAG 444
    |||||

Qy 301 GCGGGACCG 309
    |||||
Db 445 GCGGGACCG 453
    |||||

RESULT 6
US-09-933-797-165
; Sequence 165, Application US/09933797
; Patent No. US20020155119A1
; GENERAL INFORMATION:
; APPLICANT: Robert A. Sikes et al.
; TITLE OF INVENTION: Isolation and Use of Fetal Urogenital ;
; FILE REFERENCE: 9901-007-999
; CURRENT APPLICATION NUMBER: US/09/933,797
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US/09/482,933
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: PCT/US99/10746
; PRIOR FILING DATE: 1999-05/14
; PRIOR APPLICATION NUMBER: 60/085,383
; PRIOR FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 811
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 165
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; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-081-280-5
  Query Match          11.8%; Score 37.2; DB 9; Length 1438;
  Best Local Similarity 47.6%; Pred. No. 0.51;
  Matches 108; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 78 GCGTTCGCGCGCGTGGCGACTCGGCAGGTGGCTTCTGCACGCCCGCTATATGAGCTG 137
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 392 GCGCGCGCTGCTCCATAGCCTTCGACGGCGCGCCAGGGGCTTCCCGGCTCCGTGCTC 333
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 138 CTTCGGGATGACAGACCCAGCCACCCCTTCGCGGGGCCCGCTCGGTGCCCTGGCA 197
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 332 TGCCCGTCGTGCTTCAGCCCTTCAGCCCGCGCGAGGGCCCGCCCGCGCTCGAGA 273
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 198 GGATGACGCTTCATCCGAGGGCGGCCCAAGCAAGGCAAGGAAGTGGGCTGCGGGC 257
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 272 AGGCCCGCTGCGGGCGGGGAGGCGGGGCCCGCCAGCAACCGAGTCCGACCGAG 213
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 258 AGTGGCCCTGGCTTCAAGATACCGAAGTGACAACGACACCGCGG 304
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 212 GTGCCCGCTGCTCGGCTAGACCTGAGCTCATTAGGCGCAGCGG 166
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
US-10-112-793-5/c
; Sequence 5, Application US/10112793
; Publication No. US2002019279A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,793
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-793-5
  Query Match          11.8%; Score 37.2; DB 9; Length 1438;
  Best Local Similarity 47.6%; Pred. No. 0.51;
  Matches 108; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 78 GCGTTCGCGCGCGTGGCGACTCGGCAGGTGGCTTCTGCACGCCCGCTATATGAGCTG 137
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 392 GCGCGCGCTGCTCCATAGCCTTCGACGGCGCGCCAGGGGCTTCCCGGCTCCGTGCTC 333
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 138 CTTCGGGATGACAGACCCAGCCACCCCTTCGCGGGGCCCGCTCGGTGCCCTGGCA 197
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 332 TGCCCGTCGTGCTTCAGCCCTTCAGCCCGCGCGAGGGCCCGCCCGCGCTCGAGA 273
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 198 GGATGACGCTTCATCCGAGGGCGGCCCAAGCAAGGCAAGGAAGTGGGCTGCGGGC 257
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 272 AGGCCCGCTGCGGGCGGGGAGGCGGGGCCCGCCAGCAACCGAGTCCGACCGAG 213
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 258 AGTGGCCCTGGCTTCAAGATACCGAAGTGACAACGACACCGCGG 304
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 212 GTGCCCGCTGCTCGGCTAGACCTGAGCTCATTAGGCGCAGCGG 166
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
US-10-112-193-5/c
; Sequence 5, Application US/10112193
; Publication No. US20030004313A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,193
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/928,069
; FILING DATE: 11-Sep-1997
; APPLICATION NUMBER: 60/026943
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1052R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-193-5
  Query Match          11.8%; Score 37.2; DB 9; Length 1438;
  Best Local Similarity 47.6%; Pred. No. 0.51;
  Matches 108; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 78 GCGTTCGCGCGCGTGGCGACTCGGCAGGTGGCTTCTGCACGCCCGCTATATGAGCTG 137
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 392 GCGCGCGCTGCTCCATAGCCTTCGACGGCGCGCCAGGGGCTTCCCGGCTCCGTGCTC 333
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 138 CTTCGGGATGACAGACCCAGCCACCCCTTCGCGGGGCCCGCTCGGTGCCCTGGCA 197
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 392 GCGCGCGCTGCTCCATAGCCTTCGACGGCGCGCCAGGGGCTTCCCGGCTCCGTGCTC 333
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 138 CTTCGGGATGACAGACCCAGCCACCCCTTCGCGGGGCCCGCTCGGTGCCCTGGCA 197
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 332 TGCCCGCTCGTTCAGCCCGCGCCGCGCCGCGCCGCGCGCTGAGT 273  
Qy 198 GGATGACGCTTCATCCGAGGCGCGCCGCGCCGCGCCGCGCGCTGAGT 257  
Db 272 AGGGCGCGCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 213  
Qy 258 AOTGCCCTCGGCTTCGAGATACCGAAGTACGACACCGCGCGG 304  
Db 212 GTGCCCCCTCTGCTCGGCTAGACCTGAGCTCATTAGCGCGCGG 166

RESULT 12

US-09-884-733-5/c  
; Sequence 5, Application US/09884733  
; Patent No. US20020123116A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: Apo-2 Ligand Inhibitor  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/884,733  
; FILING DATE: 19-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/304,003  
; FILING DATE: 14-JUNE-2000  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-5416  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1438 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-884-733-5  
Query Match 11.8%; Score 37.2; DB 10; Length 1438;  
Best Local Similarity 47.6%; Pred. No. 0.51;  
Matches 108; Conservative 0; Mismatches 119; Indels 0; Gaps 0;  
Qy 78 GCGTTCGGCGCCGCTGCGCTCGGCGCGCGCGCGCGCGCGCTATATGAGT 137  
Db 392 GCGGCGCGCTGCTCCATAGCCCTCCGACGCGCGCGCGCGCGCTCGCTCTC 333  
Qy 138 CCGTCCGGATGACGACGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 197  
Db 332 TGCCCGCTCGTTCGCGCTTCAGCGCGCGCGCGCGCGCGCGCGCGCG 273  
Qy 198 GGATGACGCTTCATCCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 257  
Db 272 AGGGCGCGCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 213  
Qy 258 AGTGCCCTCGGCTTCGAGATACCGAAGTACGACACCGCGCGG 304

Db 212 GTGCCCCCTCTGCTCGGCTAGACCTGAGCTCATTAGCGCGCGG 166  
RESULT 13  
US-09-993-234-5/c  
; Sequence 5, Application US/09993234  
; Patent No. US20020146768A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/993,234  
; FILING DATE: 19-NO. US20020146768A1-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/828,683  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1007P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-5416  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1438 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-993-234-5  
Query Match 11.8%; Score 37.2; DB 10; Length 1438;  
Best Local Similarity 47.6%; Pred. No. 0.51;  
Matches 108; Conservative 0; Mismatches 119; Indels 0; Gaps 0;  
Qy 78 GCGTTCGGCGCCGCTGCGCTCGGCGCGCGCGCGCGCGCGCTATATGAGT 137  
Db 392 GCGGCGCGCTGCTCCATAGCCCTCCGACGCGCGCGCGCGCGCTCGCTCTC 333  
Qy 138 CCGTCCGGATGACGACGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 197  
Db 332 TGCCCGCTCGTTCGCGCTTCAGCGCGCGCGCGCGCGCGCGCGCGCG 273  
Qy 198 GGATGACGCTTCATCCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 257  
Db 272 AGGGCGCGCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 213  
Qy 258 AGTGCCCTCGGCTTCGAGATACCGAAGTACGACACCGCGCGG 304;  
Db 212 GTGCCCCCTCTGCTCGGCTAGACCTGAGCTCATTAGCGCGCGG 166  
RESULT 14  
US-09-945-901-44/c  
; Sequence 44, Application US/09945901  
; Patent No. US20020161215A1



QY 193 TCGCAGGATGACGCCCTTCATCCGGAGGGGGCGGCCCCANGCAAGGGCAAGAACTGGGGCTG 252  
Db 2746 AAGCACATCGACTGCGCCTGCGCAAGCGCTTGCAGGCGGAGTGGCCGTCGGGGCGGGCG 2687  
QY 253 CCGGCAGTGGCCCTGGGCTTCCAAGATACCGAAGTG 288  
Db 2686 CAGGGGGGGCGGTGCACCCAGCGGGCGAGAGCTG 2651

Search completed: February 23, 2003, 07:52:43  
Job time : 22.4885 secs



US-09-008-097-1

Query Match 99.7%; Score 313; DB 4; Length 314;  
Best Local Similarity 100.0%; Pred. No. 7.1e-71;  
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTCATGTTTAAAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACGCTGGGT 60  
Db 1 ATGTCATGTTTAAAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACGCTGGGT 60

Qy 61 GAACCAATGGCAGAGGTTTCGGGGCCCTGCTGCTAAAGTGGATGAACGGAACACGCTGGGT 120  
Db 61 GAACCAATGGCAGAGGTTTCGGGGCCCTGCTGCTAAAGTGGATGAACGGAACACGCTGGGT 120

Qy 121 CCCCTATATAGCTGCTCCGGGATGACAGCCACACGCCCCCCTCGGGCCCC 180  
Db 121 CCCCTATATAGCTGCTCCGGGATGACAGCCACACGCCCCCCTCGGGCCCC 180

Qy 181 CCTCGTGCCCTGCGGAGTACGCTTTCATCCGAGGGGGCCCGCCANGCAAGGCAAG 240  
Db 181 CCTCGTGCCCTGCGGAGTACGCTTTCATCCGAGGGGGCCCGCCANGCAAGGCAAG 240

Qy 241 GAACGCGGCTCGGGCAGTGGCTTTCGAGATACCGAAGTGAACACGACACG 300  
Db 241 GAACGCGGCTCGGGCAGTGGCTTTCGAGATACCGAAGTGAACACGACACG 300

Qy 301 GCGGACCGCTGAA 314  
Db 301 GCGGACCGCTGAA 314

RESULT 2

US-09-008-097-5  
; Sequence 5, Application US/090808097  
; Patent No. 6306830  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. Kirk  
; APPLICANT: Insel, Paul A.  
; APPLICANT: Ping, Peipei  
; APPLICANT: Post, Steven R.  
; APPLICANT: Gao, Meihua  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE  
; TITLE OF INVENTION: HEART FAILURE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/008,097  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dylan, Tyler M  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 22000-20567.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 3549 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1...3501  
; OTHER INFORMATION:  
US-09-008-097-5

Query Match 94.0%; Score 295.2; DB 4; Length 3549;  
Best Local Similarity 97.1%; Pred. No. 3.4e-66;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ATGTCATGTTTAAAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACGCTGGGT 60  
Db 1 ATGTCATGTTTAAAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACGCTGGGT 60

Qy 61 GAACCAATGGCAGAGGTTTCGGGGCCCTGCTGCTAAAGTGGATGAACGGAACACGCTGGGT 120  
Db 61 GAACCAATGGCAGAGGTTTCGGGGCCCTGCTGCTAAAGTGGATGAACGGAACACGCTGGGT 120

Qy 121 CCCCTATATAGCTGCTCCGGGATGACAGCCACACGCCCCCCTCGGGCCCC 180  
Db 121 CCCCTATATAGCTGCTCCGGGATGACAGCCACACGCCCCCCTCGGGCCCC 180

Qy 181 CCTCGTGCCCTGCGGAGTACGCTTTCATCCGAGGGGGCCCGCCANGCAAGGCAAG 240  
Db 181 CCTCGTGCCCTGCGGAGTACGCTTTCATCCGAGGGGGCCCGCCANGCAAGGCAAG 240

Qy 241 GAACGCGGCTCGGGCAGTGGCTTTCGAGATACCGAAGTGAACACGACACG 300  
Db 241 GAACGCGGCTCGGGCAGTGGCTTTCGAGATACCGAAGTGAACACGACACG 300

Qy 301 GCGGACCG 309  
Db 301 GCGGACCG 309

RESULT 3

US-09-474-076-1  
; Sequence 1, Application US/09474076  
; Patent No. 6465237  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, James E.  
; APPLICANT: COR Therapeutics, Inc.  
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL  
; TITLE OF INVENTION: CYCLASE  
; FILE REFERENCE: 44481-5028-01-US  
; CURRENT APPLICATION NUMBER: US/09/474,076  
; CURRENT FILING DATE: 1999-12-12  
; PRIOR APPLICATION NUMBER: PCT/US98/13694  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/070,904  
; PRIOR FILING DATE: 1997-07-01  
; PRIOR APPLICATION NUMBER: 08/886,550  
; PRIOR FILING DATE: 1997-07-01  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4942  
; TYPE: DNA  
; ORGANISM: human type VI adenylyl cyclase  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (145)..(3648)  
US-09-474-076-1

Query Match 94.0%; Score 295.2; DB 4; Length 4942;  
Best Local Similarity 97.1%; Pred. No. 3.5e-66;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ATGTCATGTTTAAAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACGCTGGGT 60



Db 131 ATGTCGTGGTTAGTGGCTCCTGCTCCCAAAAGTGGATGAACGGAACAGACGCTTGGGT 190  
Qy 61 GAACCAATGGCAGAACGTTTCGGGGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120  
Db 191 GAACCAATGGCAGAACGTTTCGGGGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 247  
Qy 121 CCCGCTATATGAGTGGCTTCGGGATGCGAGCCACCCAGCCCCCTGCGGGCCCC 180  
Db 248 CCCGCTATATGAGTGGCTTCGGGATGCGAGCCACCCAGTCCCAACCCCTGCGGCTCCC 307  
Qy 181 CCTGGTGGCTTGGCAGATGACGCCCTTCATCGGAGGGGGGGCCGANGCAAGGCGAAG 240  
Db 308 CCTGGTGGCTTGGCAGATGAGGCCCTTCATCGGAGAGCGCGCCCGGGAAGGCGACG 367  
Qy 241 GAACCTGGGGCTGCGGGCAGTGGCCCTGGCTTCGAAGATACCGAAG 286  
Db 368 GAGTGGGGCTGCGGGCGGTGGCCCTGGGCTTCGAGGACATGAGG 413

RESULT 6  
US-08-726-214-11  
; Sequence 11, Application US/08726214  
; Patent No. 6107076  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Wei-Jen  
; APPLICANT: Gilman, Alfred G.  
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLIC CYCLASE  
; TITLE OF INVENTION: AND USES THEREFOR  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,214  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/005,498  
; FILING DATE: 04-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L.  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: UTSD:450  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4131 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-726-214-11

Query Match 63.1%; Score 198.2; DB 3; Length 4131;  
Best Local Similarity 79.9%; Pred. No. 1.2e-41;  
Matches 246; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

Qy 1 ATGTCATGGTTAGTGGCTCCTGCTCCCTAAAGTGGATGAACGGAACAGCCTTGGGT 60  
Db 56 ATGTCATGGTTAGTGGCTCCTGCTCCCTAAAGTGGATGAACGGAACAGCCTTGGGT 115  
Qy 61 GAACCAATGGCAGAACGTTTCGGGGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120

Db 116 GAACCAATGGCAGAACGTTTCGGGGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 172  
Qy 121 CCCGCTATATGAGTGGCTTCGGGATGCGAGCCACCCAGCCACCCCTCGGGGGCCCC 180  
Db 173 CCCGCTATATGAGTGGCTTCAGGAATGTGGAGCCACCCAGCCACCCCTCGGCAGCTCG 232  
Qy 181 CCTGGTGGCTTGGCAGATGACGCCCTTCATCGGAGGGGGGGCCGANGCAAGGCGAAG 240  
Db 233 ACTCGTGGCTTGGCAGATGACGCCCTTCATCGGAGGGCTGGCCCGGGAAGGGGTGTG 292  
Qy 241 GAACCTGGGGCTGCGGGCAGTGGCCCTTCGAGTTCGAAGATACCGAAGTGCACACGACCG 300  
Db 293 GAGCTTGGGGCTGCGGTGCTGAGTGGCTTGGTTCGATGACACTGAGGTGACCCACCGATG 352  
Qy 301 GCGGGACG 308  
Db 353 GGGACAGC 360

RESULT 7  
US-09-404-650-12/c  
; Sequence 12, Application US/09404650  
; Patent No. 6309858  
; GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; APPLICANT: McGivern, Joseph G.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; TITLE OF INVENTION: AND USES  
; FILE REFERENCE: R0043B-REG sequence listing  
; CURRENT APPLICATION NUMBER: US/09/404,650  
; CURRENT FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 6503  
; TYPE: DNA  
; ORGANISM: Rattus sp.  
US-09-404-650-12

Query Match 12.3%; Score 38.6; DB 4; Length 6503;  
Best Local Similarity 55.2%; Pred. No. 0.31;  
Matches 74; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 141 CCGGATGCGAGCAGCCACCCAGCCCTGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 200  
Db 173 CCGGCTGGAGAGGAGGACCCCGCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 114  
Qy 201 TGACGCTTCATCCGAGGG 260  
Db 113 GCGGG 54  
Qy 261 GCGGCTGGGGTTCG 274  
Db 53 GCGGGGGGGGGTCCG 40

RESULT 8  
US-07-793-961A-1/c  
; Sequence 1, Application US/07793961A  
; Patent No. 5334521  
; GENERAL INFORMATION:  
; APPLICANT: Yoshihiro Ishikawa  
; TITLE OF INVENTION: Cloning and Character-  
; TITLE OF INVENTION: ization of a Cardiac Adenyllyl Cyclase  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Alan M. Gordon  
; ADDRESSEE: American Cyanamid Company  
; STREET: 1937 West Main Street,  
; CITY: Stamford  
; STATE: Connecticut  
; COUNTRY: USA



```
;
;
; ZIP: 06904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII from DW4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/793,961A
; FILING DATE: 19911118
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,705
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203 321 2719
; TELEFAX: 203 321 2971
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4046 base pairs listed
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-793-961A-1

Query Match 12.0%; Score 37.6; DB 1; Length 4046;
Best Local Similarity 49.2%; Pred. No. 0.52;
Matches 97; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 90 CCGTGGCAGCTCGGCGAGGTGGCTTCTGCACGCCCGCTATATAGAGCTGCCTCCGGGATGC 149
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 462 CCGGGGTCACGTCAGGCGCCACCTCCAGTGCCTCCACACCGCTGACATGGCCTCAGTGTC 403
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 150 AGAGCCACCCAGCCACCCCTCGGGGCCCGCTCGGTGCCCTCGGAGGATGACGCGCTT 209
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 402 TCAGAGCCAGGCGCCAGCCCGCCAGCTCCAGTGCCTCCACACCGCTGACATGGCCTC 343
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 210 CATCCGGAGGGCGGCCANGCAAGGCAAGAACTGGGGCTCGGGGAGTGGCCCTGGG 269
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 342 CGGATGAAGGCCCTCATCTCCAGGGGACCGAGGGGGCCGCGAGGGTGGGACTGGG 283
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 270 CTTGGAAGATACCGAAG 286
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 282 GGCTGCGCATCCCGGAG 266
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
US-08-240-357-1/G
; Sequence 1, Application US/08240357
; Patent No. 5578481
; GENERAL INFORMATION:
; APPLICANT: Ishikawa, Yoshihiro
; TITLE OF INVENTION: Cloning and Characterization of a
; TITLE OF INVENTION: Cardiac Adenylyl Cyclase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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;
;
; APPLICATION NUMBER: US/08/240,357
; FILING DATE: 10-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,705-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4046 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 131..3625
; US-08-240-357-1

Query Match 12.0%; Score 37.6; DB 1; Length 4046;
Best Local Similarity 49.2%; Pred. No. 0.52;
Matches 97; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 90 CCGTGGCAGCTCGGCGAGGTGGCTTCTGCACGCCCGCTATATAGAGCTGCCTCCGGGATGC 149
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 462 CCGGGGTCACGTCAGGCGCCACCTCCAGTGCCTCCACACCGCTGACATGGCCTCAGTGTC 403
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 150 AGAGCCACCCAGCCACCCCTCGGGGCCCGCTCGGTGCCCTCGGAGGATGACGCGCTT 209
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 402 TCAGAGCCAGGCGCCAGCCCGCCAGCTCCAGTGCCTCCACACCGCTGACATGGCCTC 343
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 210 CATCCGGAGGGCGGCCANGCAAGGCAAGAACTGGGGCTCGGGGAGTGGCCCTGGG 269
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 342 CGGATGAAGGCCCTCATCTCCAGGGGACCGAGGGGGCCGCGAGGGTGGGACTGGG 283
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 270 CTTGGAAGATACCGAAG 286
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 282 GGCTGCGCATCCCGGAG 266
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
5498529-5
; Patent No. 5498529
; APPLICANT: BERKA, THOMAS R.; FORNWALD, JAMES A.; GORNIAK,
; JOSEFINA G.; ROSENBERG, MARTIN; STRICKLER, JAMES E.; TAYLOR, DEAN P.
; TITLE OF INVENTION: PROTEIN PROTEASE INHIBITORS FROM
; STREPTOMYCES
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,506
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 894,167
; FILING DATE: 03-JUN-1992
; APPLICATION NUMBER: 346,119
; FILING DATE: 16-FEB-1989
; APPLICATION NUMBER: 897,245
; FILING DATE: 18-AUG-1986
; SEQ ID NO: 5
; LENGTH: 668
; 5498529-5

Query Match 11.8%; Score 37.2; DB 6; Length 668;
Best Local Similarity 49.4%; Pred. No. 0.49;
Matches 126; Conservative 0; Mismatches 121; Indels 8; Gaps 1;

QY 57 GGGTGAACGCAATGGGCGAGAGCGTTTCGGCGGCCCTGGGCACTGCGGCGAGGTGGCTTCTG 116
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 130 GGATGCACAAATGGGCAACACCGCGGCTGGGCGAGCCACCTGCGCCTCAGGCCACCG 189
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RESULT 13
US-08-231-193A-44/c
; Sequence 44, Application US/08231193A
; Patent No. 5849895
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie P.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
; TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231.193A
; FILING DATE: 20-APR-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/052,459
; FILING DATE: 20-APR-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3243 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...3243
; US-08-231-193A-44

Query Match      11.7%; Score 36.6; DB 2; Length 3243;
Best Local Similarity   45.7%; Pred No. 0.89;
Matches 126; Conservative    0; Mismatches 150; Indels    0; Gaps    0;

Qy  13  AGTGGCCCTCGGTGTCCTAAAGTTGGATGAACGAAAACAAGCCTGGGGTGGAAGCAATGGG  72
     || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  2926  AGAGCCCCCAGGCCGCGGAGAGCCGAGAGCGGTGCCTGTACAGSGTGAAGGTGAGGA  2867

Qy  73  CAGAAGCGCTTCGGGGCGCGCTGGCACTCGGGCAGGTGGCTTGTGCACGCCCGCGCTATATG  132
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  2866  CAGACAGCCCCCAGCACAAATGGAGGTGGGGCTGGGGCTGCAGGCAGACGCTGCTCTG  2807

Qy  133  AGCTGCTTCGGGGATGCAGACCACCCAGCCCACCCCTGCGGGCCCCCCTCGGTGCCCC  192
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  2806  TGCCTGCCAGCGGGGGCCCTTCGCTGCTCGCCCTCTTGGCAGGSCCTCCCGGTAGATCGGC  2747

Qy  193  TGGCAGGATGACGCTTCATCGGAGGGGGCCCCANGCAAGGCAAGGAACCTGGGGCTG  252
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  2746  AAGCAATCATGCTGCGCTTGCGCCAAGCGCCTGCAGGCGAGTGGCCGTGGGGCGGGCG  2687

Qy  253  CGGGCATGGGCCCTGGGCTTTCGAAGATAACCGAAGTG  288
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

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Db 2686 CAGCGGGGCGCGTGTACACCGAGGGGCACCGAGCTG 2651

RESULT 14
; Sequence 44, Application US/08486273A
; Patent No. 5985586
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie P.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA
; TITLE OF INVENTION: ENCODING SAME AND USES THEREFOR
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,273A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/231,193
; FILING DATE: 20-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9383B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3243 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...3243
; US-08-486-273A-44

Query Match 11.7%; Score 36.6; DB 2; Length 3243;
Best Local Similarity 45.7%; Pred. No. 0.89;
Matches 126; Conservative 0; Mismatches 150; Indels 0; Gaps

Qy 13 AGTGGCCCTCTGTTCCTTAAGTGGATGAACGAAACAGACCTGGGGTGACAGCAATGGG 72
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2926 AGAGGCCCGCCAGCGCGGAGAGCCAGAGCGCTGGCTGTACAGGCTGGAGGTGAGGA 2867
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 73 CAGAAGCGTTTCGGGGCGCGTGCACCTCGGGCAGGTGGCTTCTGCACGCCCGCCCTCGT 132
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2866 CAGACACCGCCCGAGCACATGTCAGGTGGGGCTGGGGCGTGCAGGCACACGTGCTG 2807
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 133 AGCTGCCTCCGGGATGCAGAGCCACCGACCGCCCGCCCTCGGGGGCCCCCTCGGTGCC 192
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2806 TGCTGCCAGCGGGGGCCCTGCTGCTCTCGCCCTCTTGGCAGGCCCTCCCGGTAGATCGG 2747
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 193 TGGCAGGATGACGCCCTTATCCGGAGGGGCGGCCCGCAGGCAAGGCAAGGCACTGGGGCTG 252
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2746 AAGCACATGCACTGGCCCTGCGCCAGAGCCCTGTCAGGCCGAGTGGCGCTGCGGGCGGCG 2687
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Result No.	Query %			Length	DB	ID	Description
	Score	Match					
1	313	99.7	314	22	AA080561	Human partial card	
2	313	99.7	1217	19	AAV23246	Human adenylyl cycl	
3	295.2	94.0	3549	22	AA080563	Human cardiac aden	
4	295.2	94.0	3552	22	AA080567	Human cardiac aden	
5	295.2	94.0	3582	22	AA080568	Human modified car	
6	295.2	94.0	4942	20	AA000451	Human type VI aden	
7	227.4	72.4	4046	14	AAQ42525	Cardiac adenylyl c	
8	199.2	63.4	5841	24	AB1996680	Mouse ischaemic co	
9	198.2	63.1	4131	21	AAA53923	TypeVI adenylyl c	

```
XX 27-DEC-1999; 99US-0472667.
XX (REGC ) UNIV CALIFORNIA.
XX Hammond HK, Gao M;
XX WPI; 2001-418260/44.
XX P-PSDB; AAE04308.
XX Novel polynucleotide encoding a modified adenylyl cyclase polypeptide
XX useful for enhancing cardiac function in mammalian hearts, and for
XX treating heart disease, especially congestive heart failure -
XX Example 5; Page 114; 153pp; English.
XX The present invention relates to methods and compositions for enhancing
XX cardiac function in mammalian hearts by inserting transgenes encoding
XX beta-adrenergic signalling proteins (beta-ASP) which increase
XX beta-adrenergic responsiveness within the myocardium using in vivo
XX gene therapy. The beta-ASPs of the invention include beta-adrenergic
XX receptors (beta-AR), adenylyl cyclases (also referred as adenylyl cyclase,
XX adenylyl cyclase and cAMP synthetase) and G-protein receptor kinase
XX (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
XX in mammalian hearts and for treating heart disease, especially
XX congestive heart failure. The present cDNA sequence encodes human
XX partial cardiac adenylyl cyclase VI (ACVI) isoform which is used for
XX generating a third beta-ASP transgene, used in the exemplification
XX of the invention.
XX Sequence 314 BP; 60 A; 98 C; 108 G; 47 T; 1 other;
Query Match 99.7%; Score 313; DB 22; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.7e-69;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTCATGTTTAGTGGCTCTCTGTCCTCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60
Db 1 ATGTCATGTTTAGTGGCTCTCTGTCCTCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60
QY 61 GAACGCAATGGGCAGAAAGCGTTCCGGCGCGCGTGGGCACATCGGGCAGGTGCTTCTGCACG 120
Db 61 GAACGCAATGGGCAGAAAGCGTTCCGGCGCGCGTGGGCACATCGGGCAGGTGCTTCTGCACG 120
QY 121 CCCCCTATATGAGTGCCTCTCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180
Db 121 CCCCCTATATGAGTGCCTCTCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180
QY 181 CCTCGTGCCCTCGGAGATGACGCTTTCATCCGAGGGGGGGCCCGCCANGAAGGCAAG 240
Db 181 CCTCGTGCCCTCGGAGATGACGCTTTCATCCGAGGGGGGGCCCGCCANGAAGGCAAG 240
QY 241 GAACTGGGGCTGGGGCAGTGGCCCTGGCTTTCGAAGATACCGAAGTGACACGACACCG 300
Db 241 GAACTGGGGCTGGGGCAGTGGCCCTGGCTTTCGAAGATACCGAAGTGACACGACACCG 300
QY 301 GCGGGACCGCTGAA 314
Db 301 GCGGGACCGCTGAA 314
RESULT 2
AAV23246
ID AAV23246 standard; cDNA; 2127 BP.
XX AAV23246;
AC AAV23246;
XX 17-JUL-1998 (first entry)
XX Human adenylyl cyclase isoform VI encoding cDNA.
XX Human; adenylyl cyclase VI; AC-VI; beta-adrenergic signalling protein;
XX transgene; gene therapy; congestive heart failure; cardiac function;
KW
```

```
adenovirus; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 1..2127
XX FT /*tag= a
XX FT /*product= "adenylyl cyclase isoform VI"
XX FT /*transl_except= (pos:229..231,aa:Xaa)
XX FT /*transl_except= (pos:315..317,aa:Xaa)
XX FT /*note= "no stop codon given; Xaa = unknown"
XX FT misc_difference 315
XX FT /*tag= b
XX FT /*note= "n indicates a gap of about 0.5 kb"
XX WO9810085-A2.
XX 12-MAR-1998.
XX 05-SEP-1997; 97WO-US15610.
XX 16-JUN-1997; 97US-0048933.
XX 05-SEP-1996; 96US-0708661.
XX (COLL-) COLLATERAL THERAPEUTICS.
XX (REGC ) UNIV CALIFORNIA.
XX Gao M, Hammond HK, Insel PA, Ping P, Post SR;
XX WPI; 1998-193633/17.
XX P-PSDB; AAW53345.
XX Vectors containing transgene(s) encoding beta-adrenergic signalling
XX proteins - useful for gene therapy of congestive heart failure
XX Claim 60; Fig 12A; 114pp; English.
XX The present sequence encodes human adenylyl cyclase isoform VI (AC-VI)
XX from the present invention. The present invention describes a
XX recombinant replication-defective viral particle (I) comprising a gene
XX encoding a beta-adrenergic signalling protein (beta-ASP) operably
XX linked to a promoter. Also described are: (1) a recombinant pro-viral
XX plasmid (Ia) comprising a gene encoding a beta-ASP, as above, operably
XX linked to a promoter and further comprising a replication-defective
XX viral genome; (2) a (mammalian) cell transfected with (I) or (Ia); (3)
XX an isolated polynucleotide comprising a sequence encoding a human
XX adenylyl cyclase isoform VI (AC-VI), or a variant having AC activity;
XX (4) a human AC-VI encoded by (3); (5) an isolated polynucleotide
XX sequence which hybridises at high stringency to (3); and (6) a vector
XX comprising the polynucleotide of (3). (I) can be used to form a
XX filtered adenovirus particle preparation. (I) is used to enhance
XX cardiac function in mammals.
XX Sequence 2127 BP; 421 A; 637 C; 615 G; 452 T; 2 other;
Query Match 99.7%; Score 313; DB 19; Length 2127;
Best Local Similarity 100.0%; Pred. No. 2.2e-69;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTCATGTTTAGTGGCTCTCTGTCCTCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60
Db 1 ATGTCATGTTTAGTGGCTCTCTGTCCTCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60
QY 61 GAACGCAATGGGCAGAAAGCGTTCCGGCGCGCGTGGGCACATCGGGCAGGTGCTTCTGCACG 120
Db 61 GAACGCAATGGGCAGAAAGCGTTCCGGCGCGCGTGGGCACATCGGGCAGGTGCTTCTGCACG 120
QY 121 CCCCCTATATGAGTGCCTCTCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180
Db 121 CCCCCTATATGAGTGCCTCTCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180
QY 181 CCTCGTGCCCTCGGAGATGACGCTTTCATCCGAGGGGGGGCCCGCCANGAAGGCAAG 240
Db 181 CCTCGTGCCCTCGGAGATGACGCTTTCATCCGAGGGGGGGCCCGCCANGAAGGCAAG 240
```

Db 181 CCTCGGTCCTCGCAGGATGACGCCTTCATCCGAGGGCGGCCGCAAGGCAAG 240  
 QY 241 GAACTGGGGCTGCGGGCAGTGGCCCTGGCTTCGAAAGTACCGAAGTGACAACGACACCG 300  
 Db 241 GAACTGGGGCTGCGGGCAGTGGCCCTGGCTTCGAAAGTACCGAAGTGACAACGACACCG 300  
 QY 301 GCGGACCGGTGAA 314  
 Db 301 GCGGACCGGTGAA 314

RESULT 3  
 AAD08563  
 ID AAD08563 standard; DNA; 3549 BP.  
 XX  
 AC AAD08563;  
 XX  
 DT 04-SEP-2001 (first entry)  
 XX  
 DE Human cardiac adenylycyclase VI (ACVI) isoform #1 DNA.  
 XX  
 KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;  
 KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
 KW adenylycyclase; adenylate cyclase; CAMP synthetase;  
 KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
 KW cardiac adenylycyclase VI; ACVI isoform; beta-ASP transgene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT CDS 1..3504  
 FT /\*tag= a  
 FT /product= "Human cardiac adenylycyclase VI isoform #1"  
 FT /EC\_number= "4.6.1.1"  
 XX  
 PN WO200148164-A2.  
 XX  
 PD 05-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000WO-US35411.  
 XX  
 PR 27-DEC-1999; 99US-0472667.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Hammond HK, Gao M;  
 XX  
 DR WPI; 2001-418260/44.  
 DR P-PSDB; AAE04310.  
 XX  
 PT Novel polynucleotide encoding a modified adenylycyclase polypeptide  
 PT useful for enhancing cardiac function in mammalian hearts, and for  
 PT treating heart disease, especially congestive heart failure -  
 XX  
 PS Example 5; Page 122-129; 153pp; English.  
 XX  
 CC The present invention relates to methods and compositions for enhancing  
 CC cardiac function in mammalian hearts by inserting transgenes encoding  
 CC beta-adrenergic signalling proteins (beta-ASP) which increase  
 CC beta-adrenergic responsiveness within the myocardium using in vivo  
 CC gene therapy. The beta-ASPs of the invention include beta-adrenergic  
 CC receptors (beta-AR), adenylyclases (also referred as adenylycyclase,  
 CC adenylate cyclase and CAMP synthetase) and G-protein receptor kinase  
 CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
 CC in mammalian hearts and for treating heart disease, especially  
 CC congestive heart failure. The present DNA sequence encodes human  
 CC cardiac adenylycyclase VI (ACVI) isoform which is used for generating  
 CC a third beta-ASP transgene, used in the exemplification  
 CC of the invention.  
 XX  
 SQ Sequence 3549 BP; 699 A; 1025 C; 1061 G; 764 T; 0 other;

Query Match 94.0%; Score 295.2; DB 22; Length 3549;

Best Local Similarity 97.1%; Pred. No. 7.1e-65;  
 Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGGTTTACTGGCTCCTCGTCCCTAAAGTGAATGAACGAAACAGCCTGGGGT 60  
 Db 1 ATGTCATGGTTTACTGGCTCCTCGTCCCTAAAGTGAATGAACGAAACAGCCTGGGGT 60  
 QY 61 GAACGCAATGGGCAGAACGCTTCGCGGCGCGCTGCCTCGGAGGTGGCTTCTGCACG 120  
 Db 61 GAACGCAATGGGCAGAACGCTTCGCGGCGCGCTGCCTCGGAGGTGGCTTCTGCACG 120  
 QY 121 CCCGCTATATGAGCTGCCTCCGGGATGCGAGCCACCCACCCCTGCGGGGCC 180  
 Db 121 CCCGCTATATGAGCTGCCTCCGGGATGCGAGCCACCCACCCCTGCGGGGCC 180  
 QY 181 CCTCGTGCCCTGCGAGGATGACGCTTCATCCGAGGGCGGCCGCAAGGCAAG 240  
 Db 181 CCTCGTGCCCTGCGAGGATGACGCTTCATCCGAGGGCGGCCGCAAGGCAAG 240  
 QY 241 GAACTGGGGCTGCGGGCAGTGGCCCTCGAGGTTCGAAAGTACCGAAGTGACAACGACCG 300  
 Db 241 GAGCTGGGGCTGCGGGCAGTGGCCCTCGAGGTTCGAGGATACCGAGGTGACAACGACCG 300  
 QY 301 GCGGACCG 309  
 Db 301 GCGGACCG 309

RESULT 4  
 AAD08567  
 ID AAD08567 standard; DNA; 3552 BP.  
 XX  
 AC AAD08567;  
 XX  
 DT 04-SEP-2001 (first entry)  
 XX  
 DE Human cardiac adenylycyclase VI (ACVI) isoform #2 DNA.  
 XX  
 KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;  
 KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
 KW adenylycyclase; adenylate cyclase; CAMP synthetase;  
 KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
 KW cardiac adenylycyclase VI; ACVI isoform; beta-ASP transgene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT CDS 1..3507  
 FT /\*tag= a  
 FT /product= "Human cardiac adenylycyclase VI isoform #2"  
 FT /EC\_number= "4.6.1.1"  
 XX  
 PN WO200148164-A2.  
 XX  
 PD 05-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000WO-US35411.  
 XX  
 PR 27-DEC-1999; 99US-0472667.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Hammond HK, Gao M;  
 XX  
 DR WPI; 2001-418260/44.  
 DR P-PSDB; AAE04311.  
 XX  
 PT Novel polynucleotide encoding a modified adenylycyclase polypeptide  
 PT useful for enhancing cardiac function in mammalian hearts, and for  
 PT treating heart disease, especially congestive heart failure -  
 XX  
 PS Claim 6; Page 134-140; 153pp; English.  
 XX

CC The present invention relates to methods and compositions for enhancing  
 CC cardiac function in mammalian hearts by inserting transgenes encoding  
 CC beta-adrenergic signalling proteins (beta-ASP) which increase  
 CC beta-adrenergic responsiveness within the myocardium using in vivo  
 CC gene therapy. The beta-ASPs of the invention include beta-adrenergic  
 CC receptors (beta-AR), adenylyl cyclases (also referred as adenylyl cyclase,  
 CC adenylylate cyclase and cAMP synthetase) and G-protein receptor kinase  
 CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
 CC in mammalian hearts and for treating heart disease, especially  
 CC congestive heart failure. The present DNA sequence encodes human  
 CC cardiac adenylyl cyclase VI (ACVI) isoform which is used for generating  
 CC a fourth beta-ASP transgene, used in the exemplification  
 CC of the invention.  
 XX  
 SQ Sequence 3552 BP; 686 A; 1037 C; 1068 G; 761 T; 0 other;

Query Match 94.0%; Score 295.2; DB 22; Length 3552;  
 Best Local Similarity 97.1%; Pred. No. 7.1e-65;  
 Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 ATGTCATGTTAGTGGCTCCTGCTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60  
 DB 1 ATGTCATGTTAGTGGCTCCTGCTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60  
 QY 61 GAACGCAATGGGAGAGCGTTTCGGCGCCGCTGGGCACATCGGGCAGGTGGCTTCTGCACG 120  
 DB 61 GAACGCAATGGGAGAGCGTTTCGGCGCCGCTGGGCACATCGGGCAGGTGGCTTCTGCACG 120  
 QY 121 CCCCCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180  
 DB 121 CCCCCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180  
 QY 181 CCTCGTGCCCTTGGCAGGATGACGCTTTCATCCGGAGGGGGGCCANGCAAGGCAAG 240  
 DB 181 CCTCGTGCCCTTGGCAGGATGACGCTTTCATCCGGAGGGGGGCCANGCAAGGCAAG 240  
 QY 241 GAACCTGGGCTGGGGCAGTGGCCCTGGGCTTCGGAAGATACCGAAGTGACAGCACCG 300  
 DB 241 GAGCTGGGCTGGGGCAGTGGCCCTGGGCTTCGAGGATACCGAAGTGACAGCACCG 300  
 QY 301 GCGGGACCG 309  
 DB 301 GCGGGACCG 309

RESULT 5  
 AAD08568  
 ID AAD08568 standard; cDNA; 3582 BP.  
 XX  
 AC AAD08568;  
 XX  
 DT 04-SEP-2001 (first entry)  
 XX  
 DE Human modified cardiac adenylyl cyclase VI (ACVI) isoform cDNA.  
 XX  
 KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;  
 KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
 KW adenylyl cyclase; adenylylate cyclase; cAMP synthetase;  
 KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
 KW cardiac adenylyl cyclase VI; ACVI isoform; beta-ASP transgene; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.

XX  
 FH Key Location/Qualifiers  
 FT CDS 22..3525  
 FT /\*tag= a  
 FT /product= "Human modified cardiac ACVI isoform"  
 XX  
 PN W0200148164-A2.  
 XX  
 PD 05-JUL-2001.  
 XX

PF 26-DEC-2000; 2000WO-US35411.  
 XX  
 PR 27-DEC-1999; 99US-0472667.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Hammond HK, Gao M;  
 XX  
 DR WPI; 2001-418260/44.  
 XX  
 DR P-PSDB; AAE04312.  
 XX

Novel polynucleotide encoding a modified adenylyl cyclase polypeptide  
 useful for enhancing cardiac function in mammalian hearts, and for  
 treating heart disease, especially congestive heart failure -

Claim 4; Page 143-150; 153pp; English.

CC The present invention relates to methods and compositions for enhancing  
 CC cardiac function in mammalian hearts by inserting transgenes encoding  
 CC beta-adrenergic signalling proteins (beta-ASP) which increase  
 CC beta-adrenergic responsiveness within the myocardium using in vivo  
 CC gene therapy. The beta-ASPs of the invention include beta-adrenergic  
 CC receptors (beta-AR), adenylyl cyclases (also referred as adenylyl cyclase,  
 CC adenylylate cyclase and cAMP synthetase) and G-protein receptor kinase  
 CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
 CC in mammalian hearts and for treating heart disease, especially  
 CC congestive heart failure. The present cDNA sequence encodes human  
 CC modified cardiac adenylyl cyclase VI (ACVI) isoform which is used for  
 CC generating a beta-ASP transgene, used in the exemplification of the  
 CC invention.  
 XX

SQ Sequence 3582 BP; 703 A; 1036 C; 1067 G; 776 T; 0 other;

Query Match 94.0%; Score 295.2; DB 22; Length 3582;  
 Best Local Similarity 97.1%; Pred. No. 7.1e-65;  
 Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 ATGTCATGTTAGTGGCTCCTGCTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60  
 DB 22 ATGTCATGTTAGTGGCTCCTGCTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 81  
 QY 61 GAACGCAATGGGAGAGCGTTTCGGCGCCGCTGGGCACATCGGGCAGGTGGCTTCTGCACG 120  
 DB 82 GAACGCAATGGGAGAGCGTTTCGGCGCCGCTGGGCACATCGGGCAGGTGGCTTCTGCACG 141  
 QY 121 CCCCCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180  
 DB 142 CCCCCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 201  
 QY 181 CCTCGTGCCCTTGGCAGGATGACGCTTTCATCCGGAGGGGGGCCANGCAAGGCAAG 240  
 DB 202 CCTCGTGCCCTTGGCAGGATGACGCTTTCATCCGGAGGGGGGCCANGCAAGGCAAG 261  
 QY 241 GAACCTGGGCTGGGGCAGTGGCCCTGGGCTTCGGAAGATACCGAAGTGACAGCACCG 300  
 DB 262 GAGCTGGGCTGGGGCAGTGGCCCTGGGCTTCGAGGATACCGAAGTGACAGCACCG 321  
 QY 301 GCGGGACCG 309  
 DB 322 GCGGGACCG 330

RESULT 6  
 AAX00461  
 ID AAX00461 standard; cDNA; 4942 BP.  
 XX  
 AC AAX00461;  
 XX  
 DT 21-MAY-1999 (first entry)  
 XX  
 DE Human type VI adenylyl cyclase cDNA.  
 XX  
 KW Adenylyl cyclase type VI; human; HAC6; therapy; diagnosis; ds.



```

XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX FT CDS 145..3651
XX FT /*tag= a
XX PN WO9901547-A1.
XX PD 14-JAN-1999.
XX PF 01-JUL-1998; 98WO-US13694.
XX PR 01-JUL-1997; 97US-0886350.
XX PR 01-JUL-1997; 97US-0070904.
XX PA (CORT-) COR THERAPEUTICS INC.
XX PI Tomlinson JA;
XX DR WPI; 1999-106049/09.
XX DR P-PSDB; AAW30599.
XX PT Newly isolated and purified human type VI adenylyl cyclase (hAC6)
XX PT polypeptide - useful for identifying potential therapeutic agents
XX PT that modulate hAC6 activity, and for the diagnosis of
XX PT hAC6-associated diseases and disorders
XX PS Claim 3; Fig 1A-I; 42pp; English.
XX CC This DNA sequence encodes human type VI adenylyl cyclase (hAC6, see
XX CC AAW30599) that is expressed mainly in the heart and brain. hAC6 has
XX CC a similar putative structure to other adenylyl cyclase isoforms
XX CC but, like type V, is distinguishable in that it has a larger
XX CC N-terminus and a relatively shorter C-terminus as it lacks the C2b
XX CC region. hAC6 cDNA was initially isolated from a human heart cDNA
XX CC library using an adenylyl cyclase PCR fragment as probe. It was
XX CC used to design primers that were used in a PCR-based RACE to obtain
XX CC the full-length cDNA sequence. The invention relates to the hAC6
XX CC gene, methods for the recombinant production of purified hAC6 and
XX CC the proteins made by these methods, antibodies against hAC6,
XX CC vectors, probes and host cells (especially HEK-293) transformed by
XX CC genes encoding polypeptides having hAC6 activity, along with
XX CC diagnostic and therapeutic uses for these various reagents. hAC6
XX CC can be used as a tool to screen for agonists and antagonists that
XX CC stimulate/inhibit hAC6. Such compounds have therapeutic utility
XX CC in treating diseases caused by aberrant activity of this enzyme,
XX CC and diseases whose symptoms can be ameliorated by stimulating or
XX CC inhibiting the activity of hAC6.
XX SQ Sequence 4942 BP; 953 A; 1404 C; 1512 G; 1073 T; 0 other;

Query Match 94.0%; Score 295.2; DB 20; Length 4942;
Best Local Similarity 97.1%; Pred. No. 7.5e-65;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGGTTTACTGGCTCCTGGTCCCTAAAGTGATGAACGAAACAGCCTGGGGT 60
Db 145 ATGTCATGGTTTACTGGCTCCTGGTCCCTAAAGTGATGAACGAAACAGCCTGGGGT 204
QY 61 GAACGCAATGGCGAGAGCGTTCGCGGCGCGTGGCACTCGGGCAGGTGCTTCGCACG 120
Db 205 GAACGCAATGGCGAGAGCGTTCGCGGCGCGTGGCACTCGGGCAGGTGCTTCGCACG 264
QY 121 CCGCGCTATATAGCTGCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180
Db 265 CCGCGCTATATAGCTGCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 324
QY 181 CCTCGGTGCCCTCGCAGGATGACGCTTCATCCGAGGGCGGCCCCANGCAAGGCGAAG 240
Db 325 CCTCGGTGCCCTCGCAGGATGACGCTTCATCCGAGGGCGGCCCCANGCAAGGCGAAG 384
QY 241 GAACCTGGGGTGGCGGGCAGTGGCCCTCGGGCTTCGAAGATACCGAAGTGACAACGACCG 300

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Db 385 GAGCTGGGGTGGCGGAGTGGCCCTTCGAGGATACCGAGGTGACAAACGACACGCG 444
QY 301 GCGGGACCG 309
Db 445 GCGGGACG 453

RESULT 7
AAQ42525
ID AAQ42525 standard; DNA; 4046 BP.
XX AC AAQ42525;
XX DT 14-SEP-1993 (first entry)
XX DE Cardiac adenylyl cyclase gene.
XX KW Regulation; cardiac function; heart; heart failure; ss.
XX OS Canis familiaris.
XX PH Key Location/Qualifiers
XX FT CDS 131..3627
XX FT /*tag= a
XX PN EP543137-A.
XX PD 26-MAY-1993.
XX PF 12-OCT-1992; 92EP-0117374.
XX PR 18-NOV-1991; 91US-0793961.
XX PA (AMCY ) AMERICAN CYANAMID CO.
XX PI Ishikawa Y;
XX DR WPI; 1993-168873/21.
XX DR P-PSDB; AAR37309.
XX PT Purified DNA encoding cardiac adenylyl cyclase - useful to screen
XX PT for cpds. which stimulate activity of the cyclase
XX PS Claim 1; Fig 2; 34pp; English.
XX CC A canine heart cDNA library was constructed in lambda gt10 and was
XX CC screened with a 970 bp AatI-HincII fragment from type I adenylyl
XX CC cyclase cDNA probe (encodes the first cytoplasmic domain of adenylyl
XX CC cyclase, which has significant homology to other previously known
XX CC types of adenylyl cyclase). One positive clone, of 5.4 kb was obtd.
XX CC Positive colonies were subcloned into pUC18 and further subcloned
XX CC and sequenced bidirectionally. The 5.4 kb clone was used to
XX CC rescreen the library and on overlapping clone contg. the 5' end of
XX CC the gene was isolated. Together the two clones cover the complete
XX CC canine cardiac adenylyl cyclase gene. The gene is suspected of
XX CC being involved in the regulation of cardiac function and it is thought
XX CC that decreased activity of adenylyl cyclase in the heart may be a
XX CC major factor in the development of heart failure. Thus the adenylyl
XX CC cyclase gene is useful to screen cpds. which stimulate the activity
XX CC of the cyclase.
XX SQ Sequence 4046 BP; 743 A; 1206 C; 1254 G; 843 T; 0 other;

Query Match 72.4%; Score 227.4; DB 14; Length 4046;
Best Local Similarity 89.5%; Pred. No. 7.7e-48;
Matches 256; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGTCATGGTTTACTGGCTCCTGGTCCCTAAAGTGATGAACGAAACAGCCTGGGGT 60
Db 131 ATGTCATGGTTTACTGGCTCCTGGTCCCTAAAGTGATGAACGAAACAGCCTGGGGT 190
QY 61 GAACGCAATGGCGAGAGCGTTCGCGGCGCGTGGCACTCGGGCAGGTGCTTCGCACG 120

```

Db 191 GAACGCAATGGCAGAAAGCT---CCACGCCGGGACTCGGACCAAGTGGCTTCTGCACG 247  
 Qy 121 CCCCGCTATATGAGCTGCTCCGGGATGAGAGCCACCCAGCCACCCCTCGGGGCCCC 180  
 Db 248 CCCCGCTATATGAGCTGCTCCGGGATGAGAGCCACCCAGTCCACCCCTCGGGTCCC 307  
 Qy 181 CCTCGTGCCCTGGCAGGATGACGCTTTCATCCGGAGGGGGCCGACGCAAGGCAAG 240  
 Db 308 CCTCGTGCCCTGGCAGGATGAGGCTTTCATCCGGAGAGGGCCGCGGCAAGGCAAG 367  
 Qy 241 GAACGGGGCTGGGCACTGGCCCTGGGCTTCGAAAGATACGAAG 286  
 Db 368 GAGCTGGGGCTGGGGCGTGGCCCTGGGCTTCGAGGACACTGAGG 413

## RESULT 8

ABI99680  
ID ABI99680 standard; cDNA; 5841 BP.

XX AC ABI99680;

XX XX

DE 07-MAR-2002 (first entry)

XX Mouse ischaemic condition related cDNA sequence SEQ ID NO:716.

KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;

XX vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.

OS Mus musculus.

XX WO20018188-A2.

XX 22-NOV-2001.

PF 18-MAY-2001; 2001WO-JP04192.

XX 18-MAY-2000; 2000JP-0145977.

XX (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX WPI; 2002-034733/04.

DR P-PSDB; ABB57257.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these genes -

XX Claim 2; Page 1771-1780; 2690pp; English.

XX The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABI99202 to ABI99912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.

XX Sequence 5841 BP; 1214 A; 1558 C; 1673 G; 1396 T; 0 other;

Query Match 63.4%; Score 199.2; DB 24; Length 5841;  
 Best Local Similarity 82.3%; Pred. No. 9.8e-41;  
 Matches 241; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

Qy 1 ATGTCATGTTTAGTGGCTCCTGCTCCCTAAAGTGGATGAACGAAACAGCCTGGGT 60  
 Db 96 ATGTCATGTTTAGTGGCTCCTGCTCCCAAGTGGATGAACGAAACAGCCTGGGG 155  
 Qy 61 GAACGCAATGGCAGAAAGCTTCGGGGCGGCTCGGCACTCGGGCAGGTGGCTTCTGCACG 120  
 Db 156 GAACGCAATGGCAGAAAGC---CCACGCCAGCGGAATCGAGCCAGTGGCTTCTGCACA 212  
 Qy 121 CCCCGCTATATGAGCTGCTCCGGGATGAGAGCCACCCAGCCACCCCTCGGGGCCCC 180  
 Db 213 CCTCGCTATATGAGCTGCTCCCAAGTGGAGCCACCCAGCCACCCCTCGAGCTCAC 272  
 Qy 181 CCTCGTGCCCTGGCAGGATGACGCTTTCATCCGGAGGGGGCGGCCCAAGGCAAG 240  
 Db 273 ACTCGGTGCCCCCTGGCAGGATGAAGCCTTCATCAGAGGGGGCGGCCGAGGGGTGTG 332  
 Qy 241 GAACGGGGCTGGGGCACTGGCCCTGGGCTTCGAAAGATACGAAGTGAACAAC 293  
 Db 333 GAGCTGGGGCTGGGTCAGTGGCTTGGGGTTTGACGACACTGAGGTGACCAC 385

## RESULT 9

AA53923  
ID AA53923 standard; cDNA; 4131 BP.

XX AC AA53923;

XX 03-JAN-2001 (first entry)

DE Type VI adenylyl cyclase coding sequence.

KW Adenylyl cyclase; type I; type II; recombinant; enzyme; CAMP;  
 KW cyclic AMP; adenosine monophosphate; screening; stimulation;  
 KW inhibition; treatment; cholera; pituitary tumour; heart failure;  
 KW ischaemia; endocrine disorder; cell necrosis;  
 KW pseudohypoparathyroidism; endocrine deficiency; human; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 14..3556

FT /tag= a

FT /product= Type VI adenylyl cyclase

XX US6107076-A.

XX 22-AUG-2000.

XX 04-OCT-1996; 960S-0726214.

XX 04-OCT-1995; 950S-0005498.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Gilman AG, Tang W;

XX WPI; 2000-578539/54.

XX P-PSDB; AAB02010.

XX Novel soluble mammalian polypeptide composition comprising adenylyl cyclase activity for screening stimulators and inhibitors of adenylyl cyclase, is activated by Galpha

XX Disclosure; Columns 75-78; 73pp; English.

CC A recombinant Adenylyl cyclase is described which lacks membrane bound domains. Separation and purification of the recombinant enzyme is much easier compared with wild type enzymes and the recombinant enzyme is more stable than the wild type enzyme which allows easier screening of compounds that stimulate and inhibit Adenylyl cyclase activity. The recombinant adenylyl cyclase comprises a chimera of adenylyl cyclase C<sub>1</sub> and C<sub>2</sub> domains linked covalently.

CC The domains may be linked by a linker peptide. The recombinant  
CC adenylyl cyclase is useful for screening inhibitors and stimulators  
CC of adenylyl cyclase activity. Inhibitors of the enzyme are useful for  
CC treating cholera, pituitary tumors, heart failure, ischaemia,  
CC endocrine disorders and cell necrosis. Stimulators of adenylyl  
CC cyclase are useful for treating pseudohypoparathyroidism and other  
CC endocrine deficiencies.

XX  
SQ Sequence 4131 BP; 835 A; 1190 C; 1182 G; 924 T; 0 other;

Query Match 63.1%; Score 198.2; DB 21; Length 4131;  
Best Local Similarity 79.9%; Pred. No. 1.7e-40;  
Matches 246; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 1 ATGTCATGTTTGTAGTGGCTCCCTGCTCCCTAAAGTGATGAACGAAACAGCCTGGCGT 60  
|||||  
DB 56 ATGTCATGTTTGTAGTGGCTCCCTGCTCCCTAAAGTGATGAACGAAACAGCCTGGCGC 115  
|||||  
QY 61 GAACGCAATGGGAGAGAGCTTCGCGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120  
|||||  
DB 116 GAACGCAATGGGAGAGAGCG---CCACGCGAGCGGACCGCGCTGGCTTCTGCACG 172  
|||||  
QY 121 CCCGCTATATAGCTCCCTCCGGGATGACAGCCACCGACCCCTGGCGGCGCC 180  
|||||  
DB 173 CCCGCTATATAGCTCCCTCCGGGATGACAGCCACCGACCCCTGGCGGCTCGC 232  
|||||  
QY 181 CTTCTGGTGGCGGAGGATGACGCTTCATCGGAGGGCGGCGCCGACGAGGGCAAG 240  
|||||  
DB 233 ACTCGGTGCGCTGGCAGGATGAAGCTTCTCAGGAGGCTGGCGGAGGGGTGTG 292  
|||||  
QY 241 GAATGGGGTGGCGGAGTGGCGCTGGGCTTGAAGATACCGAAGTACACACGACACCG 300  
|||||  
DB 293 GAGCTGGGGTGGCGTCACTGAGTGGCTGGGTTTGTGACACTGAGGTGACACACCGATG 352  
|||||  
QY 301 GCGGGACC 308  
|||||  
DB 353 GGGACAGC 360  
|||||

RESULT 10

AAS11614/C  
ID AAS11614 standard; DNA; 236303 BP.

XX AAS11614;

XX 24-OCT-2001 (first entry)

DE Human genomic DNA containing exons 2-17 of the CRIM1 gene.

XX  
KW CRIM-1; Human; human chromosome 2p21-16.3; ophthalmological;  
KW neuroprotective; renal; osteopathic; dental; vulnary; immunogen;  
KW antibody; gene therapy; neurodegenerative disease; eye disorder;  
KW cataract; bone morphogenic protein; BMG; renal disease; bone abnormality;  
KW tooth abnormality; wound; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FX exon 33104..33277

FT /tag= a

FT /number= 2

FT 33278..77746

FT /tag= b

FT /number= 2

FT 77747..77989

FT /tag= c

FT /number= 3

FT 77990..79103

FT /tag= d

FT /number= 3

FT 79104..79224

FT /tag= e

FT /number= 4

FT intron 79225..101022

FT /tag= f

FT /number= 4

FT 101023..101144

FT /tag= g

FT /number= 5

FT 101145..113377

FT /tag= h

FT /number= 5

FT 113378..113560

FT /tag= i

FT /number= 6

FT 113561..115985

FT /tag= j

FT /number= 6

FT 115986..116183

FT /tag= k

FT /number= 7

FT 116184..135707

FT /tag= l

FT /number= 7

FT 135708..135836

FT /tag= m

FT /number= 8

FT 135837..146471

FT /tag= n

FT /number= 8

FT 146472..146628

FT /tag= o

FT /number= 9

FT 146629..148761

FT /tag= p

FT /number= 9

FT 148762..148883

FT /tag= q

FT /number= 10

FT 148884..150044

FT /tag= r

FT /number= 10

FT 150045..150254

FT /tag= s

FT /number= 11

FT 150255..153815

FT /tag= t

FT /number= 11

FT 153816..154031

FT /tag= u

FT /number= 12

FT 154032..158580

FT /tag= v

FT /number= 12

FT 158581..158802

FT /tag= w

FT /number= 13

FT 158803..173982

FT /tag= x

FT /number= 13

FT 173983..174177

FT /tag= y

FT /number= 14

FT 174178..181006

FT /tag= z

FT /number= 14

FT 181007..181129

FT /tag= aa

FT /number= 15

FT 181130..183612

FT /tag= ab

FT /number= 15

FT 183613..183800

FT /tag= ac

FT /number= 16

FT 183801..185152

FT		/tag= ad	
FT	exon	/number= 16	
FT		185153..187765	
FT		/tag= ae	
FT		/number= 17	
XX			
XX	WO200138519-A1.		
XX			
PD	31-MAY-2001.		
XX			
XX	24-NOV-2000; 200WO-AU01435.		
PF			
XX			
XX	26-NOV-1999; 99AU-0004348.		
PR			
XX	(UYQU ) UNIV QUEENSLAND.		
PA			
XX			
XX	Little M, Yamada T, Holmes G, Georgas K, Kolle G, Wilkinson L;		
PI			
XX	WPI; 2001-343951/36.		
DR			
XX			
XX	Nucleic acids from human chromosome 2p21-16.3 and the encoded peptide,		
PT	useful for preventing, diagnosing and treating e.g. eye disease,		
PT	especially cataract formation -		
PT			
XX			
XX	Claim 4; Fig 3; 169pp; English.		
PS			
CC	The invention relates to nucleic acids from human chromosome 2p21-16.3		
CC	and the encoded peptide (and mouse and chicken orthologues) that		
CC	comprises a PEGCPLP group, an insulin-like growth factor binding protein		
CC	(IGFBP)-like domain, cysteine-rich domains, an RGD (undefined) group		
CC	and a transmembrane domain. The protein, e.g. CRIM1, interacts with		
CC	peptides of the transforming growth factor superfamily. A composition		
CC	comprising an expression construct comprising the nucleic acids of the		
CC	invention or a mimetic which antagonises or mimics an activity of a CRIM1		
CC	polypeptide may be used in a method for modulating the biological		
CC	activity of a polypeptide of the bone morphogenic protein (BMP) family.		
CC	In this way they may be used to prevent or treat an eye disease,		
CC	especially cataract formation. They may also be used to treat		
CC	neurodegenerative diseases, renal and kidney disease, bone and tooth		
CC	abnormalities, wounds and skin damage, e.g. by use of the nucleic acid in		
CC	gene therapy by using antibodies directed against CRIM1 polypeptides.		
CC	The present sequence is a Human genomic DNA containing exons 2-17 of		
CC	the CRIM1 gene.		
XX			
SQ	Sequence 236303 BP; 70199 A; 46544 C; 47996 G; 71563 T; 1 other;		
	Query Match 12.7%; Score 39,8; DB 22; Length 236303;		
	Best Local Similarity 55.4%; Pred. No. 1.8;		
	Matches 77; Conservative 0; Mismatches 62; Indels 0; Gaps 0		
OY	78 CGGTTCGGCGGCCGCTGGACATCGGCAGTGCGTCTTCGACGCCGCCGCTATATGAGCTG 137		
Db	234505 GAGTCGGGGGCCCGCGGGAGTGGCGGGAGCCTCCCTACCCCTCGCCCGACCGGCAG 234446		
OY	138 CCTCGGGATGCAGACGACCACCCACCCCTCGGGGCCCCCCCTCGGTGCCCTTGGCA 197		
Db	234445 CCCTACGCGCCGAGCTCTCTCCCTGGCCCTCTTCGCGCCGACGGGGAGTCTCCCGCCC 234386		
OY	198 GGATGACGCCCTTCATCCGG 216		
Db	234385 TCTCGCCTCTTCCTCCGG 234367		
RESULT 11			
AAS06036/c			
ID	AAS06036 standard; DNA; 3050 BP.		
XX			
AC	AAS06036;		
XX			
DT	12-SEP-2001 (first entry)		
XX			
DE	Angiotensin converting enzyme (ACEV) splice variant DNA #36.		
XX			

```
Db 2443 AAGCACATCGACTCGCTGCGCGAAGCGCTGACGCCGAGTGGCTGCGGCGGGCG 2384
QY 253 CGGCGACTGGCCCTGGCTTCGAGATACCGAAGTG 288
Db 2383 CAGCGGGGGCGGCGACCCAGCGGCGAGCGCTG 2348

RESULT 12
AAC77370
ID AAC77370 standard; cDNA; 3174 BP.
XX
AC AAC77370;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human ORFX ORF2925 polynucleotide sequence SEQ ID NO:5849.
XX
KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive; ss.
XX
OS Homo sapiens.
XX
PN W0200058473-A2.
XX
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US08621.
XX
PR 31-MAR-1999; 99US-0127607.
PR 02-APR-1999; 99US-0127636.
PR 05-APR-1999; 99US-0127728.
PR 30-MAR-2000; 2000US-0540763.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
XX WPI; 2000-602362/57.
XX P-PSDB; AAB43161.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
XX
XX Claim 5; Page 5022-5024; 5507pp; English.
XX
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC antithyroid; and antianaemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
```

```
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX
SQ Sequence 3174 BP; 737 A; 897 C; 904 G; 620 T; 16 other;

Query Match 12.2%; Score 38.2; DB 21; Length 3174;
Best Local Similarity 53.4%; Pred. No. 2.4;
Matches 79; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 137 GCCTCGGGATGCAGAGCCACCCAGCCCTGCGGGCGGCCCTCGGTGCCCTGGC 196
Db 2049 GCCCTTCAGGCTCAGCTTCCAAACCACAGCTCCCGGTCGCCACATTGCCCTCAGC 2108
QY 197 AGGATGACGCTTTCATCCGGAGGGCGGCCCGCAGGCGAAGCAACTGGGCTGCGGG 256
Db 2109 AGGCTTAGTCCAGTTCCTGGGTGGGGGCGAGCAGCTGCCCTGGCACAGTGGCCAGG 2168
QY 257 CAGTGGCCCTGGGCTTCGAGATACCGA 284
Db 2169 CAGGCGCCCTGGCTAGCTGGACATCCA 2196

RESULT 13
AAQ79401/c
ID AAQ79401 standard; cDNA; 3243 BP.
XX
AC AAQ79401;
XX
DT 06-JUL-1995 (first entry)
XX
DE Human NMDAR2 receptor subunit clone NMDA24 gene.
XX
KW N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel;
KW glutamate; hippocampus; rat; pcDNA1; NMDA receptor; antagonist; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 1..822
FT /*tag= a
FT /product= part of the NMDAR2C receptor subunit
FT misc_feature 540..551
FT /*tag= b
FT /note= "11 bp insertion found in clone NMDA24"
FT misc_feature 1501..1525
FT /*tag= c
FT /note= "24 bp insertion found in clone NMDA24"
XX
XX W09424284-A.
XX
XX 27-OCT-1994.
XX
XX 20-APR-1994; 94WO-US04387.
XX
XX 20-APR-1993; 93US-0052449.
XX
XX (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
XX Daggett LP, Ellis SB, Liaw CW, Lu C;
XX WPI; 1994-341863/42.
XX P-PSDB; AAR66059.
XX
XX Isolated DNA encoding a human N-methyl-D-aspartate receptor
XX subunit - used as probes in the identification and isolation of
XX nucleic acids encoding related receptor subunits.
XX
XX Claim 11; Page 99-104; 156pp; English.
```

XX The nucleotide sequence of the novel N-methyl-D-aspartate (NMDA)  
 CC receptor 2C (NMDAR2C) gene clone NMDA24. This clone covers bases  
 CC 861-4068 of the complete NMDAR2C gene (AAQ79372) with an insertion of 11  
 CC bp between bases 1300-1 and an insertion of 24 bp between bases 2350-1.  
 CC The 11 bp insert adds an extra 3 a.a. to the peptide sequence but causes  
 CC a reading frame shift which terminates the peptide at residue 494 of the  
 CC NMDAR2C sequence. The NMDA receptor contains two subunits: subunit R1  
 CC (AAQ79370) and subunit R2 selected from the subunits 2A (AAQ79375), 2B  
 CC (AAQ79377), 2C and 2D (AAQ79378). The receptor forms part of a family of  
 CC NMDA receptors which have cation-selective channels and bind glutamate  
 CC and NMDA. The NMDAR2C gene was obtained by amplifying cDNA derived from  
 CC human brain tissues with primers corresponding to sequences in the rat  
 CC NMDAR2A receptor DNA and using the resultant fragments as probes to  
 CC screen a cDNA library derived from human hippocampal RNA. 4 basic clones  
 CC were isolated: NMDA21 (AAQ79399), NMDA22 (AAQ79400), NMDA24 (AAQ79401)  
 CC and NMDA26 (AAQ79402). The clones are thought to be splice variants of  
 CC each other. Based on the sequence of the 4 clones, a series of variants  
 CC (AAQ79403-7) of the NMDAR2C receptor were constructed. The expression of  
 CC the genes allows the reconstruction of the NMDA receptor. The complete  
 CC receptor can be used to identify compounds which bind or are antagonistic  
 CC to the human NMDA receptor.

XX Sequence 3243 BP; 540 A; 1115 C; 1024 G; 564 T; 0 other;

Query Match 12.2%; Score 38.2; DB 15; Length 3243;  
 Best Local Similarity 46.0%; Pred. No. 2.5;  
 Matches 127; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY 13 AGTGGCCCTCTGGTCCCTAAAGTGATGAACGGAACACAGCCTGGGTCAACGCAATGGG 72  
 Db 2926 AGAGCCCCCAGGCCCCCGAGGAGCCAGAGCGCTGGTGGCAGAGGTGAAGGTGAGGA 2867

QY 73 CAGAAAGCGTTTCGGCGCGCGTGGCACTCGGCGAGGTGGCTTCTGCACGCCCGCTATATG 132  
 Db 2866 CAGACAGCCCCCAGCAAAATGGCAGGTGGCGGTGGCGTGCGAGCAGAGTGCTGTCTG 2807

QY 133 AGCTGCTTCGGGATGCAGAGCACCACCCAGCCCTCGGGGCCCCCTCGGTGCCCC 192  
 Db 2806 TGCTGCCAGGGGGGGCCCTCGCTCGGCCCTCTGGCAGGCGCTCCCGTAGATCGGC 2747

QY 193 TGGCAGGATGAGCGCTTCATCGGAGGGGGCGGCCANGCAAGGCAAGAACTGGGGCTG 252  
 Db 2746 AAGCACATCGACTGCGCTGCGCCAGCGCTGAGGCGGAGTGTCGTCGGGGCGGGCG 2687

QY 253 CGGCGAGTGGCCCTGGGCTTGAAGATACCCGAAGTG 288  
 Db 2686 CAGGCGGGCGGTGCACCCAGCGGGCAGCGAGCTG 2651

RESULT 14  
 AAQ79400/c  
 ID AAQ79400 standard; cDNA; 3698 BP.

XX AC AAQ79400;  
 XX DT 06-JUL-1995 (first entry)  
 XX DE Human NMDAR2 receptor subunit clone NMDA22.  
 XX KW N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel;  
 XX KW glutamate; hippocampus; rat; pcDNA1; NMDA receptor; antagonist; ds.  
 XX OS Homo sapiens.  
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 XX FT misc\_feature 1034..1045  
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FT FT /\*tag= C  
 FT FT /note= "15 bp deletion of NMDAR2C sequence between  
 XX XX these bases"  
 PN W09424284-A.  
 XX 27-OCT-1994.  
 PD 20-APR-1994; 94WO-US04387.  
 XX 20-APR-1993; 93US-0052449.  
 XX (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
 PA Daggett LP, Ellis SB, Liaw CW, Lu C;  
 PI WPI; 1994-341863/42.  
 XX P-PSDB; AAR66058.  
 DR Isolated DNA encoding a human N-methyl-D-aspartate receptor  
 DR subunit - used as probes in the identification and isolation of  
 XX nucleic acids encoding related receptor subunits.  
 PS Claim 11; Page 99-104; 156pp; English.  
 XX The nucleotide sequence of the novel N-methyl-D-aspartate (NMDA)  
 CC receptor 2C (NMDAR2C) gene clone NMDA22. This clone covers bases  
 CC 367-4068 of the complete NMDAR2C gene (AAQ79372) with an insertion of 11  
 CC bp between bases 1300-1 and a 15 bp deletion of bases 1960-74. The 11 bp  
 CC insert adds an extra 3 a.a. to the peptide sequence but causes a reading  
 CC frame shift which terminates the peptide at residue 494 of the NMDAR2C  
 CC sequence. The NMDA receptor contains two subunits: subunit R1 (AAQ79370)  
 CC and subunit R2 selected from the subunits 2A (AAQ79375), 2B (AAQ79377),  
 CC 2C and 2D (AAQ79378). The receptor forms part of a family of NMDA  
 CC receptors which have cation-selective channels and bind glutamate and  
 CC NMDA. The NMDAR2C gene was obtained by amplifying cDNA derived from  
 CC human brain tissues with primers corresponding to sequences in the rat  
 CC NMDAR2A receptor DNA and using the resultant fragments as probes to  
 CC screen a cDNA library derived from human hippocampal RNA. 4 basic clones  
 CC were isolated: NMDA21 (AAQ79399), NMDA22 (AAQ79400), NMDA24 (AAQ79401)  
 CC and NMDA26 (AAQ79402). The clones are thought to be splice variants of  
 CC each other. Based on the sequence of the 4 clones, a series of variants  
 CC (AAQ79403-7) of the NMDAR2C receptor were constructed. The expression of  
 CC the genes allows the reconstruction of the NMDA receptor. The complete  
 CC receptor can be used to identify compounds which bind or are antagonistic  
 CC to the human NMDA receptor.

XX Sequence 3698 BP; 610 A; 1280 C; 1164 G; 644 T; 0 other;

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 Best Local Similarity 46.0%; Pred. No. 2.5;  
 Matches 127; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

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QY 73 CAGAAAGCGTTTCGGCGCGCGTGGCACTCGGCGAGGTGGCTTCTGCACGCCCGCTATATG 132  
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QY 133 AGCTGCTTCGGGATGCAGAGCACCACCCAGCCCTCGGGGCCCCCTCGGTGCCCC 192  
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QY 193 TGGCAGGATGAGCGCTTCATCGGAGGGGGCGGCCANGCAAGGCAAGAACTGGGGCTG 252  
 Db 3201 AAGCACATCGACTGCGCTGCGCCAGCGCTGAGGCGGAGTGTCGTCGGGGCGGGCG 3142

QY 253 CGGCGAGTGGCCCTGGGCTTGAAGATACCCGAAGTG 288  
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RESULT 15  
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XX AC AAQ79407;  
XX DT 06-JUL-1995 (first entry)  
XX XX Human NMDAR2 receptor subunit clone NMDAR2C-delta15-delta51 gene.  
XX KW N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel;  
XX KW glutamate; hippocampus; rat; pcdna1; NMDA receptor; antagonist; ds.  
XX OS Homo sapiens.  
XX XX  
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XX PE 20-APR-1994; 94WO-0504387.  
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XX PR 20-APR-1993; 93US-0052449.  
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XX PA (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
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XX PI Daggett LP, Ellis SB, Liaw CW, Lu C;  
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XX DR WPI; 1994-341863/42.  
XX DR P-PSDB; AAR66065.  
XX XX  
XX PT Isolated DNA encoding a human N-methyl-D-aspartate receptor  
XX PT subunit - used as probes in the identification and isolation of  
XX PT nucleic acids encoding related receptor subunits.  
XX XX  
XX PS Claim 11; Page 99-104; 156pp; English.  
XX XX  
XX CC The nucleotide sequence of the novel N-methyl-D-aspartate (NMDA)  
XX CC receptor 2C (NMDAR2C) gene clone NMDAR2C-delta15-delta51. This clone  
XX CC contains bases 1-1959, 1975-2350 and 2402-4068 of the complete NMDAR2C  
XX CC sequence (AAQ79372). The variant differs from the full length sequence by  
XX CC a 15 bp deletion of bases 1960-74 and a 51 bp deletion of bases  
XX CC 2351-2401. A series of variants (AAQ79403-7) of the NMDAR2C receptor  
XX CC were constructed, by recombination, based on the sequence of the 4 basic  
XX CC clones: NMDA21 (AAQ79399), NMDA22 (AAQ79400), NMDA24 (AAQ79401) and  
XX CC NMDA26 (AAQ79402). The NMDA receptor contains two subunits: subunit R1  
XX CC (AAQ79370) and subunit R2 selected from the subunits 2A (AAQ79375), 2B  
XX CC (AAQ79377), 2C and 2D (AAQ79378). The receptor forms part of a family of  
XX CC NMDA receptors which have cation-selective channels and bind glutamate  
XX CC and NMDA. The expression of the genes allows the reconstruction of the  
XX CC NMDA receptor. The complete receptor can be used to identify compounds  
XX CC which bind or are antagonistic to the human NMDA receptor.  
XX XX  
XX SQ Sequence 4274 BP; 713 A; 1462 C; 1331 G; 768 T; 0 other;

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Best Local Similarity 46.0%; Pred. No. 2.6;  
Matches 127; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY 13 AGTGGCCTCGTGGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGTGAACGCAATGGG 72

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QY 73 CAGAAAGCGTTTCGGGGCGCCGCTGGCACTCGGGCAGGTGGCTTCTGCACGCCGCCGCTATATG 132  
Db 3625 CAGACAGCCCCCAGCAAAATGGCAGGTGGGCGTGGCGCTGCAGGCAGACGTGCTGTCTG 3566  
QY 133 AGCTGCTCCGGGATGCAGAGCCACCCAGCCACCCCTGCGGGCCCCCCTCGGTGCCCC 192  
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QY 253 CGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTG 288  
Db 3445 CAGCGGGGGCGGTGCACCCAGCGGGCAGCGAGCTG 3410





GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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12: gb\_sy:\*

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30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

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34: em\_htg\_pln:\*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	313	99.7	314	6	AR189757	AR189757 Sequence
3	295.2	94.0	3549	6	AR174473	AR174473 Sequence
4	295.2	94.0	3549	6	AR189761	AR189761 Sequence
5	295.2	94.0	3552	6	AR189766	AR189766 Sequence
6	295.2	94.0	3582	6	AR189768	AR189768 Sequence
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8	295.2	94.0	205248	2	AC117498	AC117498 Homo sapi
9	293.6	93.5	193283	2	AC021647	AC021647 Homo sapi
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19	196.6	62.6	6036	10	RATADC	L01115 Rattus norv
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21	186.2	59.3	108689	2	AC096835	AC096835 Rattus no
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23	57.8	18.4	61901	5	U72484	U72484 Fugu rubrip
24	46.6	14.8	125020	9	AF429315	AF429315 Homo sapi
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AUTHORS		Hammond H.Kirk., Insel, P.A., Ping, P., Post, S.R. and Gao, M.							
TITLE		Gene therapy for congestive heart failure							
JOURNAL		Patent: US 6306830-A 1 23-OCT-2001;							
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ACCESSION AX189757
VERSION AX189757.1 GI:15143133
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 314)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
JOURNAL 1 (bases 1 to 314)
AUTHORS Hammond, H. K. and Gao, M.
TITLE Gene therapy for congestive heart failure
JOURNAL Patent: WO 0148164-A 1 05-JUL-2001;
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VERSION AX174473.1 GI:17914793
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3549)
AUTHORS Hammond, H. Kirk., Insel, P. A., Ping, P., Post, S. R. and Gao, M.
TITLE Gene therapy for congestive heart failure
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ACCESSION AX189761
VERSION AX189761.1 GI:15143135
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SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3549)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
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REFERENCE 1 (bases 1 to 3549)
AUTHORS Hammond,H.K. and Gao,M.
TITLE Gene therapy for congestive heart failure
JOURNAL Patent: WO 0148164-A 5 05-JUL-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
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Best Local Similarity 97.1%; Pred. No. 4.8e-56;
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VERSION AX189766.1 GI:15143139
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SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3552)
AUTHORS Hammond,H.K. and Gao,M.
TITLE Gene therapy for congestive heart failure
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LOCUS AX189768 3582 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 12 from Patent WO0148164.
ACCESSION AX189768
VERSION AX189768.1 GI:15143140
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 3582)
AUTHORS Hammond,H.K. and Gao,M.
TITLE Gene therapy for congestive heart failure
JOURNAL Patent: WO 0148164-A 12 05-JUL-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
FEATURES
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        Location/Qualifiers
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                /note="Modified AC-VI"
BASE COUNT 703 a 1036 c 1067 g 776 t
ORIGIN
Query Match 94.0%; Score 295.2; DB 6; Length 3582;
Best Local Similarity 97.1%; Pred. No. 4.8e-56;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGGTTTAGTGCCCTCCTGGTCCCTAAAGTGATGAACGGAAACAGCCTGGGGT 60
    |||
Db 22 ATGTCATGGTTTAGTGCCCTCCTGGTCCCTAAAGTGATGAACGGAAACAGCCTGGGGT 81
    |||
QY 61 GAACGCAATGGCAGAGCGTTCCGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
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Db 82 GAACGCAATGGCAGAGCGTTCCGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 141
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QY 121 CCGCGCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGGCCCC 180
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Db 142 CCGCGCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGGCCCC 201
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QY 181 CCTCGGTGCCCTCGGAGGATGAGCGCTTCATCCGAGGGCGGCCANGCAAGGGCAAG 240
    |||
Db 202 CCTCGGTGCCCTCGGAGGATGAGCGCTTCATCCGAGGGCGGCCANGCAAGGGCAAG 261
    |||
QY 241 GAACCTGGGGTGGCGGCGAGTGGCCCTGGGCTTCGAAAGTACCCGAAGTACAAACGACACCG 300
    |||
Db 262 GAGCTGGGGTGGCGGCGAGTGGCCCTGGGCTTCGAGGATACCCGAGGTGACAAACGACACCG 321
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QY 301 GCGGGACCG 309
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Db 322 GCGGGACCG 330
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RESULT 7
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AB007882  
LOCUS AB007882 5877 bp mRNA linear PRI 10-MAY-2002  
DEFINITION Homo sapiens KIAA0422 mRNA, partial cds.  
ACCESSION AB007882  
VERSION AB007882.2 GI:20521044  
KEYWORDS KIAA0422.  
SOURCE Homo sapiens male brain cDNA to mRNA, clone\_lib:pBluescriptII SK  
plus clone:hh01205sl.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Ishikawa, K., Nagase, T., Nakajima, D., Seki, N., Ohira, M.,  
Miyajima, N., Tanaka, A., Kotani, H., Nomura, N. and Ohara, O.  
Prediction of the coding sequences of unidentified human genes.  
VIII. 78 new cDNA clones from brain which code for large proteins  
in vitro  
DNA Res. 4 (5), 307-313 (1997)  
JOURNAL  
MEDLINE 98116655  
PubMed 9455477  
REFERENCE 2 (bases 1 to 5877)  
AUTHORS Ohara, O.  
TITLE Direct Submission  
JOURNAL Submitted (06-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute,  
Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba  
292-0812, Japan (E-mail:cdna@info.kazusa.or.jp, Tel:+81-438-52-3913,  
Fax:+81-438-52-3914)  
COMMENT On May 9, 2002 this sequence version replaced gi:2887418.  
Sequence updated (05-Jan-1998).  
FEATURES  
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/db\_xref="GI:20521045"

## gene

## CDS

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BASE COUNT  
ORIGIN  
-- Query Match

94.0%; Score 295.2; DB 9; Length 5877;

Best Local Similarity 97.1%; Pred. No. 4.4e-56;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 ATGTCTATGTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 60  
DB 137 ATGTCTATGTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGGT 196  
QY 61 GAACGCAATGGGCGAGAGCGTTTCGGCGCGCGTGGGCACATCGGCGAGTGGCTTCTGCACG 120  
DB 197 GAACGCAATGGGCGAGAGCGTTTCGGCGCGCGTGGGCACATCGGCGAGTGGCTTCTGCACG 256  
QY 121 CCCCGCTATATGAGTGGCTCCGCGGATGCAGCCACCCAGCCCGCCCTCGGGGCCCC 180  
DB 257 CCCCGCTATATGAGTGGCTCCGCGGATGCAGCCACCCAGCCCGCCCTCGGGGCCCC 316  
QY 181 CCTCGTGGCCCTCGGAGATGACGCTTCATCCGAGGGGGGGCCGANGCAGGCGAAG 240  
DB 317 CCTCGTGGCCCTCGGAGATGACGCTTCATCCGAGGGGGGGCCGANGCAGGCGAAG 376  
QY 241 GAACGCGGCTCGGGCAGTGGCCCTGGGCTTTCGAAGATACGAAAGTGCACAGCACCG 300  
DB 377 GAGCTGGGCTCGGGCAGTGGCCCTGGGCTTTCGAGGATACGAGGTGCACAGCACCG 436  
QY 301 GCGGGGACCG 309  
DB 437 GCGGGGACG 445  
RESULT 8  
AC117498/c  
LOCUS AC117498 205248 bp DNA linear, HTG 31-JUL-2002  
DEFINITION Homo sapiens clone RP11-422021, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 20  
unordered pieces.  
ACCESSION AC117498  
VERSION AC117498.4 GI:22002346  
KEYWORDS HTG: HTGS\_PHASE1.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 205248)  
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-oshan, F.R., Allen, C.,  
Albrooks, S.L., Amarantunge, H.C., Are, J.R., Ayale, M., Banks, T.,  
Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonin, D.,  
Bowley, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,  
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,  
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,  
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,  
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,  
Dalla, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,  
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,  
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,  
Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,  
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,  
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,  
Gorell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,  
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,  
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,  
Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,  
Jacobson, B., Jia, J., Johnson, R., Jollivet, S., Joudah, S.,  
Karlssoon, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,  
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,  
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louised, H.,  
Lorado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,  
Maheshwar, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,  
Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mel, G., Metzger, M.,  
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,  
Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,  
Nguyen, N., Nickerson, E., Nwokenko, S., Ogih, M., Okwuonu, G.,  
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,  
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,  
Rivers, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G.,  
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,

Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tanssey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

Direct Submission  
Unpublished  
2 (bases 1 to 205248)  
Worley, K.C.

Direct Submission  
Submitted (10-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 205248)  
Worley, K.C.

Direct Submission  
Submitted (31-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Jul 29, 2002 this sequence version replaced gi:21956504.

## COMMENT

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Drafting Center Code: WUGSC  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: HEAU  
Center clone name: RP11-422021  
----- Summary Statistics  
Sequencing vector: Plasmid  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 216840 bases at least Q40  
Consensus quality: 220255 bases at least Q30  
Consensus quality: 222408 bases at least Q20  
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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 20 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 2025: contig of 2025 bp in length  
\* 2026 2125: gap of unknown length  
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\* 4438 4537: gap of unknown length  
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\* 6634 9149: gap of unknown length  
\* 9149 9249: gap of unknown length  
\* 9249 11635: contig of 2387 bp in length  
\* 11636 11735: gap of unknown length  
\* 11736 13780: contig of 2045 bp in length  
\* 13781 13880: gap of unknown length  
\* 13881 16697: contig of 2817 bp in length  
\* 16698 16797: gap of unknown length  
\* 16798 20089: contig of 3292 bp in length  
\* 20090 20189: gap of unknown length  
\* 20190 23014: contig of 2825 bp in length  
\* 23015 23114: gap of unknown length  
\* 23115 25345: contig of 2231 bp in length  
\* 25346 25445: gap of unknown length  
\* 25446 31033: contig of 5588 bp in length  
\* 31034 31133: gap of unknown length  
\* 31134 35863: contig of 4730 bp in length

\* 35864 35963: gap of unknown length  
\* 35964 49814: contig of 13851 bp in length  
\* 49815 49914: gap of unknown length  
\* 49915 64385: contig of 14471 bp in length  
\* 64386 81100: contig of unknown length  
\* 81101 81200: contig of 16615 bp in length  
\* 81201 97966: contig of 16766 bp in length  
\* 97967 98066: gap of unknown length  
\* 98067 115533: contig of 17467 bp in length  
\* 115534 115633: gap of unknown length  
\* 115634 139873: contig of 24240 bp in length  
\* 139874 139973: gap of unknown length  
\* 139974 175364: contig of 35391 bp in length  
\* 175365 175464: gap of unknown length  
\* 175465 205248: contig of 29784 bp in length.

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Best Local Similarity 97.1%; Pred. No. 2.6e-56;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGCTTTAGTGGCTTCTGCTCCCTAAAGTGGATGACGAAACAGCTGGGGT 60  
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QY 241 GAATCGGGGCTCGCGGAGTGGCCCTCGGCTTCGAAAGTACCGAAGTACACACACACG 300  
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Db 168879 GAGCTGGGGTCTCGCGGAGTGGCCCTCGGCTTCGAGGATACCGAGGTGACACACACG 168820  
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QY 301 GCGGGACCG 309  
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Db 168819 GCGGGACG 168811

RESULT 9  
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LOCUS  
DEFINITION  
Homo sapiens chromosome 12 clone RP11-455122, WORKING DRAFT  
SEQUENCE, 8 unordered pieces.  
AC021647  
AC021647.18 GI:20335444  
VERSION  
HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
KEYWORDS  
SOURCE  
Homo sapiens  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 193283)  
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, E.R., Allen, C.,  
Alsbrooks, S.L., Amaratunga, H.C., Are, J.R., Ayele, M., Banks, T.,  
Barbata, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,  
Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,  
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,  
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,  
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,

Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, P., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hognes, M., Holloway, C., Hollins, B., Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jollivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mahoney, E., McLeod, M.P., Meador, M., Mel, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, S., Nguyen, N., Nickerson, E., Nwokkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peary, J., Perez, L., Peters, L., Pickers, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Uman, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

COMMENT

Unpublished  
2 (bases 1 to 193283)  
Worley, K.C.

Direct Submission  
Submitted (19-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 193283)  
Worley, K.C.

Direct Submission  
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Apr 28, 2002 this sequence version replaced gi:15809061.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: HAAF

Center clone name: RP11-455122

----- Summary Statistics

Sequencing vector: Plasmid;

Sequencing vector: M13;

Chemistry: Dye-terminator Big Dye; 98% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 219180 bases at least Q40

Consensus quality: 233400 bases at least Q30

Consensus quality: 243367 bases at least Q20

Estimated insert size: 209025; sum-of-contigs estimation

Quality coverage: 10x in Q20 bases; sum-of-contigs estimation

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\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 8 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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\* 5401 5500: gap of unknown length  
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\* 7890 7989: gap of unknown length  
\* 7990 35656: contig of 27667 bp in length  
\* 35657 35756: gap of unknown length  
\* 35757 65618: contig of 29861 bp in length  
\* 65619 104448: contig of 38731 bp in length  
\* 104449 104548: gap of unknown length  
\* 104549 145966: contig of 41418 bp in length  
\* 145967 146066: gap of unknown length  
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FEATURES  
Location/Qualifiers

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BASE COUNT 49273 a 48888 c 46863 g 47544 t 715 others

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Query Match 93.5%; Score 293.6; DB 2: Length 193283;  
Best Local Similarity 96.8%; Pred. No. 6.1e-56;  
Matches 299; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ATGTCATGCTTTAGTGGCTCCTCTGCTCCTAAAGTGGATGAACGAAACAGCTGGGT 60  
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DB 74711 GAACGCAATGGCAGAAAGCGTTTCGGCGGCCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 74652

QY 121 CCCCCTATATGATGCTGCTCCGGATGAGAGCCACCCACCCCTCGGGGCCCC 180  
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DB 74651 CCCCCTATATGATGCTGCTCCGGATGAGAGCCACCCACCCCTCGGGGCCCC 74592

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DB 74591 CCTCGGTGCCCCCTGGCAGGATGACGCTTCATCCGAGGGGGGGCCGAGGAGGCAAG 74532

QY 241 GAATGGGGCTCGGGCAGTGGCCCTTGGCTTCGAAGATACCGAAGTGACACGACACCG 300  
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DB 74531 GAGCTGGGGCTCGGGCAGTGGCCCTTGGCTTCGAAGATACCGAAGTGACACGACACCG 74472

QY 301 GCGGGACCG 309  
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DB 74471 GCGGGACG 74463

RESULT 10

AF250226

LOCUS

DEFINITION

AF250226

ACCESSION

AF250226.1

KEYWORDS

GI:9049782

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 6463)

AUTHORS

TITLE

AF250226 6463 bp mRNA linear PRI 15-SEP-2000  
Homo sapiens adenylyl cyclase type VI mRNA, complete cds.

AF250226  
AF250226.1

GI:9049782

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 6463)

Wicker, R., Catalan, A.G., Caillieux, A., Starenki, D., Stengel, D.,

Sarasin, A., and Suarez, H.G.

Cloning and expression of human adenylyl cyclase type VI in normal

[illegible]

\* 26430 33594: contig of 7165 bp in length  
\* 33595 33694: gap of unknown length  
\* 42148 42148: contig of 8454 bp in length  
\* 42149 42248: gap of unknown length  
\* 42249 42248: contig of 10142 bp in length  
\* 52391 52490: gap of unknown length  
\* 52491 62388: contig of 9898 bp in length  
\* 62389 62488: gap of unknown length  
\* 62489 72408: contig of 9920 bp in length  
\* 72409 72508: gap of unknown length  
\* 72509 84743: contig of 12235 bp in length  
\* 84744 84843: gap of unknown length  
\* 84844 97522: contig of 12679 bp in length  
\* 97523 97622: gap of unknown length  
\* 97623 110884: contig of 13262 bp in length  
\* 110885 126977: gap of unknown length  
\* 126978 127077: contig of 15993 bp in length  
\* 127078 146137: contig of 19060 bp in length  
\* 146138 146237: gap of unknown length  
\* 146238 171945: contig of 25708 bp in length.

## FEATURES

Location/Qualifiers

source

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33695..42148  
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52491..62388  
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ORIGIN

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Matches 299; Conservative 0; Mismatches 9; Indels 1; Gaps 1;  
QY 1 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGGAACACACGCTGGGT 60

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Db 79560 ATGTCATGTTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGGAACACACGCTGGGT 79501  
QY 61 GAACCAATGGCAGAGCGTTTCGGGGCCCGTGGCACTCGGCAGGTGGCTTCTGCACG 120  
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Db 79500 GAACCAATGGCAGAGCGTTTCGGGGCCCGTGGCACTCGGCAGGTGGCTTCTGCACG 79441  
QY 121 CCCCCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCGCCCTCGGGGCC 180  
Db 79440 CCCCCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCGCCCTCG-GGCC 79382  
QY 181 CCTCGTGCCCTGCGAGGATGACGCCCTTCATCCGAGGGGGCCCGCCANGCAAGGCAAG 240  
Db 79381 CCTCGTGCCCTGCGAGGATGACGCCCTTCATCCGAGGGGGCCCGCCANGCAAGGCAAG 79322  
QY 241 GAACCTGGGGCTGGGGCAGTGGCTTCGAGATACCGAGTGCACGACGACACG 300  
Db 79321 GAGCTGGGGCTGGGGCAGTGGCTTCGAGGATACCGAGTGCACGACGACGCG 79262  
QY 301 GCGGGACCG 309  
Db 79261 GCGGGACG 79253  
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RESULT 12  
DOGADENCYC 4046 bp mRNA linear MAM 27-APR-1993  
LOCUS  
DEFINITION Canis familiaris adenylyl cyclase type VI mRNA sequence.  
ACCESSION M94968  
VERSION M94968.1 GI:163896  
KEYWORDS adenylyl cyclase type VI.  
SOURCE Canis familiaris cardiac muscle cDNA to mRNA.  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 4046)  
AUTHORS Katsushika,S., Chen,L., Kawabe,J., Nilakantan,R., Halnon,N.J.,  
Homcy,C.J. and Ishikawa,Y.  
TITLE Cloning and characterization of a sixth adenylyl cyclase isoform:  
types V and VI constitute a subgroup within the mammalian adenylyl  
cyclase family  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (18), 8774-8778 (1992)  
MEDLINE 92409599  
PUBMED 1528892  
FEATURES  
Location/Qualifiers  
Source  
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BASE COUNT 743 a 1206 c 1254 g 843 t  
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Best Local Similarity 89.5%; Pred. No. 6.2e-41;  
Matches 256; Conservative 0; Mismatches 27; Indels 3; Gaps 1;  
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Db 131 ATGTCGTTAGTGGCTCCTGGTCCCAAGTGGATGAACGGAAGACAGCTGGGT 190  
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QY 121 CCCCCTATATGAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCGCCCTCGGGGCC 180  
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QY 181 CCTCGTGCCCTGCGAGGATGACGCCCTTCATCCGAGGGGGCCCGCCANGCAAGGCAAG 240  
Db 308 CCTCGTGCCCTGCGAGGATGACGCCCTTCATCCGAGGGGGCCCGCCANGGCAAGGCAAG 367  
QY 241 GAACCTGGGGCTGGGGCAGTGGCTTCGAGATACCGAGTGCACGACGACGCG 286



RESULT	14
AX305965	
LOCUS	5841 bp DNA linear PAT 11-DEC-2001
DEFINITION	Sequence 716 from Patent WO0188188.
AX305965	
ACCESSION	
VERSION	AX305965.1 GI:17645322
KEYWORDS	house mouse.
SOURCE	Mus musculus
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1
AUTHORS	Ishikawa,K., Asai,S., Takahashi,Y., Nagata,T. and Ishii,Y.
TITLE	Method for examining ischemic conditions
JOURNAL	Patent: WO 0188188-A 716 22-NOV-2001;
FEATURES	School Juridical Person Nihon University (JP) Location/Qualifiers 1..5841 /organism="Mus musculus" /db_xref="taxon:10090"
BASE COUNT	1214 a 1558 c 1673 g 1396 t
ORIGIN	
Query Match	63.4%; Score 199.2; DB 6; Length 5841;

Best Local Similarity 82.3%; Pred. No. 1..1e-34;  
Matches 241; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

QY 1 ATGTCATGGTTTAAAGTGCCCTCGGTCCCTAAAGTGGATGAACGGAACCAAGCCTGGGGT 60  
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96 ATGTCATGGTTTAAAGTGCCCTCGGTCCCTAAAGTGGATGAACGGAACCAAGCCTGGGG 155  
QY 61 GAACGCAATGGCGAGAAGCGTTCCGCCGCCGCTGGCACTCGGCAGGTGGCTTCTGCACG 120  
Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
156 GAACGCAATGGCGAGAAGCG---CCCACGCCACGCGAATCGAGCCACTGGCTTCTGCACA 212  
QY 121 CCCGCTATATAGTCCTCCGGGATGACAGCCACCAGCCCCACCCCTCGCGGCCCC 180  
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213 CCTCGTACATAGTCCTCCAAGATGCGGAGCACCCAGCCCCACTCTCTGCAGCTCAC 272  
QY 181 CTTCTGGTCCCTCGGAGGATGACGCCCTTCATCGGAGGGCGGCCCCANGCAAGCGCAAG 240  
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273 ACTCGTGCCTCGGAGGATGAAGCCTTCATCAGGAGGGCGGCCCGCAGGGTGTG 332  
QY 241 GAACCTGGGGTGGCGGAGTGGCCCTGGGCTTGAAGATACCGAAGTGACAAC 293  
Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
333 GAGCTGGGGTGGCGTCACTGGGCTTGGGTTTTGACGACACTGAGGTGACCAC 385

RESULT 15  
MUSADCYC                5841 bp      mRNA      linear      ROD 27-APR-1993  
LOCUS                  Mouse adenylyl cyclase type VI mRNA, complete cds.  
DEFINITION             M33422  
ACCESSION             M33422.1 GI:191690  
VERSION                adenylyl cyclase; adenylyl cyclase type VI.  
KEYWORDS               Mus musculus cDNA to mRNA.  
SOURCE                Mus musculus  
ORGANISM               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
REFERENCE               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
AUTHORS               Yoshimura,M. and Cooper,D.M.  
TITLE                   Cloning and expression of a Ca(2+)-inhibitable adenylyl cyclase  
JOURNAL                from NCB-20 cells  
MEDLINE               Proc. Natl. Acad. Sci. U.S.A. 89 (15), 6716-6720 (1992)  
PUBMED                92357702  
FEATURES               1379717  
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                         AVGIESVLVFTSAIEMNTCHNPTRTCAARMNLTPADVTAHQQLNQLSYGLDPA  
                         ICEGAPTCSFPFYFVGNVLLSLASSVFLHSSIGKLTAMTFILGTFTYLVLLGP  
                         AIFDNVDLLGVGHGLASSNETFDGLDCPAGRVALKYMTPVILLVFALYLHAOOVE  
                         STARVDFLNKLGATKEKEMEELQATNRLLNLPLPKDVAHFLEARNRDELYYSC  
                         ECVAWNFSIANFSEFYEELEANNEGVECLRLNLEIADFDEISEERFQDEIKTI  
                         VTYMAAGSLNASTDOVGRRSHITALADYAMRLMEQMKIHNEFSFNFMQKIGLNNP  
                         GGAGTCAGKPOYDIWGNTVNVYSRMDKTPGVDIRIQVTTDLTVLAAGKQLECRGW

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BASE COUNT      1214 a 1558 c 1673 g 1396 t
ORIGIN
Query Match      63.4%; Score 199.2; DB 10; Length 5841;
Best Local Similarity 82.3%; Pred. No. 1.1e-34;
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QY 1 ATGTCATGTTTAGTGGCTCCTGTGTCCTAAAGTGGATGAACGGAAAAACAGCCCTGGGGT 60
Db 96 ATGTCATGTTTAGTGGCTCCTGTGTCCTCCAAAGTGGATGAACGGAAAAACAGCTTGGGG 155
QY 61 GAACGCAATGGCAGAGGTTTCGGCGCCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
Db 156 GAACGCAATGGCAGAGG---CCACGCCACGGCAATCGAGCCAGTGGCTTCTGCACG 212
QY 121 CCCCCTATATAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCGCCCTCGGGGCCCC 180
Db 213 CCTCGCTACATGAGCTGCCCTCAAGATGGGAGCCACCCAGCCCTCCTGCAGCTCAC 272
QY 181 CCTCGTGCCCTGGCAGGATGACGCCCTTCATCCGGAGGGGGGGCCCCANGCAAGGGCAAG 240
Db 273 ACTCGGTGCCCTGGCAGGATGAAGCCTTCATCAGGAGGGGGGGCCCGGGCAGGGGTGTG 332
QY 241 GAACCTGGGGCTCGGGCAGTGGCCCTTGGGCTTCGAAGATACCGAAGTGACAC 293
Db 333 GAGCTGGGGGCTCGGGTCACTGGGCTTGGGGTTTGACGACACTGAGGTGACCAC 385
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Job time : 953.507 secs

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2	90	15.8	277	4	O8W445	O8W445 homo sapien	
3	84.5	14.8	174	6	O95JT1	O95JT1 macaca fasc	
4	80.5	14.1	533	4	O96JK4	O96JK4 homo sapien	
5	78.5	13.8	1492	4	O9NU93	O9NU93 homo sapien	
6	78	13.7	2033	12	O9E940	O9E940 gallid herp	
7	78	13.7	2033	12	O9E938	O9E938 gallid herp	
8	77.5	13.6	1285	11	O7O305	O7O305 mus musculus	
9	77	13.5	167	10	O9AWN2	O9AWN2 oryza sativ	
10	77	13.5	389	6	O8SO95	O8SO95 nyctimene a	
11	76	13.3	285	16	O9RWY8	O9RWY8 deinococcus	
12	75	13.2	4203	5	O965G2	O965G2 caenorhabdi	
13	75	13.2	4219	5	O9NL87	O9NL87 caenorhabdi	
14	75	13.2	4488	5	O9TXK2	O9TXK2 caenorhabdi	
15	74.5	13.1	1014	2	O9RA53	O9RA53 thermus the	
16	74	13.0	1173	11	O63624	O63624 rattus norv	

RP SEQUENCE FROM N.A.

[illegible]

Best Local Similarity 36.0%; Pred. No. 8.6;  
Matches 18; Conservative 1; Mismatches 24; Indels 7; Gaps 1;  
QY 15 RKTAWGERNGKRSRRRCCTAGGCTCTPRYMSCLRDAPSPPTAGPPRC 64  
Db 20 RPAGNAARRSLPRTARRGGGAVAYP-----SAGPPPRGFGAPPRGP 62

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AC Q9AWN2;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE P0504D03.17 protein (OSUNBa0054L14.26 protein).  
GN P0504D03.17.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. NIPPONBARE;  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC  
clone:P0504D03."  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. NIPPONBARE;  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC  
clone:OSJNBa0054L14."  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP002970; BAB32968.1; -  
DR EMBL; AP003213; BAB60930.1; -  
SQ SEQUENCE 167 AA; 18298 MW; E992470613213752 CRC64;

Query Match 13.5%; Score 77; DB 10; Length 167;  
Best Local Similarity 34.0%; Pred. No. 1.1;  
Matches 33; Conservative 3; Mismatches 31; Indels 30; Gaps 5;  
QY 15 RKTAWGERNGKRSRRR-----GTRAGGCTCTPRYMSCLRDAPSPPTAG-PPRCPPWQ 66  
Db 24 RKT--CKRGQRDFARSLVCHGSLAGS-----PRPPAGVGPTC--- 63  
QY 67 DDAFIRRGPGXKGLGLRAVALGFEDTEVTTTPAGP 103  
Db 64 --QVRVRDGRGKGRKCTRAAALLTCGTRRPRGP 98

RESULT 10  
Q8SQ95 PRELIMINARY: PRT; 389 AA.  
AC Q8SQ95;  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Alpha 2B adrenergic receptor (Fragment).  
GN ADRA2B.  
OS Nymtiumene albiventer (common tube-nosed fruit bat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;  
OC Pteropodinae; Nymtiumene.  
OX NCBI\_TaxID=48988;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21819367; PubMed=11805285;  
RA Teeling E.C., Madsen O., Van Den Bussche R.A., de Jong W.W.,  
RA Stanhope M.J., Springer M.S.;  
RT "Microbat paraphyly and the convergent evolution of a key innovation

RT in Old World rhinolophoid microbats.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:1431-1436(2002).  
DR EMBL; AJ4119805; CAD11972.1; -  
KW Receptor.  
FT NON\_TER 1  
FT NON\_TER 389  
SQ SEQUENCE 389 AA; 42907 MW; C203401584C560EE CRC64;

Query Match 13.5%; Score 77; DB 6; Length 389;  
Best Local Similarity 34.9%; Pred. No. 2.7;  
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QY 26 KRSRRRTRAGGCTCTPRYMSCLRDAPSP--TPAGP---PRCPQDDAFIRRGPGXK 80  
Db 187 KRSHRGPRAGK-----GLRDSKQPHRVPGPSTLASCLATSGEASRSKPTKEK 238

QY 81 ELGLRAVALGFEDTEVTTTPAGP 103  
Db 239 EQG-----ETEDPGSPVLP 252

RESULT 11  
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AC Q9RWY8;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-WAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Hypothetical protein DR0527.  
GN DR0527.  
OS Deinococcus radiodurans.  
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;  
OC Deinococcaceae; Deinococcus.  
OX NCBI\_TaxID=1299;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=R1;  
RX MEDLINE=20036896; PubMed=10567266;  
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,  
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,  
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,  
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,  
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,  
RA Fraser C.M.;  
RT "Genome sequence of the radioresistant bacterium Deinococcus  
radiodurans R1."  
RL Science 286:1571-1577(1999).  
DR EMBL; AE001911; AAF10109.1; -  
DR TIGR; DR0527; -  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 285 AA; 31219 MW; 02FDDFAD6D9351E3 CRC64;

Query Match 13.3%; Score 76; DB 16; Length 285;  
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QY 3 WESGLLVKPVDERK---TAWGERNGKR--SRRRGTAGGCTCTPRYMSCLRDAPSPPT 56  
Db 189 WAGHVLAQRVDYTRKPYRARAWGAHDAALYVSRASAARA----LPGYF-----PK 234

QY 57 PAGPPR-----CFWQDDAFIRRG---GPXKKGKELG 83  
Db 235 PSRPERWGLGPCPWGKAAGRRAYERGSGAGGRDLG 269

RESULT 12  
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AC Q965G2;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)



Query Match 13.1%; Score 74.5; DB 2; Length 1014;  
Best Local Similarity 31.0%; Pred. No. 14;  
Matches 31; Conservative 8; Mismatches 38; Indels 23; Gaps 6;

Search completed: February 19, 2003, 15:35:17  
Job time : 96 secs



GenCore version 5.1.1.3  
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# OM protein - protein search, using sw model

Run on: February 19, 2003, 15:22:28 ; Search time 12 Seconds  
(without alignments)  
359,462 Million cell updates/sec

Title: US-09-750-240-2

Perfect score: 570

Sequence: 1 MSWFGSLLPVKDERKTAWG.....RAVALGFEDTEVTTPAGPL 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	545	95.6	1168	1	CYA6_HUMAN
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4	428	75.1	1166	1	CYA6_RAT
5	75	13.2	289	1	KLFD_MOUSE
6	73.5	12.9	719	1	DEND_RAT
7	73	12.8	512	1	IE63_HSV11
8	73	12.8	1168	1	MYSC_ACACA
9	72	12.6	232	1	VEGA_HUMAN
10	71.5	12.5	1816	1	AF6_HUMAN
11	69.5	12.2	1061	1	RNE_ECOLI
12	69.5	12.2	2205	1	POLN_RUBVT
13	69	12.1	384	1	A2AB_ELEMA
14	69	12.1	615	1	MENI_HUMAN
15	68.5	12.0	1250	1	TP3A_DROME
16	68.5	12.0	1265	1	CYA5_CANFA
17	68	11.9	1323	1	NME4_MOUSE
18	68	11.9	1323	1	NME4_RAT
19	67.5	11.8	511	1	IE63_HSV1E
20	67	11.8	425	1	I450_HUMAN
21	66.5	11.7	283	1	IPF1_HUMAN
22	66.5	11.7	365	1	IB01_SAGOE
23	66	11.6	251	1	HXB4_HUMAN
24	66	11.6	489	1	ACHE_XENLA
25	66	11.6	778	1	TAST_HUMAN
26	65.5	11.5	283	1	IPF1_MESAU
27	65.5	11.5	284	1	IPF1_MOUSE
28	65.5	11.5	365	1	IA01_SAGOE
29	65.5	11.5	659	1	VST2_HEVME
30	65.5	11.5	946	1	IP3L_HUMAN
31	65	11.4	269	1	CEBD_HUMAN
32	65	11.4	340	1	NIF1_HUMAN
33	65	11.4	376	1	VASP_MOUSE

## ALIGNMENTS

### RESULT 1

ID	CYA6_HUMAN	STANDARD;	PRT;	1168 AA.
AC	O43306; Q9NR75;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Adenylate cyclase, type VI (EC 4.6.1.1) (ATP pyrophosphate-lyase)			
DE	CA(2+)-inhibitable adenyl cyclase.			
GN	ADCY6 OR KIAA0422.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Thyroid.			
RA	Wicker R., Gascon Catalan A., Cailleux A.-F., Starenki D., Stengel D.,			
RA	Sarasin A., Suarez H.G.;			
RT	"Cloning and expression of human adenyl cyclase type VI from normal			
RT	thyroid tissues.";			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBDJ databases.			
RP	[2]			
RP	SEQUENCE OF 142-1168 FROM N.A.			
RC	TISSUE=Brain;			
RA	MEDLINE=98116655; Pubmed=9455477;			
RA	Ishikawa K.-I., Nagase T., Nakajima D., Seki N., Ohira M.,			
RA	Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;			
RT	"Prediction of the coding sequences of unidentified human genes. VIII.			
RT	78 new cDNA clones from brain which code for large proteins in			
RT	vitro.";			
RL	DNA Res. 4:307-313(1997).			
CC	-I- FUNCTION: THIS A MEMBRANE-BOUND, CA(2+)-INHIBITABLE ADENYL CYCLASE (BY SIMILARITY).			
CC	-I- CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.			
CC	-I- ENZYME REGULATION: INHIBITION BY CA(2+) IN THE SUBMICROMOLAR			
CC	CONCENTRATION RANGE (BY SIMILARITY).			
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-I- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.			
CC	-I- SIMILARITY: BELONGS TO ADENYL CYCLASE CLASS-4/GUANYLYL CYCLASE FAMILY.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; AF250226; AAP82478.1; -			
CC	EMBL; AB007882; BAA24852.1; -			
CC	HSSP; P19754; IAWK.			
CC	Genew; HGNC:237; ADCY6.			
CC	MIM; 600294; -			
CC	InterPro; IPR001054; G_cyclase.			

34	64.5	11.3	250	1	HXB4_MOUSE
35	64.5	11.3	669	1	COTE_HUMAN
36	64	11.2	245	1	VE4_HPV5B
37	64	11.2	423	1	PPAL_HUMAN
38	64	11.2	519	1	ERR1_HUMAN
39	64	11.2	913	1	UBPK_HUMAN
40	64	11.2	928	1	RB_HUMAN
41	64	11.2	2167	1	SHK1_RAT
42	63.5	11.1	365	1	IA24_HUMAN
43	63.5	11.1	365	1	IC01_SAGOE
44	63.5	11.1	660	1	VST2_HEVBU
45	63.5	11.1	660	1	VST2_HEVNY

PI0284	mus musculus
P81408	homo sapien
P26550	human papil
P11117	homo sapien
P11474	homo sapien
Q9Y2K6	homo sapien
P06400	homo sapien
Q9WV48	rattus norv
P05534	homo sapien
P30517	sagunus oe
P29336	hepatitis e
Q04611	hepatitis e

```
DR Pfam; PF00211; guanylate_cyc; 2.
DR SMART; SM00044; CYCC; 2.
DR PROSITE; PS00452; GUANYLATE_CYCLASES.1; 2.
DR PROSITE; PS00452; GUANYLATE_CYCLASES.2; 2.
KW Lyase; CAMP synthesis; Transmembrane; Glycoprotein; Repeat.
FT DOMAIN 1 151
FT TRANSMEM 152 168
FT TRANSMEM 181 197
FT TRANSMEM 214 230
FT TRANSMEM 239 255
FT TRANSMEM 259 275
FT TRANSMEM 289 305
FT DOMAIN 306 673
FT TRANSMEM 674 691
FT TRANSMEM 702 718
FT TRANSMEM 743 759
FT DOMAIN 760 819
FT TRANSMEM 820 836
FT TRANSMEM 839 855
FT TRANSMEM 897 913
FT TRANSMEM 914 1168
FT CARBOHYD 793 793
FT CONFLICT 762 814
FT CONFLICT 762 814
SQ SEQUENCE 1168 AA; 130615 MW; 127BB6E67F73AA61 CRC64;

Query Match          95.6%; Score 545; DB 1; Length 1168;
Best Local Similarity 97.1%; Pred. No. 9.9e-46;
Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSWFSGLLPKVDERTKATWANGKRRGCTRAGGCTPRYMSCLRDAPSPPTPAGP 60
DB 1 MSWFSGLLPKVDERTKATWANGKRRGCTRAGGCTPRYMSCLRDAPSPPTPAGP 60
QY 61 PRCPQDDAFIRRGPGXKGKELGRAVALGFEDTEVTTPAG 102
DB 61 PRCPQDDAFIRRGPGXKGKELGRAVALGFEDTEVTTPAG 102

RESULT 2
CYA6_CANFA
ID CYA6_CANFA STANDARD; PRT; 1165 AA.
AC P30804;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Adenylate cyclase, type VI (EC 4.6.1.1) (ATP pyrophosphate-lyase)
DE (Ca(2+)-inhibitable adenylate cyclase).
GN ADCY6.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=92409599; PubMed=1528892;
RA Katsushika S., Chen L., Kawabe J., Nilakantan R., Halnon N.J.,
RA Homcy C.J., Ishikawa Y.;
RT "Cloning and characterization of a sixth adenylate cyclase isoform:
RT types V and VI constitute a subgroup within the mammalian adenylate
RT cyclase family."
RT Proc. Natl. Acad. Sci. U.S.A. 89:8774-8778(1992).
CC -!- FUNCTION: THIS A MEMBRANE-BOUND, CA(2+)-INHIBITABLE ADENYLATE
CC CYCLASE.
CC -!- CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.
CC -!- ENZYME REGULATION: INHIBITION BY CA(2+) IN THE SUBMICROMOLAR
CC CONCENTRATION RANGE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO ADENYLATE CYCLASE CLASS-4/GUANYLYL CYCLASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M94968; -; NOT_ANNOTATED_CDS.
DR PIR; A46180; A46180.
DR HSP; P19754; 1ANK.
DR InterPro; IPR001054; G_cyclase.
DR Pfam; PF00211; guanylate_cyc; 2.
DR SMART; SM00044; CYCC; 2.
DR PROSITE; PS00452; GUANYLATE_CYCLASES.1; 2.
DR PROSITE; PS00452; GUANYLATE_CYCLASES.2; 2.
KW Lyase; CAMP synthesis; Transmembrane; Glycoprotein; Repeat.
FT DOMAIN 1 149
FT TRANSMEM 150 166
FT TRANSMEM 179 195
FT TRANSMEM 212 228
FT TRANSMEM 237 253
FT TRANSMEM 257 273
FT TRANSMEM 287 303
FT DOMAIN 304 670
FT TRANSMEM 671 688
FT TRANSMEM 699 715
FT TRANSMEM 740 756
FT DOMAIN 757 816
FT TRANSMEM 817 833
FT TRANSMEM 836 852
FT TRANSMEM 894 910
FT DOMAIN 911 1165
FT CARBOHYD 790 790
FT CARBOHYD 875 875
SQ SEQUENCE 1165 AA; 130323 MW; BA9D2D329120615E CRC64;

Query Match          82.9%; Score 472.5; DB 1; Length 1165;
Best Local Similarity 83.2%; Pred. No. 1.2e-38;
Matches 89; Conservative 2; Mismatches 11; Indels 5; Gaps 2;

QY 1 MSWFSGLLPKVDERTKATWANGKRRGCTRAGGCTPRYMSCLRDAPSPPTPAGP 60
DB 1 MSWFSGLLPKVDERTKATWANGKRRGCTRAGGCTPRYMSCLRDAPSPPTPAGP 59
QY 61 PRCPQDDAFIRRGPGXKGKELGRAVALGFEDTEVTTPAG 103
DB 61 PRCPQDDAFIRRGPGXKGKELGRAVALGFEDTEVTTPAG 103

RESULT 3
CYA6_MOUSE
ID CYA6_MOUSE STANDARD; PRT; 1165 AA.
AC Q01341;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Adenylate cyclase, type VI (EC 4.6.1.1) (ATP pyrophosphate-lyase)
DE (Ca(2+)-inhibitable adenylate cyclase).
GN ADCY6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92357702; PubMed=1379717;
RA Yoshimura M., Cooper D.M.F.;
RT "Cloning and expression of a Ca(2+)-inhibitable adenylate cyclase from
RT NCB-20 cells."
RT Proc. Natl. Acad. Sci. U.S.A. 89:6716-6720(1992).
RN [2]
RP SEQUENCE OF 10-1165 FROM N.A.
RX MEDLINE=93076707; PubMed=1332848;
```

60 TRCPQDEAFIRRAPGPGRGVELGRLSRVALGFDDTEV-TTPMG 100

Db

RESULT 4

CYA6\_RAT

ID	CYA6_RAT	STANDARD;	PRT; 1166 AA.
AC	Q03343;		
DT	01-OCT-1993 (Rel. 27, Created)		
DT	01-OCT-1993 (Rel. 27, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Adenylate cyclase, type VI (EC 4.6.1.1) (ATP pyrophosphate-lyase)		
DE	(Ca(2+)-inhibitable adenyl cyclase).		
GN	ADCY6.		
OS	Eukaryote (Rat).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus		
OC	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=93077589; PubMed=1332969;		
RA	Krupinski J., Lehman T.C., Frankenfield C.D., Zwaagstra J.C.,		
RA	Watson P.A.;		
RT	"Molecular diversity in the adenyl cyclase family. Evidence for		
RT	eight forms of the enzyme and cloning of type VI.";		
RL	J. Biol. Chem. 267:24858-24862(1992).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Liver;		
RX	MEDLINE=93028552; PubMed=1409703;		
RA	Premont R.T., Chen J., Ma H.-W., Ponnappalli M., Iyengar R.;		
RT	"Two members of a widely expressed subfamily of hormone-stimulated		
RT	adenyl cyclases.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 89:9809-9813(1992).		
CC	-1- FUNCTION: THIS A MEMBRANE-BOUND, CA(2+)-INHIBITABLE ADENYLYL CYCLASE.		
CC	-1- CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.		
CC	-1- ENZYME REGULATION: INHIBITION BY CA(2+) IN THE SUBMICROMOLAR CONCENTRATION RANGE.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.		
CC	-1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE FAMILY.		
CC	-----		
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CC	-----		
DR	EMBL; L01115; AAA40676.1; -		
DR	EMBL; M96160; AAA40678.1; ALT_INIT.		
DR	PIR; A45145; A45145.		
DR	HSP; P19754; IAWK.		
DR	InterPro; IPR001054; G_cyclase.		
DR	Pfam; PF00211; guanylate_cyc; 2.		
DR	SMART; SM00044; CYC; 2		
DR	PROSITE; PS00452; GUANYLATE_CYCLASES_1; 2.		
DR	PROSITE; PSS01125; GUANYLATE_CYCLASES_2; 2.		
KW	Lyase; CAMP synthesis; Transmembrane; Glycoprotein; Repeat.		
FT	DOMAIN 1 149		
FT	TRANSMEM 150 166		
FT	TRANSMEM 179 195		
FT	TRANSMEM 212 228		
FT	TRANSMEM 237 253		
FT	TRANSMEM 257 273		
FT	TRANSMEM 287 303		
FT	DOMAIN 304 671		
FT	TRANSMEM 672 689		
FT	TRANSMEM 700 716		
FT	TRANSMEM 741 757		
FT	DOMAIN 758 817		
FT	EXTRACELLULAR (POTENTIAL)		

```
FT TRANSMEM 818 834 POTENTIAL.
FT TRANSMEM 837 853 POTENTIAL.
FT TRANSMEM 895 911 POTENTIAL.
FT DOMAIN 912 1166 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 791 791 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 876 876 K -> E (IN REF. 2).
FT CONFLICT 80 130 R -> P (IN REF. 2).
FT CONFLICT 130 130 R -> P (IN REF. 2).
FT CONFLICT 538 538 G -> A (IN REF. 2).
FT CONFLICT 790 790 I -> L (IN REF. 2).
SQ SEQUENCE 1166 AA; 130506 MW; 5042C650546E4E79 CRC64;

Query Match 75.1%; Score 428; DB 1; Length 1166;
Best Local Similarity 78.4%; Pred. No. 2.6e-34;
Matches 80; Conservative 8; Mismatches 12; Indels 2; Gaps 2;

QY 1 MSWESGLLVKPKYDERKTANGERNQKRSRRCTRAGGCTPRYMSCLRDAPSPPTPACG 60
Db 1 MSWESGLLVKPKYDERKTANGERNQKRP-RQATRARGFCAPRYMSCLKNVPPSPPTPAAR 59
QY 61 PRCPWQDDAFIRRGFPKXKELGLRAVALGFEDTEVTTTPAG 102
Db 60 TRCPWQDEAFIRRGFGVKGKGLRSLVALGPDTEV-TTPMG 100

RESULT 5
KLFID_MOUSE
ID KLFID_MOUSE STANDARD; PRT; 289 AA.
AC Q9JZ6: Q9JH9: Q9ESX3;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE kruepel-like factor 13 (Transcription factor BTEB3) (Basic
DE transcription element binding protein 3) (BTE-binding protein 3)
DE (RANTES factor of late activated T lymphocytes-1) (RFLAT-1) (Erythroid
DE transcription factor FKLF-2).
GN KLF13 OR BTEB3 OR FKLF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=20115087; PubMed=10642511;
RA Martin K.M., Cooper W.N., Metcalfe J.C., Kemp P.R.;
RT "Mouse BTEB3, a new member of the basic transcription element binding
RT protein (BTEB) family, activates expression from GC-rich minimal
RT promoter regions";
RL Biochem. J. 345:529-533(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B6D2F2; TISSUE=Yolk;
RX MEDLINE=20287401; PubMed=10828046;
RA Asano H., Li X.S., Stamatiyanopoulos G.;
RT "FKLF-2: a novel Kruppel-like transcriptional factor that activates
RT globin and other erythroid lineage genes.";
RL Blood 95:3578-3584(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=20541714; PubMed=11087666;
RA Schohy S., Gabant P., Van Reeth T., Hertveldt V., Dreze P.-L.,
RA Van Vooren P., Riviere M., Szpirer J., Szpirer C.;
RT "Identification of KLF13 and KLF14 (SP6), novel members of the SP/XKLF
RT transcription factor family.";
RL Genomics 70:93-101(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Song A., Thamatrakoln K., Krensky A.M.;
RT "Identification of Mus musculus cDNA for RANTES factor of late
RT activated T lymphocytes-1.";
```

```
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Transcription factor that activates expression from GC-
CC rich minimal promoter regions, including genes in the cells of the
CC erythroid lineage.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: BELONGS TO THE SP1 FAMILY OF C2H2-TYPE ZINC-FINGER
CC PROTEINS.
CC -----
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CC -----
CC EMBL; AJ245644; CAB75887.1; -
CC EMBL; AF251796; AAF73964.1; -
CC EMBL; AJ275987; CAC06697.1; -
CC EMBL; AF252285; AAF65826.1; -
CC HSSP; P08047; 1SP2.
CC TRANSFAC; T05052; -
CC MGD; MGI:1354948; Klf13.
CC InterPro; IPR000822; Znf_C2H2.
CC Pfam; PF00096; zf_C2H2; 6.
CC ProDom; PD000003; Znf_C2H2; 1.
CC SMART; SM00355; Znf_C2H2; 3.
CC PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
CC PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
CC Transcription regulation; DNA-binding; Activator; Nuclear protein;
KW Repeat; Zinc-finger; Metal-binding.
FT DOMAIN 2 146 ALA/PRO-RICH.
FT DOMAIN 149 169 ARG/LYS-RICH (BASIC).
FT DOMAIN 168 250 ZINC FINGERS.
FT 2N_FING 168 192 C2H2-TYPE.
FT ZN_FING 198 222 C2H2-TYPE.
FT 2N_FING 228 250 C2H2-TYPE.
FT DOMAIN 265 288 SER-RICH.
FT CONFLICT 13 30 ECLVSMSSRAVVHEPREG -> SASCPQPSRARAAGR
FT CONFLICT 32 32 E -> R (IN REF. 1).
FT CONFLICT 43 43 P -> L (IN REF. 1).
SQ SEQUENCE 289 AA; 31136 MW; E248EF12890DA090 CRC64;

Query Match 13.2%; Score 75; DB 1; Length 289;
Best Local Similarity 27.6%; Pred. No. 1.9;
Matches 29; Conservative 7; Mismatches 41; Indels 28; Gaps 4;

QY 9 VPKVDERKTA-----WGRNGQ-----KSRRRGTGAGGCTPRYMSCLRDAP 51
Db 45 LPRVDERRDGKDSALFVVVARILADLNQAPAPAPAPAEERREGAARAKRTPCRLPPAPPAP 104
QY 52 PPSP-----TPAGPRCPQDD--AFIRGGPKKGLR 85
Db 105 PPGPEPSPGQAGAPAAPSPAWSEPEAALEQEPGAGSGEPLR 149

RESULT 6
DEND_RAT
ID DEND_RAT STANDARD; PRT; 719 AA.
AC P50617;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Dendrin (Fragment).
GN DDN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
```

RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
RX MEDLINE=97073143; PubMed=8915891;  
RA Neuner-Jehle M., Denzot J.P., Borbely A.A., Mallet J.;  
RT "Characterization and sleep deprivation-induced expression modulation  
of dendrin, a novel dendritic protein in rat brain neurons.";  
RL J. Neurosci. Res. 46:138-151(1996).  
CC -!- MISCELLANEOUS: MODULATED BY SLEEP DEPRIVATION.  
CC  
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CC or send an email to license@isb-sib.ch).  
CC  
CC EMBL: X96589; CAA65407.1; --  
DR NON\_TER 1  
FT  
SQ SEQUENCE 719 AA; 77208 MW; 89E2ED094514EAFB CRC64;  
Query Match 12.9%; Score 73.5; DB 1; Length 719;  
Best Local Similarity 28.9%; Pred. No. 6.5;  
Matches 26; Conservative 7; Mismatches 30; Indels 27; Gaps 3;  
  
QY 13 DERKTAWGNGOKRRRRGTRAGG-----FCTPRYMSCLRDAP----- 52  
Db 124 EKRAASQEREAKETKRR-KKAGDAGVPSAPPRAPELRRAAQPTGPFVFSRPERFGQ 182  
QY 53 -----PSPTPAGPPRCPWQDDAFIRGGP 76  
Db 183 VGRAPRPSALPOGDGPVAVAGWGMGRDRPGP 212  
  
RESULT 7  
IE63\_HSV11  
ID IE63\_HSV11 STANDARD; PRT; 512 AA.  
AC P10238;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Transcriptional regulator IE63 (VIM63) (ICP27).  
GN UL54.  
OS Herpes simplex virus (type 1 / strain 17).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Simplexvirus.  
OX NCBI\_TaxID=10299;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88274327; PubMed=2839594;  
RA McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,  
RA McNab D., Perry L.J., Scott J.E., Taylor P.;  
RT "The complete DNA sequence of the long unique region in the genome of  
herpes simplex virus type 1.";  
RL J. Gen. Virol. 69:1531-1574 (1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89036163; PubMed=2846760;  
RA Perry L.J., McGeoch D.J.;  
RT "The DNA sequences of the long repeat region and adjoining parts of  
the long unique region in the genome of herpes simplex virus type  
1.";  
RL J. Gen. Virol. 69:2831-2846 (1988).  
CC -!- FUNCTION: INVOLVED IN THE DOWN-REGULATION OF VIRAL IMMEDIATE-EARLY  
CC GENES AND ACTS IN COMBINATION WITH ICP0 AND ICP4 AS AN ACTIVATOR  
CC OF LATE GENES.  
CC -!- PTM: PHOSPHORYLATED.  
CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL54,  
CC HSV-2 UL54, EBV-1 5, VZV 4, EBV BMLF1, HCMV UL69, AND HVS-1 57.  
CC  
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CC or send an email to license@isb-sib.ch).  
CC  
CC EMBL: D10879; BAA01700.1; --  
DR EMBL: X14112; CAA32290.1; --  
DR PIR: I30089; WMBEY4.  
KW Early protein; Transcription regulation; DNA-binding; Phosphorylation.  
SQ SEQUENCE 512 AA; 55252 MW; 97DF74A2B7E63A85 CRC64;  
Query Match 12.8%; Score 73; DB 1; Length 512;  
Best Local Similarity 27.5%; Pred. No. 5.2;  
Matches 30; Conservative 8; Mismatches 53; Indels 18; Gaps 4;  
  
QY 8 LVPKVDKRTAWGNGOKRRRRG--TRAGGCTPRYMSCLRDAPSPPTPAGP-PRCP 64  
Db 127 LQPPPTKAQPARGRRGRGRRGCGCAADGLSDPR-----RRAPTRNRPGGPRGAG 181  
QY 65 WQDDAFIRGGPXKKGK-----LGLRAVALGFEDTEVTTTPAGP 103  
Db 182 WTDGPGAPHGCEAWRGSEQDPDPGGQRTGRVGRQAPPLMTLAIAPPPADP 230  
  
RESULT 8  
MYSC\_ACACA  
ID MYSC\_ACACA STANDARD; PRT; 1168 AA.  
AC P10569;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Myosin IC heavy chain.  
GN MIC.  
OS Acanthamoeba castellanii (Amoeba).  
OC Eukaryota; Acanthamoebidae; Acanthamoeba.  
OX NCBI\_TaxID=5755;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88016163; PubMed=3477803;  
RA Jung G., Korn E.D., Hammer J.A. III;  
RT "The heavy chain of Acanthamoeba myosin IB is a fusion of myosin-like  
and non-myosin-like sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:6720-6724 (1987).  
RN [2]  
RP PARTIAL SEQUENCE FROM N.A.  
RX MEDLINE=86259656; PubMed=3014500;  
RA Hammer J.A. III, Jung G., Korn E.D.;  
RT "Genetic evidence that Acanthamoeba myosin I is a true myosin.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:4655-4659 (1986).  
RN [3]  
RP PHOSPHORYLATION SITE.  
RX MEDLINE=90037074; PubMed=2530230;  
RA Brzeska H., Lynch T.J., Martin B., Korn E.D.;  
RT "The localization and sequence of the phosphorylation sites of  
Acanthamoeba myosins I. An improved method for locating the  
phosphorylated amino acid.";  
RL J. Biol. Chem. 264:19340-19348 (1989).  
CC -!- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAS ATPASE  
CC ACTIVITY THAT IS ACTIVATED BY F-ACTIN.  
CC -!- SUBUNIT: MYOSIN I HEAVY CHAIN IS SINGLE-HEADED. DIMER OF A HEAVY  
CC AND A LIGHT CHAIN. INABILITY TO SELF-ASSEMBLE INTO FILAMENTS.  
CC -!- DOMAIN: TH.1 BINDS DIRECTLY TO ANIONIC PHOSPHOLIPID MEMBRANES;  
CC MYOSINS I CAN THEREFORE MOVE ACTIN RELATIVE TO MEMBRANES AND VICE  
CC VERSA. TH.2 AND SH3 BIND TIGHTLY TO F-ACTIN; THIS TOGETHER WITH  
CC THE NUCLEOTIDE-SENSITIVE SITE IN THE HEAD, ALLOWS SINGLE MOLECULES  
CC OF MYOSIN I TO CROSS-LINK ACTIN FILAMENTS.  
CC -!- MISCELLANEOUS: THIS ORGANISM EXPRESSES AT LEAST THREE ISOFORMS OF  
CC MYOSIN I HEAVY-CHAIN, ENCODED BY GENES MIA, MIB, AND MIT.  
CC -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.  
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
CC -!- CAUTION: WAS ORIGINALLY THOUGHT TO BE MYOSIN IB.  
CC  
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CC EMBL; J02974; AAA27707.1; -.
CC PIR; A33891; MWAXIC.
CC HSSP; P08799; 1MND.
CC InterPro; IPR001452; SH3.
CC InterPro; IPR001609; myosin_head.
CC Pfam; PF00018; SH3; 1.
CC Pfam; PF00063; myosin_head; 1.
CC PRINTS; PR00193; MYOSINHEAVY.
CC PRINTS; PR00452; SH3DOMAIN.
CC ProDom; PD000066; SH3; 1.
CC ProDom; PD000355; myosin_head; 1.
CC SMART; SM00242; MYSC; 1.
CC SMART; SM00326; SH3; 1.
CC PROSITE; PS00002; SH3; 1.
KW Myosin; ATP-binding; Phosphorylation; Multigene family; SH3 domain.
FT DOMAIN 1 670
FT MYOSIN HEAD-LIKE.
FT TAIL HOMOLGY REGION 1 (TH.1).
FT DOMAIN 671 922
FT GLY/PRO/ALA-RICH (TH.2).
FT DOMAIN 923 975
FT SH3.
FT DOMAIN 976 1035
FT SH3.
FT DOMAIN 1036 1168
FT GLY/PRO/ALA-RICH (TH.2).
FT BIND 101 108
FT ATP (POTENTIAL).
FT MOD_RES 311 311
FT PHOSPHORYLATION.
SQ SEQUENCE 1168 AA; 127309 MW; D07084B373A37A32 CRC64;

Query Match 12.8%; Score 73; DB 1; Length 1168;
Best Local Similarity 25.8%; Pred. NO. 12;
Matches 24; Conservative 13; Mismatches 32; Indels 24; Gaps 4;

QY 1 MSWFSGLLPVKYDERKTAW--GERNGKRSRRRGTRAGGCTFPRYMSCLRDAPSPPTA 58
Db 995 LTFNEGAVVTIVNKSPNDWGEELNGQR-----GVFPASVVELIPRAAAPGPGS 1044

QY 59 GPPR-----CPWODDAFIR-RGGFXKG 79
Db 1045 GGP RPAPP GKGSGRAAPMGPGMRGCGPAPG 1077

RESULT 9
VEGA_HUMAN
ID VEGA_HUMAN STANDARD; PRT; 232 AA.
AC P15692; Q16889; O60720; O75875; Q9UL23; Q9UH58; Q9H1W9; Q9H1W8;
AC Q96NW5;
DT 01-APR-1990 (Rel. 14, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE permeability factor) (VPF).
GN VEGF OR VEGFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS VEGF189 AND VEGF165).
RX MEDLINE=90069608; PubMed=2479986;
Leung D.W., Cachianes G., Kiang W.-J., Goeddel D.V., Ferrara N.;
RT "Vascular endothelial growth factor is a secreted angiogenic
RT mitogen.";
RL Science 246:1306-1309(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM VEGF189). AND PARTIAL SEQUENCE.
RX MEDLINE=90069609; PubMed=2479987;
Keck P.J., Hauser S.D., Krivi G., Sanzo K., Warren T., Feder J.,
RA Connolly D.T.;
RT "Vascular permeability factor, an endothelial cell mitogen related to
RT PDGF.";
RL Science 246:1309-1312(1989).
```

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RN [3]
RP SEQUENCE FROM N.A. (ISOFORM VEGF189).
RX MEDLINE=91268072; PubMed=1711045;
Tischer E., Mitchell R., Hartman T., Silva M., Gospodarowicz D.,
RA Fiddes J.C., Abraham J.A.;
RT "The human gene for vascular endothelial growth factor. Multiple
RT protein forms are encoded through alternative exon splicing.";
RL J. Biol. Chem. 266:11947-11954(1991).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM VEGF206).
RX MEDLINE=92168017; PubMed=1791831;
Houck K.A., Ferrara N., Winer J., Cachianes G., Li B., Leung D.W.;
RA "The vascular endothelial growth factor family: identification of a
RT fourth molecular species and characterization of alternative splicing
RT of RNA.";
RL Mol. Endocrinol. 5:1806-1814(1991).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM VEGF165).
RX MEDLINE=92231879; PubMed=1567395;
Weindel K., Marne D., Weich H.A.;
RA "AIDS-associated Kaposi's sarcoma cells in culture express vascular
RT endothelial growth factor.";
RL Biochem. Biophys. Res. Commun. 183:1167-1174(1992).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM VEGF145).
RX MEDLINE=97207275; PubMed=9054410;
Poltorak Z., Cohen T., Sivan R., Kandellis Y., Spira G., Vlodavsky I.,
RA Keshet E., Neufeld G.;
RA "VEGF145, a secreted vascular endothelial growth factor isoform that
RT binds to extracellular matrix.";
RL J. Biol. Chem. 272:7151-7158(1997).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM VEGF183).
RC TISSUE=Kidney;
RX MEDLINE=99096474; PubMed=9878851;
Lei J., Jiang A., Pei D.;
RT "Identification and characterization of a new splicing variant of
RT vascular endothelial growth factor: VEGF183.";
RL Biochim. Biophys. Acta 1443:400-406(1998).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM VEGF165).
RC TISSUE=Breast;
RX MEDLINE=98119755; PubMed=9450968;
Claffey K.P., Shih S.-C., Mullen A., Dziennis S., Cusick J.L.,
RA Abrams K.R., Lee S.W., Detmar M.;
RT "Identification of a human VPE/VEGF 3' untranslated region mediating
RT hypoxia-induced mRNA stability.";
RL Mol. Biol. Cell 9:469-481(1998).
RN [9]
RP SEQUENCE OF 114-209 FROM N.A. (ISOFORM VEGF183).
RC TISSUE=Retina;
RX MEDLINE=99165303; PubMed=10067980;
Jingjing L., Xue Y., Agarwal N., Roque R.S.;
RT "Human Muller cells express VEGF183, a novel spliced variant of
RT vascular endothelial growth factor.";
RL Invest. Ophthalmol. Vis. Sci. 40:752-759(1999).
RN [10]
RP SEQUENCE FROM N.A. (ISOFORM VEGF165).
RC TISSUE=Hemangioendothelioma;
RA Murata H., Fukushima J., Hattori S., Okuda K., Yanagi H.;
RT "Human cDNA for the vascular endothelial growth factor isoform
RT VEGF165.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A. (ISOFORM VEGF148).
RC TISSUE=Renal glomerulus;
RX MEDLINE=99394945; PubMed=10464055;
Whittle C.J., Gillespie K.M., Harrison R., Mathieson P.W.,
RA Harper S.J.;
RT "Heterogeneous vascular endothelial growth factor (VEGF) isoform mRNA
RT and receptor mRNA expression in human glomeruli, and the
RT identification of VEGF148 mRNA, a novel truncated splice variant.";
RL Clin. Sci. 97:303-312(1999).
```

RT [12] SEQUENCE FROM N.A. (ISOFORM VEGF121).  
RP Sato J.D., Whitney R.G.;  
RA "Human cDNA for vascular endothelial growth factor isoform VEGF121.";  
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
RN [13]  
RN SEQUENCE FROM N.A.  
RA Williams S.;  
RP Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [14]  
RN SEQUENCE OF 23-232 FROM N.A. (VEGF165).  
RA Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,  
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;  
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [15]  
RN PRELIMINARY SEQUENCE OF 27-36; 43-50 AND 59-81.  
RX MEDLINE=90062112; PubMed=2584205.  
RA Connolly D.T., Olander J.V., Heuvelman D., Nelson R., Monsell R.,  
RA Siegel N., Haymore B.L., Leimgruber R., Feder J.;  
RT "Human vascular permeability factor. Isolation from U937 cells.";  
RL J. Biol. Chem. 264:20017-20024(1989).  
RN [16]  
RN SEQUENCE OF 27-41.  
RX MEDLINE=93145946; PubMed=7678805;  
RA Fiebig B.L., Jaeger B., Schoellmann C., Weindel K., Wilting J.,  
RA Kochs G., Marne D., Hug H., Weich H.A.;  
RT "Synthesis and assembly of functionally active human vascular  
endothelial growth factor homodimers in insect cells.";  
RL Eur. J. Biochem. 211:19-26(1993).  
RN [17]  
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 34-135.  
RX MEDLINE=97352774; PubMed=9207067;  
RA Muller Y.A., Li B., Christinger H.W., Wells J.A., Cunningham B.C.,  
RA de Vos A.M.;  
RT "Vascular endothelial growth factor: crystal structure and functional  
mapping of the kinase domain receptor binding site.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:7192-7197(1997).  
RN [18]  
RN X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 34-135.  
RX MEDLINE=98035455; PubMed=9351807;  
RA Muller Y.A., Christinger H.W., Keyt B.A., de Vos A.M.;  
RT "The crystal structure of vascular endothelial growth factor (VEGF)  
refined to 1.93-A resolution: multiple copy flexibility and receptor  
binding.";  
RL Structure 5:1325-1338(1997).  
RN [19]  
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 39-134.  
RX MEDLINE=99119204; PubMed=9922142;  
RA Wiesmann C., Christinger H.W., Cochran A.G., Cunningham B.C.,  
RA Fairbrother W.J., Keenan C.J., Meng G., de Vos A.M.;  
RT "Crystal structure of the complex between VEGF and a receptor-blocking  
peptide.";  
RL Biochemistry 37:17765-17772(1998).  
RN [20]  
RN STRUCTURE BY NMR OF 34-135.  
RX MEDLINE=97477915; PubMed=9336848;  
RA Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,  
RA Starovasnik M.A.;  
RT "1H, 13C, and 15N backbone assignment and secondary structure of the  
receptor-binding domain of vascular endothelial growth factor.";  
RL Protein Sci. 6:2250-2260(1997).  
RN [21]  
RN STRUCTURE BY NMR OF 137-215.  
RX MEDLINE=98298440; PubMed=9634701;  
RA Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,  
RA Starovasnik M.A.;  
RT "Solution structure of the heparin-binding domain of vascular  
endothelial growth factor.";  
RL Structure 6:637-648(1998).  
RN [22]  
RN FUNCTION.  
RX MEDLINE=21320570; PubMed=11427521;  
RA Murphy J.F., Fitzgerald D.J.;

RT "Vascular endothelial growth factor induces cyclooxygenase-dependent  
proliferation of endothelial cells via the VEGF-2 receptor.";  
RL FASEB J. 15:1667-1669(2001).  
CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and  
endothelial cell growth. It induces endothelial cell  
proliferation, promotes cell migration, inhibits apoptosis, and  
induces permeabilization of blood vessels. It binds to the  
CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and  
CC heparin. Neuropilin-1 binds isoforms VEGF-165 and VEGF-145.  
CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer  
CC with PlGF (By similarity).  
CC -!- SUBCELLULAR LOCATION: VEGF121 is acidic and freely secreted.  
CC VEGF165 is more basic, has heparin-binding properties and,  
CC although a significant proportion remains cell-associated, most is  
CC freely secreted. VEGF189 is very basic; it is cell-associated  
CC after secretion and is bound avidly by heparin and the  
CC extracellular matrix, although it may be released as a soluble  
CC form by heparin, heparinase or plasmin.  
CC -!- ALTERNATIVE PRODUCTS: 7 isoforms; VEGF206 (shown here), VEGF189,  
CC VEGF183, VEGF165/VEGF, VEGF148, VEGF145 and VEGF121; may be  
CC produced by alternative splicing.  
CC -!- TISSUE SPECIFICITY: The VEGF189, VEGF-165 and VEGF-121 isoforms  
CC are widely expressed, whereas the VEGF206 and VEGF-145 are  
CC uncommon.  
CC -!- INDUCTION: Regulated by growth factors, cytokines, gonadotropins,  
CC nitric oxide, hypoxia, hypoglycemia and oncogenic mutations.  
Query Match 12.6%; Score 72; DB 1; Length 232;  
Best Local Similarity 32.8%; Pred. NO. 3.1;  
Matches 21; Conservative 5; Mismatches 16; Indels 22; Gaps 3;  
QY 10 PKVD---ERKTAWGERNGKRRRRRTRAGGCTPRYMS-----CLRDAPPSPT 56  
DB 132 PKDRARQEKSKYVGKGGKGRKRKKS-----RYKSNVYVGRCCLMPWSLPGPH 182  
QY 57 PAGP 60  
DB 183 PCGP 186  
RESULT 10  
AF6\_HUMAN  
ID AF6\_HUMAN STANDARD; PRT; 1816 AA.  
AC P51196; O75087; O75088; O75089; Q9NU92;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE AF-6 protein.  
GN MLLT4 OR AF6.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
OX [1]  
RN SEQUENCE FROM N.A. (ISOFORM 1).  
RP MEDLINE=94061833; PubMed=8242616;  
RX Prasad R., Gu Y., Alder H., Nakamura T., Canaani O., Saito H.,  
RA Huebner K., Gale R.P., Nowell P.C., Kuriyama K., Miyazaki Y.,  
RA Croce C.M., Canaani E.;  
RT "Cloning of the ALL-1 fusion partner, the AF-6 gene, involved in  
RT acute myeloid leukemias with the t(6;11) chromosome translocation.";  
RL Cancer Res. 53:5624-5628(1993).  
RN [2]  
RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RP TISSUE=Fetal brain;  
RX MEDLINE=98344142; PubMed=9679199;  
RA Saito S., Matsushima M., Shirahama S., Minaguchi T., Kanamori Y.,  
RA Minami M., Nakamura Y.;  
RT "Complete genomic structure, DNA polymorphisms, and alternative  
RT splicing of the human AF-6 gene.";  
RL DNA Res. 5:115-120(1998).  
RN [3]  
RN SEQUENCE OF 337-1816 FROM N.A. (ISOFORM 2).  
RP

RA Williams S.;  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 CC !- FUNCTION: MAY ACT AS AN INTRACELLULAR SIGNALING COMPONENT  
 CC CONTROLLED BY RAS SIGNALING PATHWAYS.  
 CC !- SUBUNIT: BINDS DIRECTLY TO ZO-1 AND OCCLUDIN.  
 CC !- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
 CC !- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1, 2 (SHOWN HERE) AND 3; ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC !- DISEASE: INVOLVED IN ACUTE LEUKEMIAS BY A CHROMOSOMAL  
 CC TRANSLOCATION T(6;11)(Q27;Q23) THAT INVOLVES MLLT4 AND MLL/HRX.  
 CC THE RESULT IS A ROGUE ACTIVATOR PROTEIN.  
 CC !- SIMILARITY: CONTAINS 1 DILUTE DOMAIN.  
 CC !- SIMILARITY: CONTAINS 1 FHA DOMAIN.  
 CC !- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AB011399; BAA32484.1; -;  
 CC EMBL; AB011399; BAA32483.1; -;  
 CC EMBL; AB011399; BAA32485.1; -;  
 CC EMBL; U02478; AAC50059.1; -;  
 CC EMBL; AL049698; CAB76850.1; -;  
 CC HSSP; Q12923; 3PDZ.  
 CC Genew; HGNC:7137; MLLT4.  
 CC MIM; 159559; -;  
 CC InterPro; IPR002710; DIL.  
 CC InterPro; IPR000253; FHA\_domain.  
 CC InterPro; IPR001478; PDZ.  
 CC InterPro; IPR000159; RA\_domain.  
 CC Pfam; PF00498; FHA; 1.  
 CC Pfam; PF00595; PDZ; 1.  
 CC Pfam; PF00788; RA; 2.  
 CC Pfam; PF01843; DIL; 1.  
 CC ProDom; PD003376; DIL; 1.  
 CC SMART; SM00240; FHA; 1.  
 CC SMART; SM00228; PDZ; 1.  
 CC SMART; SM00314; RA; 2.  
 CC PROSITE; PS0106; PDZ; 1.  
 CC Chromosomal translocation; Proto-oncogene; Alternative splicing.  
 FT DOMAIN 36 206  
 FT DOMAIN 425 491  
 FT DOMAIN 804 910  
 FT DOMAIN 991 1077  
 FT DOMAIN 162 174  
 FT DOMAIN 1349 1356  
 FT DOMAIN 1371 1376  
 FT DOMAIN 1561 1571  
 FT SITE 26 26  
 FT VARSPLIC 1588 1611  
 FT VARSPLIC 1612 1816  
 FT VARSPLIC 1666 1743  
 FT VARSPLIC 1744 1816  
 FT CONFLICT 373 373  
 FT CONFLICT 391 391  
 FT CONFLICT 744 744  
 FT CONFLICT 1031 1031  
 FT CONFLICT 1408 1408  
 FT CONFLICT 1816 AA; 205604 MW; EB1FE7F04879CE8F CRC64;  
 Query Match 12.5%; Score 71.5; DB 1; Length 1816;  
 Best Local Similarity 26.5%; Pred. No. 25;

Matches 27; Conservative 15; Mismatches 45; Indels 15; Gaps 3;  
 QY 13 DERKTAWGERNGOKRSRR-----GTRAGGCTPRYMSCLRDAPPSPTPA--GP 60  
 Db 1631 EKRRQEEGYSLAEARRRQHDDEAARRLLEPEAPGLCRP---PLPRDYEPSPSPAPGAP 1687  
 QY 61 PRCPWQDDAFIRRGPPXKGKELGRLAVALGFEDTEVTTPAG 102  
 Db 1688 PPPQPNASYLKTQVLSPLDFTAKFVAYNEEEEDCSLAG 1729  
 RESULT 11  
 RNE\_ECOLI  
 ID RNE\_ECOLI STANDARD; PRT: 1061 AA.  
 AC P21513; P77591;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ribonuclease E (EC 3.1.4.-) (RNase E).  
 GN RNE OR AMS OR HMP1 OR B1084.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=97061202; PubMed=8905232;  
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
 RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
 RA Yano M., Horiuchi T.;  
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome  
 RT corresponding to the 12.7-28.0 min region on the linkage map.";  
 RL DNA Res. 3:137-155(1996).  
 RN [3]  
 RP SEQUENCE OF 1-1025 FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=93078265; PubMed=1447789;  
 RA Casaregola S., Jacq A., Laoudj D., McGurk G., Margaron S.,  
 RA Tempete M., Norris V., Holland I.B.;  
 RT "Cloning and analysis of the entire Escherichia coli *ams* gene. *ams* is  
 RT identical to *hmp1* and encodes a 114 kDa protein that migrates as a  
 RT 180 kDa protein.";  
 RL J. Mol. Biol. 228:30-40(1992).  
 RN [4]  
 RP SEQUENCE OF 1-844 FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=91131576; PubMed=1704367;  
 RA Claverie-Martin F., Diaz-Torres M., Yancey S.D., Kushner S.R.;  
 RT "Analysis of the altered mRNA stability (*ams*) gene from Escherichia  
 RT coli. Nucleotide sequence, transcriptional analysis, and homology of  
 RT its product to *MRP3*, a mitochondrial ribosomal protein from  
 RT *Neurospora crassa*.";  
 RL J. Biol. Chem. 266:2843-2851(1991).  
 RN [5]  
 RP PARTIAL SEQUENCE FROM N.A., AND SEQUENCE OF 1-27.  
 RC STRAIN=K12;  
 RX MEDLINE=91187608; PubMed=2011493;  
 RA Chauhan A.K., Miczak A., Taraseviciene L., Aprillon D.;  
 RT "Sequencing and expression of the *rne* gene of Escherichia coli.";



RL Nucleic Acids Res. 19:125-129(1991).  
RN [6]  
RP SEQUENCE OF 844-1061 FROM N.A., AND CHARACTERIZATION.  
RC STRAIN-K12;  
RX MEDLINE=94022304; PubMed=8415644;  
RA Cornack R.S., Genereux J.L., Mackie G.A.;  
RT "Rnase E activity is conferred by a single polypeptide:  
RT overexpression, purification, and properties of the ams/rne/hmp1 gene  
RT product.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:9006-9010(1993).  
RN [7]  
RP CHARACTERIZATION.  
RX PubMed=11328869;  
RA Walsh A.P., Tock M.R., Mallen M.H., Kabardin V.R., Gabain Av A.,  
RA McDowall K.J.;  
RT "Cleavage of poly(A) tails on the 3'-end of RNA by ribonuclease E of  
RT Escherichia coli.";  
RL Nucleic Acids Res. 29:1864-1871(2001).  
CC -!- FUNCTION: MATURES 5S RNA FROM ITS PRECURSORS FROM ALL THE RRNA  
CC GENES. IT ALSO CLEAVES RNA I, A MOLECULE THAT CONTROLS THE  
CC REPLICATION OF COLEI PLASMID DNA. IT IS THE MAJOR ENDOURIBONUCLEASE  
CC PARTICIPATING IN MRNA TURNOVER IN E.COLI. IT INITIATES THE DECAY  
CC OF RNAS BY CUTTING THEM INTERNALLY NEAR THEIR 5'-END. IT IS ABLE  
CC TO REMOVE POLY(A) TAILS BY AN ENDONUCLEOLYTIC PROCESS.  
CC -!- SUBUNIT: ORGANIZED INTO A STRUCTURE (PROCESSOME OR RNA  
CC DEGRADOSOME) CONTAINING A NUMBER OF RNA-PROCESSING ENZYMES.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: BELONGS TO THE RNE FAMILY.  
CC -!- SIMILARITY: CONTAINS 1 SI MOTIF DOMAIN.  
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 1003  
CC ONWARD AND IS SHORTER (1025 AA) DUE TO A FRAMESHIFT.  
CC -!- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN IN THE C-TERMINUS  
CC AND IS SHORTER (815 AA) DUE TO A FRAMESHIFT.  
CC -!- CAUTION: REF.5 SEQUENCE WAS ALSO INCORRECT IN MANY POSITIONS DUE  
CC TO FRAMESHIFTS.  
CC  
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CC  
CC EMBL; AE000209; AAC74168.1; -  
DR EMBL; D90744; BAA35893.1; -  
DR EMBL; X67470; CAA47818.1; ALT-FRAME.  
DR EMBL; X62747; AAB23443.1; ALT-FRAME.  
DR EMBL; X54309; CAA38206.1; ALT-FRAME.  
DR EMBL; L23942; AAA03347.1; -  
DR PIR; JG0009; JG0009.  
DR PIR; A23747; A23747.  
DR PIR; S25116; S25116.  
DR PIR; S27311; S27311.  
DR EcoGene; EGI0859; rne.  
DR InterPro; IPR004659; RNaseEG.  
DR InterPro; IPR003029; S1.  
DR Pfam; PF00575; S1; 1.  
DR SMART; SM00316; S1; 1.  
DR TIGRFAMs; TIGR00757; RNaseEG; 1.  
DR PROSITE; PS50126; S1; 1.  
KW Hydrolase; Nuclease; Endonuclease; RNA-binding; Complete proteome.  
FT DOMAIN 39 119  
FT SI MOTIF.  
FT CONFLICT 350 350 O -> H (IN REF. 4).  
FT CONFLICT 487 487 V -> L (IN REF. 1 AND 2).  
FT CONFLICT 564 564 A -> R (IN REF. 3).  
FT CONFLICT 784 784 N -> K (IN REF. 3).  
FT CONFLICT 838 838 A -> R (IN REF. 4).  
FT CONFLICT 905 905 P -> R (IN REF. 3).  
FT CONFLICT 1048 1048 H -> R (IN REF. 6).  
SQ SEQUENCE 1061 AA; 118182 MW; B911877DF03E79A8 CRC64;

Query Match

12.2%; Score 69.5; DB 1; Length 1061;

Best Local Similarity 26.4%; Pred. No. 23;  
Matches 29; Conservative 9; Mismatches 41; Indels 31; Gaps 4;  
QY 8 LVPKVDERTAW-CERNGQKRRRRRTRAGGCTTPRYMSCLRDAPPSPTPAGP-----60  
DB 501 MLPKHEEAMALPSEEEFAERKRPQPALATFAMPDV-----PPAPTAEAPAPVVA 552  
QY 61 -----PRCQWQDAFIRRGPKXKGLGRAVALGFEDTEVTTPA 101  
DB 553 PAPKAAPATPAAPQAQGLLSRRFG-----ALKALFSGGEETKPTQPA 595  
RESULT 12  
POLN\_RUBVT  
ID POLN\_RUBVT STANDARD; PRT; 2205 AA.  
AC P13889;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Nonstructural polyprotein [Contains: Nonstructural protein NSP1;  
DE Nonstructural protein NSP2; Nonstructural protein NSP3; Nonstructural  
DE protein NSP4].  
OS Rubella virus (strain Therien).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
OC Rubivirus.  
OX NCBI\_TaxID=11045;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90281585; PubMed=2353453;  
RA Dominguez G., Wang C.Y., Frey T.K.;  
RT "Sequence of the genome RNA of rubella virus: evidence for genetic  
RT rearrangement during togavirus evolution.";  
RL Virology 177:225-258(1990).  
RN [2]  
RP SEQUENCE OF 1737-2205 FROM N.A.  
RX MEDLINE=88226020; PubMed=2836271;  
RA Frey T.K., Marr L.D.;  
RT "Sequence of the region coding for virion proteins C and E2 and the  
RT carboxy terminus of the nonstructural proteins of rubella virus:  
RT comparison with alphaviruses.";  
RL Gene 62:85-99(1989).  
CC -!- PTM: SPECIFIC ENZYMTIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.  
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CC  
CC EMBL; M15240; AAA88528.1; -  
DR PIR; A35320; MNWVRN.  
DR MEROPS; C27.001; -  
DR InterPro; IPR002589; Alpp.  
DR InterPro; IPR001788; RNA\_dep\_RNapol2.  
DR InterPro; IPR000606; Viral\_helicase1.  
DR Pfam; PF00978; RNA\_dep\_RNapol2; 1.  
DR Pfam; PF01443; Viral\_helicase1; 1.  
DR Pfam; PF01661; Alpp; 1.  
DR SMART; SM00506; Alpp; 1.  
KW Polyprotein; Nonstructural protein.  
FT CHAIN 1 ? NONSTRUCTURAL PROTEIN NSP1.  
FT CHAIN ? ? NONSTRUCTURAL PROTEIN NSP2.  
FT CHAIN ? ? NONSTRUCTURAL PROTEIN NSP3.  
FT CHAIN ? 2205 NONSTRUCTURAL PROTEIN NSP4.  
SQ SEQUENCE 2205 AA; 240220 MW; 15A95F55E34C0B03 CRC64;  
Query Match 12.2%; Score 69.5; DB 1; Length 2205;  
Best Local Similarity 30.5%; Pred. No. 47;  
Matches 25; Conservative 5; Mismatches 33; Indels 19; Gaps 3;  
QY 22 RNSQKRRRRRTRAGGCTTPRYMSCLRDAPPSPTPAGPRCPWQDDAFIRRGPKXKGE 81

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DB 733 RRSQHSOARGTTP-----PAPARDPPPPAPSPAPPRA-----GDPVPPIP 774
QY 82 LGLRAVALGFEDTEVTTTPAGP 103
DB 775 AGPADRARDAE-LEVACEPSGP 795

RESULT 13
A2AB_ELEM
ID A2AB_ELEM STANDARD; PRT; 384 AA.
AC 019014;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
GN ADRA2B.
OS Elephas maximus (Indian elephant).
OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Proboscidea; Elephantiidae; Elephas.
OX NCBI_TaxID=9783;
RN 11
RP SEQUENCE FROM N.A. PubMed=9214502;
RX MEDLINE=97357151; PubMed=9214502;
RA Springer M.S., Cleven G.C., Madsen O.J., de Jong W.W., Waddell V.G.,
RA Amrine H.M., Stanhope M.J.;
RT "Endemic African mammals shake the phylogenetic tree.";
RL Nature 388:61-64(1997).
CC -1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL; Y12525; CAA73125.1; -
CC HSSP; P29274; IMMH.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G-PROTEIN_RECP_FL_1; 1.
DR PROSITE: PS0262; G-PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Multigene family;
KW Phosphorylation; Lipoprotein; Palmitate.
FT NON_TER 1 1
FT TRANSMEM <1 25 1 (POTENTIAL).
FT DOMAIN 26 36 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 37 62 2 (POTENTIAL).
FT DOMAIN 63 72 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 73 95 3 (POTENTIAL).
FT DOMAIN 96 117 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 118 140 4 (POTENTIAL).
FT DOMAIN 141 156 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 157 180 5 (POTENTIAL).
FT DOMAIN 181 348 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 349 372 6 (POTENTIAL).
FT DOMAIN 373 381 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 382 >384 7 (POTENTIAL).
FT DISULFID 72 151 BY SIMILARITY.
FT DOMAIN 281 285 ASP/GLU-RICH (ACIDIC),
FT SITE 79 79 IMPLICATED IN LIGAND BINDING (BY
SIMILARITY).
FT SITE 163 163 IMPLICATED IN CATECHOL AGONIST BINDING
(BY SIMILARITY).
FT SITE 167 167 IMPLICATED IN CATECHOL AGONIST BINDING
(BY SIMILARITY).
FT NON_TER 384 384
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SQ SEQUENCE 384 AA; 41911 MW; CF41B56CC355B94F CRC64;
Query Match 12.1%; Score 69; DB 1; Length 384;
Best Local Similarity 48.6%; Pred. No. 9.8;
Matches 18; Conservative 1; Mismatches 8; Indels 10; Gaps 2;

QY 26 KRSRRRGTRAGGCTPRYMNSCLRDAP--PSPTPAGP 60
DB 187 KRSNRGRGPRAG-----APREGEKQPHPLPAGP 215

RESULT 14
MENI_HUMAN
ID MENI_HUMAN STANDARD; PRT; 615 AA.
AC 000255; O00632;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Menin.
GN MEN1 OR SCG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A., AND VARIANTS FMEN1.
RC TISSUE=Leukocyte;
RX MEDLINE=97358940; PubMed=9103196;
RA Chandrasekharappa S.C., Guru S.C., Manickam P., Olufemi S.-E.,
RA Collins F.S., Emmert-Buck M.R., Debelenko L.V., Zhuang Z.,
RA Lubensky I.A., Liotta L.A., Crabtree J.S., Wang Y., Roe B.A.,
RA Weisenmann J., Boguski M.S., Agarwal S.K., Kester M.B., Kim Y.S.,
RA Heppner C., Dong Q., Spiegel A.M., Burns A.L., Marx S.J.;
RT "Positional cloning of the gene for multiple endocrine neoplasia-type
RT 1.";
RT Science 276:404-407(1997).
RN 12
RP VARIANTS FMEN1 AND SPORADIC MEN1.
RX MEDLINE=97358593; PubMed=9215689;
RA Agarwal S.K., Kester M.B., Debelenko L.V., Heppner C.,
RA Emmert-Buck M.R., Skarulis M.C., Doppman J.L., Kim Y.S.,
RA Lubensky I.A., Zhuang Z., Green J.S., Guru S.C., Manickam P.,
RA Olufemi S.-E., Liotta L.A., Chandrasekharappa S.C., Collins F.S.,
RA Spiegel A.M., Burns A.L., Marx S.J.;
RT "Germline mutations of the MEN1 gene in familial multiple endocrine
RT neoplasia type 1 and related states.";
RL Hum. Mol. Genet. 6:1169-1175(1997).
RN 13
RP VARIANT PARATHYROID ADENOMA LYS-26.
RX MEDLINE=97385243; PubMed=9241276;
RA Heppner C., Kester M.B., Agarwal S.K., Debelenko L.V.,
RA Emmert-Buck M.R., Guru S.C., Manickam P., Olufemi S.-E.,
RA Skarulis M.C., Doppman J.L., Alexander R.H., Kim Y.S., Saggat S.K.,
RA Lubensky I.A., Zhuang Z., Liotta L.A., Chandrasekharappa S.C.,
RA Collins F.S., Spiegel A.M., Burns A.L., Marx S.J.;
RT "Somatic mutation of the MEN1 gene in parathyroid tumours.";
RL Nat. Genet. 16:375-378(1997).
RN 14
RP VARIANTS FMEN1 D-42; P-165; D-169; S-188 AND E-289.
RX MEDLINE=98130524; PubMed=9463336;
RA Bassett J.H.D., Forbes S.A., Pannett A.A.J., Lloyd S.E.,
RA Christie P.T., Wooding C., Harding B., Besser G.M., Edwards C.R.,
RA Monson J.P., Sampson J., Wass J.A.H., Wheeler M.H., Thakker R.V.;
RT "Characterization of mutations in patients with multiple endocrine
RT neoplasia type 1.";
RL Am. J. Hum. Genet. 62:232-244(1998).
RN 15
RP VARIANTS FMEN1.
RX MEDLINE=98349969; PubMed=9683585;
RA Giraud S., Zhang C.X., Serova-Sinilnikova O., Wautot V., Salandre J.,
RA Bulsson N., Waterlot C., Batters C., Porchet N., Aubert J.-P., Emy P.,
RA Cadiot G., Delemer B., Chabre O., Niccoli P., Leprat F., Duron F.,
RA Emperauger B., Cougaut P., Salfati E., Riou J.-P.,
```

RA Guichard S., Rodier M., Meyrier A., Caron P., Vantghem M.-C.,  
RA Assayag M., Peix J.-L., Pugeat M., Rohmer V., Vallotton M., Lenoir G.,  
RA Gaudray P., Proye C., Conte-Devolx B., Chanson P., Shugart Y.Y.,  
RA Goldgar D., Murat A., Calender A.,  
RT "Germline mutation analysis in patients with multiple endocrine  
neoplasia type 1 and related disorders.";  
RL Am. J. Hum. Genet. 63:455-467(1998).  
RN [6]  
RP VARIANT FIHP LYS-260.  
RX MEDLINE=99011276; PubMed=9792884;  
RA Teh B.T., Esapa C.T., Houlston R., Grandell U., Farnebo F.,  
RA Nordenskjöld M., Pearce C.J., Carmichael D., Larsson C., Harris P.E.;  
RT "A family with isolated hyperparathyroidism segregating a missense  
MEN1 mutation and showing loss of the wild-type alleles in the  
parathyroid tumors.";  
RL Am. J. Hum. Genet. 63:1544-1549(1998).  
RN [7]  
RP VARIANT FIHP GLU-189.  
RX MEDLINE=99057176; PubMed=9843042;  
RA Fujimori M., Shirahama S., Sakurai A., Hashizume K., Hama Y., Ito K.,  
RA Shingu K., Kobayashi S., Amano J., Fukushima Y.;  
RT "Novel V184E MEN1 germline mutation in a Japanese kindred with  
familial hyperparathyroidism.";  
RL Am. J. Med. Genet. 80:221-222(1998).  
RN [8]  
RP VARIANTS FMEN1.  
RX MEDLINE=98334342; PubMed=9671267;  
RA Agarwal S.K., Debelenko L.V., Kester M.B., Guru S.C., Manickam P.,  
RA Olufemi S.E., Skarulis M.C., Heppner C., Crabtree J.S.,  
RA Lubensky I.A., Skarulis S., Kim Y.S., Chandrasekharappa S.C.,  
RA Collins F.S., Liotta L.A., Spiegel A.M., Burns A.L., Emmert-Buck M.R.,  
RA Marx S.J.;  
RT "Analysis of recurrent germline mutations in the MEN1 gene encountered  
in apparently unrelated families.";  
RL Hum. Mutat. 12:75-82(1998).  
RN [9]  
RP VARIANTS FMEN1 ILF-135 AND LYS-364.  
RX MEDLINE=98410971; PubMed=9740255;  
RA Boeni R., Vortmeyer A.O., Pack S., Park W.-S., Burg G., Hofbauer G.,  
RA Darling T., Liotta L., Zhuang Z.;  
RT "Somatic mutations of the MEN1 tumor suppressor gene detected in  
sporadic angiofibromas.";  
RL J. Invest. Dermatol. 111:539-540(1998).  
RN [10]  
RP VARIANTS FMEN1 LYS-119 DEL AND 171-GLN--LEU-173 DEL.  
RX MEDLINE=98419173; PubMed=9747036;  
RA Sakurai A., Shirahama S., Fujimori M., Katai M., Itakura Y.,  
RA Kobayashi S., Amano J., Fukushima Y., Hashizume K.;  
RT "Novel MEN1 gene mutations in familial multiple endocrine neoplasia  
type 1.";  
RL J. Hum. Genet. 43:199-201(1998).  
RN [11]  
RP VARIANTS FMEN1 GLY-45.  
RX MEDLINE=99048878; PubMed=9832038;  
RA Sato M., Matsubara S., Miyauchi A., Ohye H., Imachi H., Murao K.,  
RA Takahara J.;  
RT "Identification of five novel germline mutations of the MEN1 gene in  
Japanese multiple endocrine neoplasia type 1 (MEN1) families.";  
RL J. Med. Genet. 35:915-919(1998).  
RN [12]  
RP VARIANTS FMEN1 TRP-39; TYR-177; ASP-184; PRO-269 AND PRO-272.  
RX MEDLINE=99103464; PubMed=9888389;  
RA Poncin J., Abs R., Velkeniers B., Bonduelle M., Abramowicz M.,  
RA Legros J.-J., Verloes A., Meurisse M., van Gaal L., Verellen C.,  
RA Koulschier L., Beckers A.;  
RT "Mutation analysis of the MEN1 gene in Belgian patients with multiple  
endocrine neoplasia type 1 and related diseases.";  
RL Hum. Mutat. 13:54-60(1999).  
RN [13]  
RP VARIANTS MEN1 ASP-161 AND ARG-246.  
RX MEDLINE=99188881; PubMed=10090472;  
RA Mutch M.G., Dilley W.G., Sanjurjo F., Debenedetti M.K., Doherty G.M.,  
RA Wells S.A. Jr., Goodfellow P.J., Lairmore T.C.;

RT "Germline mutations in the multiple endocrine neoplasia type 1 gene:  
evidence for frequent splicing defects.";  
Hum. Mutat. 13:175-185(1999).  
CC -!- FUNCTION: NOT KNOWN.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- TISSUE SPECIFICITY: UBIQUITOUS.  
CC -!- DISEASE: DEFECTS IN MEN1 ARE THE CAUSE OF FAMILIAL MULTIPLE  
ENDOCRINE NEOPLASIA TYPE 1 (FMEN1); WERNER SYNDROME, AN AUTOSOMAL  
DOMINANT DISORDER CHARACTERIZED BY TUMORS OF THE PARATHYROID  
GLANDS, GASTRO-INTESTINAL ENDOCRINE TISSUE, THE ANTERIOR PITUITARY  
AND OTHER TISSUES. CUTANEOUS LESIONS AND NERVOUS-TISSUE TUMORS CAN  
EXIST. PROGNOSIS IN FMEN1 PATIENTS IS RELATED TO HORMONAL  
EXCRETION BY TUMORS, SUCH AS HYPERGASTRINEMIA CAUSING SEVERE  
PEPTIC ULCER DISEASE (ZOLLINGER-ELISON SYNDROME, ZES), PRIMARY  
HYPERPARATHYROIDISM, AND ACUTE FORMS OF HYPERINSULINEMIA.  
CC -!- DISEASE: DEFECTS IN MEN1 ARE THE CAUSE OF FAMILIAL ISOLATED  
HYPERPARATHYROIDISM (FIHP OR HRPT1). FIHP IS AN AUTOSOMAL DOMINANT  
DISORDER CHARACTERIZED BY HYPERCALCEMIA, ELEVATED PARATHYROID  
HORMONE (PTH) LEVELS, AND UNIGLANDULAR OR MULTIGLANDULAR  
PARATHYROID TUMORS.  
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CC -----  
CC EMBL: U932236; AAC51228.1; -;  
DR EMBL: U932237; AAC51229.1; -;  
DR EMBL: U932237; AAC51230.1; -;  
DR Genew: HGNC:7010; MEN1.  
DR MIM: 131100; -;  
DR MIM: 145000; -;  
DR Nuclear protein; Disease mutation; Alternative splicing; Polymorphism.  
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FT L -> R (IN FMEN1).  
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FT E -> K (IN PARATHYROID ADENOMA).  
FT VARIANTS 26 26  
FT MISSING (IN SHORT ISOFORM).  
FT L -> W (IN FMEN1).  
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FT G -> D (IN FMEN1).  
FT /FTID=VAR\_005428.  
FT E -> G (IN FMEN1).  
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FT MISSING (IN FMEN1).  
FT /FTID=VAR\_005430.  
FT MISSING (IN FMEN1).  
FT /FTID=VAR\_005431.  
FT K -> I (IN FMEN1).  
FT /FTID=VAR\_005434.  
FT H -> D (IN FMEN1).  
FT /FTID=VAR\_005432.  
FT H -> Y (IN FMEN1 AND SPORADIC MEN1).  
FT /FTID=VAR\_005433.  
FT F -> V (IN FMEN1).  
FT /FTID=VAR\_005436.  
FT G -> D (IN FMEN1).  
FT /FTID=VAR\_005437.  
FT A -> D (IN FMEN1).  
FT /FTID=VAR\_005438.  
FT MISSING (IN FMEN1).  
FT /FTID=VAR\_005439.  
FT  
Query Match 12.1%; Score 69; DB 1; Length 615;  
Best Local Similarity 25.9%; Pred. No. 15;  
Matches 28; Conservative 9; Mismatches 31; Indels 40; Gaps 5;  
QY 14 ERKTANGERNQKRRRRRTRAGGCTPRYMNSCLRDAPPSPTP----- 57

[illegible]

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OM protein - protein search, using sw model

Run on: February 19, 2003, 15:32:08 ; Search time 17 seconds  
(without alignments)  
588.116 Million cell updates/sec

Title: US-09-750-240-2

Perfect score: 570

Sequence: 1 MSWFSGLLVKVDERTKAMG.....RAVALGFEDTEVTTPAGPL 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	472.5	82.9	1165	2 A46180	adenyllyl cyclase t
2	432	75.8	1180	2 A47202	adenylate cyclase
3	431	75.6	1166	2 A49201	adenylate cyclase
4	77.5	13.6	1285	2 T14171	ataxin-2 - mouse
5	76	13.3	285	2 E75507	hypothetical prote
6	74	13.0	1173	2 T31421	C-terminal domain-
7	73	12.8	512	1 WMBEY4	UL54 protein - hum
8	73	12.8	550	2 C75557	hypothetical prote
9	73	12.8	1168	1 MWAXIC	myosin heavy chain
10	72	12.6	232	2 A41551	vascular endothell
11	72	12.6	406	2 T36632	probable oxidoredu
12	72	12.6	576	2 T36729	probable serine/th
13	70.5	12.4	357	2 S11137	class I histocompa
14	70.5	12.4	357	2 S11134	class I histocompa
15	69.5	12.2	138	2 C96734	hypothetical prote
16	69.5	12.2	337	2 S11136	class I histocompa
17	69.5	12.2	1061	1 S27311	ribonuclease E (EC
18	69.5	12.2	2205	1 MNWVRN	nonstructural poly
19	69	12.1	948	2 A57640	retinoblastoma bin
20	69	12.1	1621	2 T15264	hypothetical prote
21	68.5	12.0	144	2 E86364	hypothetical prote
22	68.5	12.0	303	2 T19289	hypothetical prote
23	68.5	12.0	357	2 S11135	class I histocompa
24	68.5	12.0	1061	2 F90811	RNase E [imported]
25	68.5	12.0	1061	2 B85671	RNase E [similarit
26	68.5	12.0	1147	2 T42627	ADP-ribosylation f
27	68	11.9	162	2 T49420	hypothetical prote
28	68	11.9	212	2 T35187	hypothetical prote
29	68	11.9	294	2 T22639	hypothetical prote

ALIGNMENTS

RESULT 1

A46180

adenyllyl cyclase type VI - dog

C:Species: Canis lupus familiaris (dog)

C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 04-Sep-1998

C:Accession: A46180

R:Katsushika S.; Chen, L.; Kawabe, J.; Nilakantan, R.; Halnon, N.J.; Homcy, C.J.; I

Proc. Natl. Acad. Sci. U.S.A. 89, 8774-8778, 1992

A:Title: Cloning and characterization of a sixth adenyllyl cyclase isoform: types V a

A:Reference number: A46180; MUID:92409599; PMID:1528892

A:Accession: A46180

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-1165 <NAI>

A:Experimental source: cardiac

A>Note: sequence extracted from NCBI backbone (NCBIN:114249, NCBIPI:114250)

C:Superfamily: human adenylate cyclase; guanylate cyclase catalytic domain homology

C:Keywords: transmembrane protein

F:319-553/Domain: guanylate cyclase catalytic domain homology <GCC>

F:924-1163/Domain: guanylate cyclase catalytic domain homology <GCC>

Query Match 82.9%; Score 472.5; DB 2; Length 1165;  
Best Local Similarity 83.2%; Pred. No. 2.3e-39;  
Matches 89; Conservative 2; Mismatches 11; Indels 5; Gaps 2;

QY 1 MSWFSGLLVKVDERTKAWGNGKRRRGCTPRYMNSCLRDAPPSPTPAGP 60

Db 1 MSWFSGLLVKVDERTKAWGNGKRRP-RRGTRTSFGCTPRYMNSCLRDAPPSPTPAGP 59

QY 61 PRCPWQDDAFIRRGPGKXKELGLRAVALGPEDETE----VTTTPAGP 103

Db 60 PRCPWQDDAFIRRGPGKXKELGLRAVALGPEDETE----VTTTPAGP 106

RESULT 2

A47202

adenylate cyclase (EC 4.6.1.1) type 6 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 16-Jul-1999

C:Accession: A47202; A45145

R:Premont, R.T.; Chen, J.; Ma, H.W.; Ponnappalli, M.; Iyengar, R.

Proc. Natl. Acad. Sci. U.S.A. 89, 9809-9813, 1992

A:Title: Two members of a widely expressed subfamily of hormone-stimulated adenyllyl

A:Reference number: A47202; MUID:93028552; PMID:1409703

A:Accession: A47202

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-1180 <PRE>

A:Experimental source: liver, kidney

A>Note: sequence extracted from NCBI backbone (NCBIPI:115851)

R:Krupinski, J.; Lehman, T.C.; Frankenfield, C.D.; Zwaagstra, J.C.; Watson, P.A.

J. Biol. Chem. 267, 24858-24862, 1992

hypothetical prote  
hypothetical prote  
2-aminobenzoyl-CoA  
N-methyl-D-asparta  
N-methyl-D-asparta  
N-methyl-D-asparta  
conserved hypothet  
class I histocompa  
UL54 protein - hum  
hypothetical prote  
hypothetical prote  
insulin promoter f  
hypothetical prote  
class I histocompa  
hypothetical prote

A:Title: Molecular diversity in the adenylcyclase family. Evidence for eight forms of  
A:Reference number: A45145; MUID:93077589; PMID:1332969

A:Accession: A45145

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 15-93, 'K', 95-463, 'V', 465-551, 'G', 553-803, 'I', 805-1180 <KRU>

A:Cross-references: GB:L0115; NID:g202712; PIDN:AAA40676.1; PID:g202713

C:Superfamily: human adenylate cyclase; guanylate cyclase catalytic domain homology

C:Keywords: phosphorus-oxygen lyase

F:333-568/Domain: guanylate cyclase catalytic domain homology <GCC>

F:939-1178/Domain: guanylate cyclase catalytic domain homology <GCC2>

Query Match

Best Local Similarity 75.8%; Score 432; DB 2; Length 1180;

Matches 81; Conservative 7; Mismatches 12; Indels 2; Gaps 2;

QY 1 MSWFSGLLPVKYDERKTAWGERNGKRSRRRTTRAGGCTPRYMSCLRDAPPSPTPAGP 60

DB 15 MSWFSGLLPVKYDERKTAWGERNGKRP-RQATRARGFCAPRYMSCLKNVEPPSPTPAAR 73

QY 61 PRCPWQDDAFIRRGPGPKGKGLGRAVALGFEDTEVTTPAG 102

DB 74 TRCPWQDEAFIRRGPGRGVGLGRSVALGFDTEV-TTPMG 114

RESULT 3

A49201

adenylate cyclase (EC 4.6.1.1) type V, calcium-inhibitable - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 16-Jul-1999

C:Accession: A49201; A46187

R:Premont, R.T.; Jacobowitz, O.; Iyengar, R.

Endocrinology 131, 2774-2784, 1992

A:Title: Lowered responsiveness of the catalyst of adenyl cyclase to stimulation by Gs

A:Reference number: A49201; MUID:93076707; PMID:1332848

A:Accession: A49201

A:Molecule type: mRNA

A:Residues: 7-1161 <PRE>

A:Cross-references: GB:M96653; NID:g191726; PIDN:AAA37182.1; PID:g191727

A:Experimental source: S49 lymphoma cells

A:Note: sequence extracted from NCBI backbone (NCBIN:119384, NCBI:P:119386)

R:Yoshimura, M.; Cooper, D.M.

Proc. Natl. Acad. Sci. U.S.A. 89, 6716-6720, 1992

A:Title: Cloning and expression of a Ca(2+)-inhibitable adenyl cyclase from NCB-20 cell

A:Reference number: A46187; MUID:92357702; PMID:1379717

A:Accession: A46187

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-46, 'K', 48-75, 'G', 77-507, 'GR', 511-737, 'V', 739-881, 'L', 883-990, 'V', 992-1166

A:Cross-references: GB:M93422; NID:g191690; PIDN:AAA37174.1; PID:g191691

A:Experimental source: NCB-20 cells

A:Note: sequence extracted from NCBI backbone (NCBI:P:110233); the authors acknowledge th

C:Superfamily: human adenylate cyclase; guanylate cyclase catalytic domain homology

C:Keywords: phosphorus-oxygen lyase; transmembrane protein

F:319-554/Domain: guanylate cyclase catalytic domain homology <GCC>

F:925-1164/Domain: guanylate cyclase catalytic domain homology <GCC2>

Query Match

Best Local Similarity 75.6%; Score 431; DB 2; Length 1166;

Matches 81; Conservative 5; Mismatches 14; Indels 2; Gaps 2;

QY 1 MSWFSGLLPVKYDERKTAWGERNGKRSRRRTTRAGGCTPRYMSCLRDAPPSPTPAGP 60

DB 1 MSWFSGLLPVKYDERKTAWGERNGKRP-RHANRARGFCAPRYMSCLNNAEPPSPTPAAH 59

QY 61 PRCPWQDDAFIRRGPGPKGKGLGRAVALGFEDTEVTTPAG 102

DB 60 TRCPWQDEAFIRRGPGRGVGLGRSVALGFDTEV-TTPMG 100

RESULT 4

T14171

ataxin-2 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999

C:Accession: T14171

R:Nechiporuk, T.T.; Figueroa, K.; Sahba, S.; Nechiporuk, A.V.; Pulst, S.M.

submitted to the EMBL Data Library, January 1998

A:Description: Mouse homolog of the SCA2 gene.

A:Reference number: Z17900

A:Accession: T14171

A:Status: preliminary; translated from GB/EMBL/DDDBJ

A:Molecule type: mRNA

A:Residues: 1-1285 <NEC>

A:Cross-references: EMBL:AF041472; NID:g3005019; PID:g3005020; PIDN:AAC09275.1

C:Genetics:

A:Gene: SCA2

Query Match

Best Local Similarity 13.6%; Score 77.5; DB 2; Length 1285;

Matches 18; Conservative 1; Mismatches 24; Indels 7; Gaps 1;

QY 15 RKTAMGERNGKRSRRRTTRAGGCTPRYMSCLRDAPPSPTPAGPRCP 64

DB 20 RAGWAARSLPRTARRGGRGAVAP-----SAGPPRGCGAPPRCP 62

RESULT 5

E75507

hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000

C:Accession: E75507

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: E75507

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-285 <WHI>

A:Cross-references: GB:AE001911; GB:AE000513; NID:g6458217; PIDN:AAE10109.1; PID:g645

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR0527

A:Map position: 1

Query Match

Best Local Similarity 13.3%; Score 76; DB 2; Length 285;

Matches 29; Conservative 7; Mismatches 31; Indels 28; Gaps 6;

QY 3 WFSGLLPVKYDERK----TAWGERNGKRR--SRRRTTRAGGCTPRYMSCLRDAPPSPT 56

DB 189 WAGHVAQRVDTKPYRARAAGAHDRALVVSASARA----LPGYF-----PK 234

QY 57 PAGPPR-----CPWQDDAFIRRG---GPXKKGKELG 83

DB 235 PSRPERWGLGCPWGKAGGRRAYRBERGSAGGRDLG 269

RESULT 6

T31421

C-terminal domain-binding protein ral - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 07-Dec-1999

C:Accession: T31421

R:Yuryev, A.; Patturajan, M.; Litington, Y.; Joshi, R.V.; Gentile, C.; Gebara, M.; C

Proc. Natl. Acad. Sci. U.S.A. 93, 6975-6980, 1996

A:Title: The C-terminal domain of the largest subunit of RNA polymerase II interacts

A:Reference number: Z21024; MUID:96293459; PMID:8692929

A:Accession: T31421

A:Status: preliminary; translated from GB/EMBL/DDDBJ

A:Molecule type: mRNA

A:Residues: 1-1173 <YUR>









RESULT 15  
C96734



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 19, 2003, 15:33:43 ; Search time 23 Seconds  
(without alignments)  
384,520 Million cell updates/sec

Title: US-09-750-240-2

Perfect score: 570

Sequence: 1 MSWFGLLVPKVDERTAWG.....RAVALGFEDTEVTTPAGPL 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 433615 seqs, 85038156 residues

Total number of hits satisfying chosen parameters: 433615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Pending\_Patents\_AA\_New.\*
- 1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep.\*
  - 2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep.\*
  - 3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep.\*
  - 4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep.\*
  - 5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep.\*
  - 6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep.\*
  - 7: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	545	95.6	453	1	PCT-US02-36759-36
2	73.5	12.9	442	5	US-09-724-676-76996
3	73.5	12.9	442	5	US-09-724-676A-76996
4	73.5	12.9	678	5	US-09-724-676-77008
5	73.5	12.9	678	5	US-09-724-676A-77008
6	73.5	12.9	1234	1	PCT-US02-14905-12
7	73.5	12.9	1239	6	US-10-218-140-4986
8	72.5	12.7	1129	1	PCT-US02-36151-44
9	72	12.6	126	5	US-09-724-676-63223
10	72	12.6	126	5	US-09-724-676-63224
11	72	12.6	126	5	US-09-724-676-63227
12	72	12.6	126	5	US-09-724-676-63228
13	72	12.6	126	5	US-09-724-676A-63223
14	72	12.6	126	5	US-09-724-676A-63224
15	72	12.6	126	5	US-09-724-676A-63227
16	72	12.6	126	5	US-09-724-676A-63228
17	72	12.6	232	1	PCT-US02-26246A-7
18	72	12.6	232	6	US-10-268-447-10
19	72	12.6	418	5	US-09-724-676-89865
20	72	12.6	418	5	US-09-724-676A-89865
21	72	12.6	503	5	US-09-724-676-89864
22	72	12.6	503	5	US-09-724-676A-89864
23	71.5	12.5	328	5	US-09-724-676-58588
24	71.5	12.5	328	5	US-09-724-676-58589
25	71.5	12.5	328	5	US-09-724-676A-58588
26	71.5	12.5	328	5	US-09-724-676A-58589

Sequence 58592, A  
Sequence 58593, A  
Sequence 58592, A  
Sequence 58593, A  
Sequence 58590, A  
Sequence 58591, A  
Sequence 58591, A  
Sequence 16, Appl  
Sequence 348, Appl  
Sequence 9, Appl  
Sequence 58582, A  
Sequence 58583, A  
Sequence 58582, A  
Sequence 58583, A  
Sequence 58586, A  
Sequence 58587, A  
Sequence 58587, A

## ALIGNMENTS

RESULT 1

PCT-US02-36759-36

Sequence 36, Application PC/TUS0236759

GENERAL INFORMATION:

APPLICANT: INCYTE GENOMICS, INC.

APPLICANT: DUGGAN, Brendan M.

APPLICANT: YANG, Junming

APPLICANT: GIETZEN, Kimberly J.

APPLICANT: LEE, Soo Yeun

APPLICANT: TANG, Y. Tom

APPLICANT: AZIMZAI, Yalda

APPLICANT: WALIA, Narinder K.

APPLICANT: WARREN, Bridget A.

APPLICANT: BARROSO, Ines

APPLICANT: BECHA, Shanya D.

APPLICANT: YUE, Henry

APPLICANT: LEHR-MASON, Patricia M.

APPLICANT: THANGAVELU, Kavitha

APPLICANT: LEE, Sally

APPLICANT: EMERLING, Brooke M.

APPLICANT: KABLE, Amy E.

APPLICANT: KHARE, Reena

APPLICANT: BAUGHN, Mariah R.

APPLICANT: GANDHI, Ameeta R.

APPLICANT: TRAN, Uyen K.

APPLICANT: RICHARDSON, Thomas W.

APPLICANT: MARQUIS, Joseph P.

APPLICANT: LAL, Preeti G.

APPLICANT: FORSYTHE, Ian J.

APPLICANT: LEE, Ernestine A.

APPLICANT: SWARNAKAR, Anita.

APPLICANT: KALLICK, Deborah A.

APPLICANT: GRIFFIN, Jennifer A.

APPLICANT: ELLIOTT, Vicki S.

APPLICANT: GORVAD, Ann E.

APPLICANT: HAFALIA, April J.A.

APPLICANT: ISON, Craig H.

APPLICANT: JIN, Pei

APPLICANT: JIANG, Xin

APPLICANT: JACKSON, Alan

APPLICANT: BHATTIA, Umesh

APPLICANT: BURRILL, John D.

APPLICANT: BLAKE, Julie J.

APPLICANT: HO, Ann

APPLICANT: ZHENG, Wenjin

APPLICANT: GAO, Jing

TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS

FILE REFERENCE: PF-1279 PCT

CURRENT APPLICATION NUMBER: PCT/US02/36759

; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: US 60/333,097  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/335,274  
; PRIOR FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: US 60/340,542  
; PRIOR FILING DATE: 2001-12-14  
; PRIOR APPLICATION NUMBER: US 60/342,166  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: US 60/347,580  
; PRIOR FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: US 60/348,687  
; PRIOR FILING DATE: 2002-01-14  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: PERL Program  
; SEQ ID NO 36  
; LENGTH: 453  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No: 7506194CD1  
PCT-US02-36759-36

Query Match 95.6%; Score 545; DB 1; Length 453;  
Best Local Similarity 97.1%; Pred. No. 1.le-36;  
Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSWFSGLLVPKVDERKTANGERNQKRSRRCTRAGGCTPRYMSCLRDADPPSPPTPAGP 60  
|||||  
DB 1 MSWFSGLLVPKVDERKTANGERNQKRSRRCTRAGGCTPRYMSCLRDADPPSPPTPAGP 60  
|||||  
QY 61 PRCPWQDDAFIRRGPGXKGLGSLRAVALGFEDTEVTTTAPG 102  
|||||  
DB 61 PRCPWQDDAFIRRGPGXKGLGSLRAVALGFEDTEVTTTAPG 102  
|||||

RESULT 2  
US-09-724-676-76996  
; Sequence 76996, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Comugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Comugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 76996  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676-76996

Query Match 12.9%; Score 73.5; DB 5; Length 442;  
Best Local Similarity 41.8%; Pred. No. 1.3e+02;  
Matches 23; Conservative 4; Mismatches 17; Indels 11; Gaps 4;

QY 30-RRGTRAGGCTPRYM-----SCLRDADPP--SPTPAGPP---RCPWQDDAFIRRG 75  
|||||  
DB 32 RRGFQMGLLRRPPIICGLYSRVAPAEPPPSRPTPAGAGWRRCPPW--NRFCRSPG 84  
|||||

RESULT 3  
US-09-724-676A-76996  
; Sequence 76996, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Comugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Comugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 76996  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676A-76996

Query Match 12.9%; Score 73.5; DB 5; Length 442;  
Best Local Similarity 41.8%; Pred. No. 1.3e+02;  
Matches 23; Conservative 4; Mismatches 17; Indels 11; Gaps 4;

QY 30 RRGTRAGGCTPRYM-----SCLRDADPP--SPTPAGPP---RCPWQDDAFIRRG 75  
|||||  
DB 32 RRGFQMGLLRRPPIICGLYSRVAPAEPPPSRPTPAGAGWRRCPPW--NRFCRSPG 84  
|||||

RESULT 4  
US-09-724-676-77008  
; Sequence 77008, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Comugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Comugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 77008  
; LENGTH: 678  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676-77008

Query Match 12.9%; Score 73.5; DB 5; Length 678;  
Best Local Similarity 41.8%; Pred. No. 1.8e+02;  
Matches 23; Conservative 4; Mismatches 17; Indels 11; Gaps 4;

QY 30 RRGTRAGGCTPRYM-----SCLRDADPP--SPTPAGPP---RCPWQDDAFIRRG 75  
|||||  
DB 32 RRGFQMGLLRRPPIICGLYSRVAPAEPPPSRPTPAGAGWRRCPPW--NRFCRSPG 84  
|||||

RESULT 5  
US-09-724-676A-77008  
; Sequence 77008, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Comugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Comugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 77008  
; LENGTH: 678  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676A-77008

Query Match 12.9%; Score 73.5; DB 5; Length 678;  
Best Local Similarity 41.8%; Pred. No. 1.8e+02;  
Matches 23; Conservative 4; Mismatches 17; Indels 11; Gaps 4;

QY 30 RRGTRAGGCTPRYM-----SCLRDADPP--SPTPAGPP---RCPWQDDAFIRRG 75  
|||||  
DB 32 RRGFQMGLLRRPPIICGLYSRVAPAEPPPSRPTPAGAGWRRCPPW--NRFCRSPG 84  
|||||

RESULT 6  
PCT-US02-14905-12  
; Sequence 12, Application PC/TUS0214905  
; GENERAL INFORMATION:  
; APPLICANT: Research Corporation Tech., Inc.

Query Match	12.9%	Score 73.5	DB 1	Length 1234
Best Local Similarity	27.9%	Pred. No. 2.8e+02		
Matches	34	Conservative	13	Mismatches 46; Indels 29; Gaps 7
OY	5	SGLLVPKVDERTKATGERNGOKRSRRRGTT-----RACGFCPTPRYMSGLDPAEP--	52	
		: : : : :         : : :		
Db	331	SGFAEP-LEIRSPPTSRGK--SSRGTAIIILLTGLEGRAGGLPTRIILAAQADPRPESM	386	
OY	53	-----PSPTPAGPPRCWQDDAFTIRGCGPKXGKEL-GLRAVALGFEDEVTTPAG	102	
		: : : : :     : : :		
Db	387	SLAVVVTGTEPSAPPA-PPSPAPDPDRFL--NSPQGGQTGGGQGVSPDPEAEAAHTPCS	443	
OY	103	PL 104		
Db	444	AL 445		

	Query Match	12.9%	Score 73.5;	DB 6;	Length 1239;
	Best Local Similarity	27.9%;	Pred. No.2,8e+02;		
	Matches	34;	Conservative	13;	Mismatches 46; Indels 29; Gaps 7
QY	5 SGLVPKYDERTAMGERGCRKRRRG	-----RAGCFCTPRMISCLDAEP--	52		
Db	336 SGFAEP-LEIRSPPTSRGG--SSRGGAILLTLGLEORASLLPPTLRLLADPADRPDM	.....:::..	391		

RESULT 8  
PCT-US02

Query Match	12.7%	Score 72.5;	DB 1	length 1129;
Best Local Similarity	32.8%	Pred. No. 3	1e+02;	
Matches	19;	Conservative	6;	Mismatches 24; Indels 9; Gaps 3
OY	50	AEEPPTPAGPR---	CPWDDAFTLRGCGPXXKGLGLRAVALGCF-DTEVTTTPAGP	103
Db	8339	SDPPEPLPHGCPNNKCAVPWGND----	GGSSSSKRTNNFEGLISQDSSTSSAKTALGP	891

## RESULT 9

[illegible]

```

; ORGANISM: Homo sapiens
US-09-724-676-63227

Query Match      12.6%; Score 72; DB 5; Length 126;
Best Local Similarity 32.8%; Pred. No. 64;
Matches 21; Conservative 5; Mismatches 16; Indels 22; Gaps 3

QY 10 PKVD---EERTAMGERNGOKRRRGRTRAGGFCPTPRYS-----CLRDAEPSPFT 56
    ||| |::| :| :||| |::| :||| |
DB 26 PKKDAROEKKS SVRGKGCGKKRKRRKS-----RYKSMsvyVGARCCLMPWSLPGPH 76
    ||| |::| :| :||| |::| :||| |

QY 57 PAGP 60
    |||
DB 77 PCGP 80

RESULT 12
US-09-724-676-63228
; Sequence 63228, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724.676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63228
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-63228

Query Match      12.6%; Score 72; DB 5; Length 126;
Best Local Similarity 32.8%; Pred. No. 64;
Matches 21; Conservative 5; Mismatches 16; Indels 22; Gaps 3

QY 10 PKVD---EERTAMGERNGOKRRRGRTRAGGFCPTPRYS-----CLRDAEPSPFT 56
    ||| |::| :| :||| |::| :||| |
DB 26 PKKDAROEKKS SVRGKGCGKKRKRRKS-----RYKSMsvyVGARCCLMPWSLPGPH 76
    ||| |::| :| :||| |::| :||| |

QY 57 PAGP 60
    |||
DB 77 PCGP 80

RESULT 13
US-09-724-676A-63223
; Sequence 63223, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724.676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63223
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-63223

Query Match      12.6%; Score 72; DB 5; Length 126;
Best Local Similarity 32.8%; Pred. No. 64;
Matches 21; Conservative 5; Mismatches 16; Indels 22; Gaps 3;

QY 10 PKVD---EERTAMGERNGOKRRRGRTRAGGFCPTPRYS-----CLRDAEPSPFT 56
    ||| |::| :| :||| |::| :||| |
DB 26 PKKDAROEKKS SVRGKGCGKKRKRRKS-----RYKSMsvyVGARCCLMPWSLPGPH 76
    ||| |::| :| :||| |::| :||| |

QY 57 PAGP 60
    |||
DB 77 PCGP 80
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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 19, 2003, 15:32:58 ; Search time 354 seconds  
(without alignments)  
189.413 Million cell updates/sec

Title: US-09-750-240-2  
Perfect score: 570  
Sequence: 1 MSWFGSLVPKVDKRTAMG.....RAVALGFEDTEVTTTTPAGPL 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues  
Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main: \*  
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10: /cgn2\_6/ptodata/1/paa/US086\_COMB.pep.\*  
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26: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep.\*  
27: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	568	99.6	104	18 US-09-472-667-2	Sequence 2, Appli
2	568	99.6	104	21 US-09-750-240-2	Sequence 2, Appli
3	545	95.6	1167	18 US-09-472-667-6	Sequence 6, Appli
4	545	95.6	1167	21 US-09-750-240-6	Sequence 6, Appli
5	545	95.6	1167	21 US-09-750-240-13	Sequence 13, Appli
6	545	95.6	1168	18 US-09-472-667-11	Sequence 11, Appli

7	545	95.6	1168	21 US-09-750-240-11	Sequence 11, Appli
8	545	95.6	1168	26 US-10-201-000-2	Sequence 2, Appli
9	472.5	82.9	1165	21 US-09-791-537-121687	Sequence 121687,
10	432	75.8	1165	21 US-09-791-537-12125	Sequence 12125, A
11	432	75.8	1180	9 US-08-538-815-12125	Sequence 12, Appli
12	432	75.8	1180	21 US-09-791-537-17912	Sequence 17912, A
13	432	75.8	1180	21 US-09-791-537-126174	Sequence 126174, A
14	431	75.6	1166	21 US-09-791-537-34515	Sequence 34515, A
15	428	75.1	1166	21 US-09-791-537-18463	Sequence 18463, A
16	395	69.3	1155	21 US-09-791-537-118669	Sequence 118669,
17	258	45.3	1171	21 US-09-791-537-104384	Sequence 104384,
18	122.5	21.5	1216	27 US-60-248-592-119	Sequence 119, App
19	112	19.6	1099	27 US-60-245-228-339	Sequence 339, App
20	86	15.1	1239	27 US-60-229-518-453	Sequence 453, App
21	86	15.1	1328	27 US-60-212-413-161	Sequence 161, App
22	84.5	14.8	514	1 PCT-US01-08656-9636	Sequence 9626, Ap
23	84	14.7	55	1 PCT-US01-08631-47109	Sequence 47109, A
24	83	14.6	160	20 US-09-617-681A-4271	Sequence 4271, Ap
25	82.5	14.5	217	16 US-09-252-991A-28321	Sequence 28321, A
26	82.5	14.5	345	16 US-09-252-991A-32377	Sequence 32377, A
27	81.5	14.3	217	25 US-10-155-881-11975	Sequence 11975, A
28	81.5	14.3	390	20 US-09-675-784A-13125	Sequence 13125, A
29	81	14.2	266	25 US-10-104-047-3114	Sequence 3114, Ap
30	81	14.2	370	19 US-09-513-996A-43007	Sequence 43007, A
31	81	14.2	370	21 US-09-708-427-54400	Sequence 54400, A
32	80.5	14.1	782	1 PCT-US01-49232-54	Sequence 54, Appli
33	79.5	13.9	146	20 US-09-617-681A-4272	Sequence 4272, Ap
34	79.5	13.9	525	25 US-10-155-881-26729	Sequence 26729, A
35	79	13.9	109	20 US-09-617-682A-952	Sequence 952, App
36	79	13.9	111	20 US-09-617-682A-951	Sequence 951, App
37	79	13.9	116	20 US-09-617-682A-950	Sequence 950, App
38	79	13.9	289	21 US-09-252-991A-23748	Sequence 23748, A
39	79	13.9	289	21 US-09-791-537-129836	Sequence 129836,
40	79	13.9	454	1 PCT-US02-24842-9	Sequence 9, Appli
41	79	13.9	454	26 US-10-213-990-9	Sequence 9, Appli
42	79	13.9	454	27 US-60-309-870-9	Sequence 2, Appli
43	78.5	13.8	465	8 US-08-447-965-2	Sequence 41289, A
44	78.5	13.8	1076	1 PCT-US01-08631-41289	Sequence 9311, Ap
45	78.5	13.8	1076	1 PCT-US01-08656-9311	

ALIGNMENTS

RESULT 1  
US-09-472-667-2  
; Sequence 2, Application US/09472667  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. Kirk  
; APPLICANT: Insel, Paul A.  
; APPLICANT: Ping, Peipei  
; APPLICANT: Post, Steven R.  
; APPLICANT: Gao, Meihua  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
; TITLE OF INVENTION: FAILURE  
; FILE REFERENCE: 220002056722  
; CURRENT APPLICATION NUMBER: US/09/472,667  
; CURRENT FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: PCT/US99/02702  
; PRIOR FILING DATE: 1999-02-09  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 09/021,773  
; PRIOR FILING DATE: 1998-02-11  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: PCT/US97/15610  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/058,209

;; PRIOR FILING DATE: 1996-09-05  
;; PRIOR APPLICATION NUMBER: PCT/US96/02631  
;; PRIOR FILING DATE: 1996-02-27  
;; PRIOR APPLICATION NUMBER: US 08/396,207  
;; PRIOR FILING DATE: 1995-02-28  
;; PRIOR APPLICATION NUMBER: US 08/485,472  
;; PRIOR FILING DATE: 1995-06-07  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 104  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: VARIANT  
;; LOCATION: (1)...(104)  
;; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-472-667-2

Query Match 99.6%; Score 568; DB 18; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.5e-47;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSWFSGLLPVKYDERKTANGERNQKRSRRGCTRAGGCTCTPRYMCLRDPAEPPSPPTAGP 60  
DB 1 MSWFSGLLPVKYDERKTANGERNQKRSRRGCTRAGGCTCTPRYMCLRDPAEPPSPPTAGP 60  
QY 61 PRCPWODDAFIRGGPKGKGLRAVALGFEDTEVTTTTPAGPL 104  
DB 61 PRCPWODDAFIRGGPKGKGLRAVALGFEDTEVTTTTPAGPL 104

RESULT 2  
US-09-750-240-2  
;; Sequence 2, Application US/09750240  
;; GENERAL INFORMATION:  
;; APPLICANT: Hammond, H. K.  
;; APPLICANT: Insel, P. A.  
;; APPLICANT: Ping, P.  
;; APPLICANT: Post, S. R.  
;; APPLICANT: Gao, M.  
;; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART FAILURE  
;; FILE REFERENCE: 220002056723  
;; CURRENT APPLICATION NUMBER: US/09/750,240  
;; CURRENT FILING DATE: 2001-10-12  
;; PRIOR APPLICATION NUMBER: US 09/472,667  
;; PRIOR FILING DATE: 1999-12-27  
;; PRIOR APPLICATION NUMBER: US 09/008,097  
;; PRIOR FILING DATE: 1998-01-16  
;; PRIOR APPLICATION NUMBER: US 08/924,757  
;; PRIOR FILING DATE: 1997-09-05  
;; PRIOR APPLICATION NUMBER: US 60/048,933  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: US 08/485,472  
;; NUMBER OF SEQ ID NOS: 13  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 104  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: VARIANT  
;; LOCATION: (1)...(104)  
;; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-750-240-2

Query Match 99.6%; Score 568; DB 21; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.5e-47;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSWFSGLLPVKYDERKTANGERNQKRSRRGCTRAGGCTCTPRYMCLRDPAEPPSPPTAGP 60

DB 1 MSWFSGLLPVKYDERKTANGERNQKRSRRGCTRAGGCTCTPRYMCLRDPAEPPSPPTAGP 60  
QY 61 PRCPWODDAFIRGGPKGKGLRAVALGFEDTEVTTTTPAGPL 104  
DB 61 PRCPWODDAFIRGGPKGKGLRAVALGFEDTEVTTTTPAGPL 104

RESULT 3  
US-09-472-667-6  
;; Sequence 6, Application US/09472667  
;; GENERAL INFORMATION:  
;; APPLICANT: Hammond, H. Kirk  
;; APPLICANT: Insel, Paul A.  
;; APPLICANT: Ping, Peipei  
;; APPLICANT: Post, Steven R.  
;; APPLICANT: Gao, Meihua  
;; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART FAILURE  
;; FILE REFERENCE: 220002056722  
;; CURRENT APPLICATION NUMBER: US/09/472,667  
;; CURRENT FILING DATE: 1999-12-27  
;; PRIOR APPLICATION NUMBER: PCT/US99/02702  
;; PRIOR FILING DATE: 1999-02-09  
;; PRIOR APPLICATION NUMBER: US 09/008,097  
;; PRIOR FILING DATE: 1998-01-16  
;; PRIOR APPLICATION NUMBER: US 09/021,773  
;; PRIOR FILING DATE: 1998-02-11  
;; PRIOR APPLICATION NUMBER: US 08/924,757  
;; PRIOR FILING DATE: 1997-09-05  
;; PRIOR APPLICATION NUMBER: PCT/US97/15610  
;; PRIOR FILING DATE: 1997-09-05  
;; PRIOR APPLICATION NUMBER: US 08/708,661  
;; PRIOR FILING DATE: 1996-09-05  
;; PRIOR APPLICATION NUMBER: US 60/048,933  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/058,209  
;; PRIOR FILING DATE: 1996-09-05  
;; PRIOR APPLICATION NUMBER: PCT/US96/02631  
;; PRIOR FILING DATE: 1996-02-27  
;; PRIOR APPLICATION NUMBER: US 08/396,207  
;; PRIOR FILING DATE: 1995-02-28  
;; PRIOR APPLICATION NUMBER: US 08/485,472  
;; PRIOR FILING DATE: 1995-06-07  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 6  
;; LENGTH: 1167  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-472-667-6

Query Match 95.6%; Score 545; DB 18; Length 1167;  
Best Local Similarity 97.1%; Pred. No. 3.8e-44;  
Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSWFSGLLPVKYDERKTANGERNQKRSRRGCTRAGGCTCTPRYMCLRDPAEPPSPPTAGP 60  
DB 1 MSWFSGLLPVKYDERKTANGERNQKRSRRGCTRAGGCTCTPRYMCLRDPAEPPSPPTAGP 60  
QY 61 PRCPWODDAFIRGGPKGKGLRAVALGFEDTEVTTTTPAG 102  
DB 61 PRCPWODDAFIRGGPKGKGLRAVALGFEDTEVTTTTPAG 102

RESULT 4  
US-09-750-240-6  
;; Sequence 6, Application US/09750240  
;; GENERAL INFORMATION:  
;; APPLICANT: Hammond, H. K.  
;; APPLICANT: Insel, P. A.  
;; APPLICANT: Ping, P.  
;; APPLICANT: Post, S. R.

APPLICANT: Gao, M.  
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
FILE REFERENCE: 220002056723  
CURRENT APPLICATION NUMBER: US/09/750,240  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: US 09/472,667  
PRIOR FILING DATE: 1999-12-27  
PRIOR APPLICATION NUMBER: US 09/008,097  
PRIOR FILING DATE: 1998-01-16  
PRIOR APPLICATION NUMBER: US 08/924,757  
PRIOR FILING DATE: 1997-09-05  
PRIOR APPLICATION NUMBER: US 60/048,933  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: US 08/708,661  
PRIOR FILING DATE: 1996-09-05  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 1167  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-750-240-6

Query Match 95.6%; Score 545; DB 21; Length 1167;  
Best Local Similarity 97.1%; Pred. No. 3.8e-44;  
Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSFSGLLVPKVDKRTAWGNGKRRRGTRAGGFCCTPRYMSCLRDAPPSPTPAGP 60  
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DB 1 MSFSGLLVPKVDKRTAWGNGKRRRGTRAGGFCCTPRYMSCLRDAPPSPTPAGP 60  
|||||  
QY 61 PRCPWQDDAFIRRGPKXKGLRAVALGFEDTEVTTTAPG 102  
|||||  
DB 61 PRCPWQDDAFIRRGPKXKGLRAVALGFEDTEVTTTAPG 102  
|||||

RESULT 5  
US-09-750-240-13  
Sequence 13, Application US/09750240  
GENERAL INFORMATION:  
APPLICANT: Hammon, H. K.  
APPLICANT: Insel, P. A.  
APPLICANT: Ping, P. A.  
APPLICANT: Post, S. R.  
APPLICANT: Gao, M.

TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
FILE REFERENCE: 220002056723  
CURRENT APPLICATION NUMBER: US/09/750,240  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: US 09/472,667  
PRIOR FILING DATE: 1999-12-27  
PRIOR APPLICATION NUMBER: US 09/008,097  
PRIOR FILING DATE: 1998-01-16  
PRIOR APPLICATION NUMBER: US 08/924,757  
PRIOR FILING DATE: 1997-09-05  
PRIOR APPLICATION NUMBER: US 60/048,933  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: US 08/708,661  
PRIOR FILING DATE: 1996-09-05  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 1167  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Modified AC-VI  
US-09-750-240-13

Query Match 95.6%; Score 545; DB 21; Length 1167;  
Best Local Similarity 97.1%; Pred. No. 3.8e-44;

Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MSFSGLLVPKVDKRTAWGNGKRRRGTRAGGFCCTPRYMSCLRDAPPSPTPAGP 60  
|||||  
DB 1 MSFSGLLVPKVDKRTAWGNGKRRRGTRAGGFCCTPRYMSCLRDAPPSPTPAGP 60  
|||||  
QY 61 PRCPWQDDAFIRRGPKXKGLRAVALGFEDTEVTTTAPG 102  
|||||  
DB 61 PRCPWQDDAFIRRGPKXKGLRAVALGFEDTEVTTTAPG 102  
|||||

RESULT 6  
US-09-472-667-11  
Sequence 11, Application US/09472667  
GENERAL INFORMATION:  
APPLICANT: Hammon, H. Kirk  
APPLICANT: Insel, Paul A.  
APPLICANT: Ping, Peipel  
APPLICANT: Post, Steven R.  
APPLICANT: Gao, Meihua  
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
TITLE OF INVENTION: FAILURE  
FILE REFERENCE: 220002056722  
CURRENT APPLICATION NUMBER: US/09/472,667  
CURRENT FILING DATE: 1999-12-27  
PRIOR APPLICATION NUMBER: PCT/US99/02702  
PRIOR FILING DATE: 1999-02-09  
PRIOR APPLICATION NUMBER: US 09/008,097  
PRIOR FILING DATE: 1998-01-16  
PRIOR APPLICATION NUMBER: US 09/021,773  
PRIOR FILING DATE: 1998-02-11  
PRIOR APPLICATION NUMBER: US 08/924,757  
PRIOR FILING DATE: 1997-09-05  
PRIOR APPLICATION NUMBER: PCT/US97/15610  
PRIOR FILING DATE: 1997-09-05  
PRIOR APPLICATION NUMBER: US 08/708,661  
PRIOR FILING DATE: 1996-09-05  
PRIOR APPLICATION NUMBER: US 60/048,933  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/058,209  
PRIOR FILING DATE: 1996-09-05  
PRIOR APPLICATION NUMBER: PCT/US96/02631  
PRIOR FILING DATE: 1996-02-27  
PRIOR APPLICATION NUMBER: US 08/396,207  
PRIOR FILING DATE: 1995-02-28  
PRIOR APPLICATION NUMBER: US 08/485,472  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 1168  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-472-667-11

Query Match 95.6%; Score 545; DB 18; Length 1168;  
Best Local Similarity 97.1%; Pred. No. 3.8e-44;  
Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSFSGLLVPKVDKRTAWGNGKRRRGTRAGGFCCTPRYMSCLRDAPPSPTPAGP 60  
|||||  
DB 1 MSFSGLLVPKVDKRTAWGNGKRRRGTRAGGFCCTPRYMSCLRDAPPSPTPAGP 60  
|||||  
QY 61 PRCPWQDDAFIRRGPKXKGLRAVALGFEDTEVTTTAPG 102  
|||||  
DB 61 PRCPWQDDAFIRRGPKXKGLRAVALGFEDTEVTTTAPG 102  
|||||

RESULT 7  
US-09-750-240-11  
Sequence 11, Application US/09750240  
GENERAL INFORMATION:  
APPLICANT: Hammon, H. K.

[illegible][illegible]

```

RESULT 10
US-09-791-537-12125
; Sequence 12125, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILIES
; FILE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12125
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-12125

Query Match 75.8%; Score 432; DB 21; Length 1165;
Best Local Similarity 79.4%; Pred. NO. 4.6e-33;
Matches 81; Conservative 6; Mismatches 13; Indels 2; Gaps 2;
QY 1 MSWPSGLLVKVDKRTAWGNGKRSRRRTAGGFCPTRYMSCLRDAPPSPPTAGP 60

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Db 1 MSWPSGLLVPKVDGRKTAWGRNQCKRP-RHNASRGFCAPRYMSCLKNAEPPSPTPAAH 59

QY 61 PRCPQDDAIFRRGQPKXKGLGRLAVALGFEDTEVTTTAPG 102  
| | | | | : | | | | | : | | | | |

Db 60 TRCPQDEAFIRRGAPRGVGLGRLSVALGFDDETEV-TTPMG 100  
| | | | | : | | | | | : | | | | |

## RESULT 11

US-08-538-815-12  
; Sequence 12, Application US/08538815  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Wei-Jen  
; APPLICANT: Gilman, Alfred G.  
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYL  
; CYCLASE AND USES THEREFOR  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/538,815  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L.  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: UTSD:450  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1180 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-538-815-12

Query Match 75.8%; Score 432; DB 9; Length 1180;

Best Local Similarity 79.4%; Pred. No. 4.6e-33;

Matches 81; Conservative 7; Mismatches 12; Indels 2; Gaps 2;

QY 1 MSWFSGLLVKVDKRTAWGNGOKRRRGTRAGGCTPRYMNSCLRDAPPSPPTAGP 60

DB 15 MSWFSGLLVKVDKRTAWGNGOKRRP-RQATRRAGFCAPRYMSCLKNVPPSPPTAAR 73

QY 61 PRCPWQDDAFIRRGCPXKKGELGLRAVALGFEDTEVTTTTPAG 102

DB 74 TRCPWQDEAFIRRAGPGRGVELGLRSLVALGFDDETEV-TTPMG 114

## RESULT 12

US-09-791-537-17912  
; Sequence 17912, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN MEMBR  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 17912  
; LENGTH: 1180  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus

US-09-791-537-17912

Query Match 75.8%; Score 432; DB 21; Length 1180;

Best Local Similarity 79.4%; Pred. No. 4.6e-33;

Matches 81; Conservative 7; Mismatches 12; Indels 2; Gaps 2;

QY 1 MSWFSGLLVKVDKRTAWGNGOKRRRGTRAGGCTPRYMNSCLRDAPPSPPTAGP 60

DB 15 MSWFSGLLVKVDKRTAWGNGOKRRP-RQATRRAGFCAPRYMSCLKNVPPSPPTAAR 73

QY 61 PRCPWQDDAFIRRGCPXKKGELGLRAVALGFEDTEVTTTTPAG 102

DB 74 TRCPWQDEAFIRRAGPGRGVELGLRSLVALGFDDETEV-TTPMG 114

## RESULT 13

US-09-791-537-126174  
; Sequence 126174, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY M  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 126174  
; LENGTH: 1180  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-791-537-126174

Query Match 75.8%; Score 432; DB 21; Length 1180;

Best Local Similarity 79.4%; Pred. No. 4.6e-33;

Matches 81; Conservative 7; Mismatches 12; Indels 2; Gaps 2;

QY 1 MSWFSGLLVKVDKRTAWGNGOKRRRGTRAGGCTPRYMNSCLRDAPPSPPTAGP 60

DB 15 MSWFSGLLVKVDKRTAWGNGOKRRP-RQATRRAGFCAPRYMSCLKNVPPSPPTAAR 73

QY 61 PRCPWQDDAFIRRGCPXKKGELGLRAVALGFEDTEVTTTTPAG 102

DB 74 TRCPWQDEAFIRRAGPGRGVELGLRSLVALGFDDETEV-TTPMG 114

## RESULT 14

US-09-791-537-34515  
; Sequence 34515, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY M  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 34515  
; LENGTH: 1166  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-791-537-34515

Query Match 75.6%; Score 431; DB 21; Length 1166;

Best Local Similarity 79.4%; Pred. No. 5.7e-33;

Matches 81; Conservative 5; Mismatches 14; Indels 2; Gaps 2;

QY 1 MSWFSGLLVKVDKRTAWGNGOKRRRGTRAGGCTPRYMNSCLRDAPPSPPTAGP 60

Db 1 MSWFSGLLVPKVDERTANGERNQKRP-RHANRSGFCAPRYMSCLNNAPPSPTPAAH 59  
 QY 61 PRCPWODDAFIRRGDPXKKGELGRAVALGFEDTEVTTTTPAG 102  
 Db 60 TRCPWODEAFIRRGDPARGVELGLRSVALGFDDTEV-TTPMG 100

RESULT 15

US-09-791-537-18463  
 ; Sequence 18463, Application US/09791537  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bionomix, Inc.  
 ; APPLICANT: Debe, Derek  
 ; APPLICANT: Danzer, Joseph  
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
 ; TITLE OF INVENTION: METHODS OF USE THEREOF  
 ; FILE REFERENCE: 261/210  
 ; CURRENT APPLICATION NUMBER: US/09/791,537  
 ; CURRENT FILING DATE: 2001-02-22  
 ; NUMBER OF SEQ ID NOS: 153055  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 18463  
 ; LENGTH: 1166  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 US-09-791-537-18463

Query Match 75.1%; Score 428; DB 21; Length 1166;  
 Best Local Similarity 78.4%; Pred. No. 1.le-32;  
 Matches 80; Conservative 8; Mismatches 12; Indels 2; Gaps 2;

QY 1 MSWFSGLLVPKVDERTANGERNQKRSRRGTRAGGCTPRYMSCLRDAPPSPTPAGP 60  
 Db 1 MSWFSGLLVPKVDERTANGERNQKRP-RQATRARGFCAPRYMSCLKNVEPPSPTPAAR 59  
 QY 61 PRCPWODDAFIRRGDPXKKGELGRAVALGFEDTEVTTTTPAG 102  
 Db 60 TRCPWODEAFIRRGDPARGVELGLRSVALGFDDTEV-TTPMG 100

Search completed: February 19, 2003, 15:42:03  
 Job time : 357 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 19, 2003, 15:35:23 ; Search time 30 Seconds  
(without alignments)  
88.569 Million cell updates/sec

Title: US-09-750-240-2  
Perfect score: 570  
Sequence: 1 MSWFGLLVPKVDKRTAMG.....RAVALGFEDTEVTTTAPGPL 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues  
Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published\_Applications\_AA.\*
- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
  - 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
  - 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
  - 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
  - 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*
  - 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
  - 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	568	99.6	104	10	US-09-750-240-2
2	545	95.6	1167	10	US-09-750-240-6
3	545	95.6	1167	10	US-09-750-240-13
4	545	95.6	1168	9	US-10-201-000-2
5	545	95.6	1168	10	US-09-750-240-11
6	77.5	13.6	213	9	US-09-975-719-27
7	73.5	12.9	1234	10	US-09-854-173A-12
8	72	12.6	232	9	US-10-060-523-9
9	72	12.6	232	9	US-09-935-726-7
10	72	12.6	232	9	US-10-084-488-7
11	72	12.6	232	10	US-09-795-006A-147
12	72	12.6	232	12	US-10-127-551-5
13	71.5	12.5	722	10	US-09-894-998-15
14	70	12.3	156	10	US-09-764-870-402
15	70	12.3	402	10	US-09-933-561-16
16	69	12.1	160	10	US-09-864-761-38608
17	69	12.1	173	10	US-09-867-550-1072
18	67.5	11.8	468	10	US-09-814-777A-2
19	67.5	11.8	468	10	US-09-814-777A-4

20	67	11.8	325	10	US-09-927-112-10	Sequence 10, Appl
21	67	11.8	427	9	US-10-007-132-4	Sequence 4, Appli
22	67	11.8	1207	10	US-09-927-112-2	Sequence 2, Appli
23	66.5	11.7	802	9	US-10-174-590-312	Sequence 312, App
24	66.5	11.7	802	9	US-10-176-758-312	Sequence 312, App
25	66.5	11.7	802	9	US-10-175-737-312	Sequence 312, App
26	66.5	11.7	802	9	US-10-173-706-312	Sequence 312, App
27	66.5	11.7	802	9	US-10-175-738-312	Sequence 312, App
28	66.5	11.7	802	9	US-10-175-752-312	Sequence 312, App
29	66.5	11.7	802	9	US-10-176-482-312	Sequence 312, App
30	66.5	11.7	802	9	US-10-176-757-312	Sequence 312, App
31	66.5	11.7	802	9	US-10-176-913-312	Sequence 312, App
32	66.5	11.7	802	9	US-10-180-553-312	Sequence 312, App
33	66.5	11.7	802	9	US-10-180-557-312	Sequence 312, App
34	66.5	11.7	802	9	US-10-173-700-312	Sequence 312, App
35	66.5	11.7	802	9	US-10-174-572-312	Sequence 312, App
36	66.5	11.7	802	9	US-10-174-579-312	Sequence 312, App
37	66.5	11.7	802	9	US-10-174-582-312	Sequence 312, App
38	66.5	11.7	802	9	US-10-174-588-312	Sequence 312, App
39	66.5	11.7	802	9	US-10-175-739-312	Sequence 312, App
40	66.5	11.7	802	9	US-10-175-740-312	Sequence 312, App
41	66.5	11.7	802	9	US-10-175-743-312	Sequence 312, App
42	66.5	11.7	802	9	US-10-176-488-312	Sequence 312, App
43	66.5	11.7	802	9	US-10-176-492-312	Sequence 312, App
44	66.5	11.7	802	9	US-10-176-747-312	Sequence 312, App
45	66.5	11.7	802	9	US-10-176-750-312	Sequence 312, App

ALIGNMENTS

RESULT 1  
US-09-750-240-2  
; Sequence 2, Application US/09750240  
; Patent No. US20020103147A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammon, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
; TITLE OF INVENTION: FAILURE  
; FILE REFERENCE: 220002056723  
; CURRENT APPLICATION NUMBER: US/09/750,240  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/472,667  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 104  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(104)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-750-240-2

Query Match 99.6%; Score 568; DB 10; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2.3e-51;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSWFGLLVPKVDKRTAMGKRRRRGTRAGGCTPRYNCLRDAPPSPTPAGP 60

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; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified AC-VI
US-09-750-240-13

Query Match      95.6%; Score 545; DB 10; Length 1167;
Best Local Similarity 97.1%; Pred. No. 7.5e-48;
Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSWFSGLLPVKVDERKTAWGERNGOKRSRRRTAGGCTPRYMSCLRDAPPSPTPAGP 60
Db 1 MSWFSGLLPVKVDERKTAWGERNGOKRSRRRTAGGCTPRYMSCLRDAPPSPTPAGP 60
Qy 61 PRCPWQDDAFIRRGPGXKGKELGLRAVALGFEDTEVTTTTPAG 102
Db 61 PRCPWQDDAFIRRGPGXKGKELGLRAVALGFEDTEVTTTTPAG 102

RESULT 4
US-10-201-000-2
; Sequence 2, Application US/10201000
; Publication No. US20020187540A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/10/201,000
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US/09/474,076
; PRIOR FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1168
; TYPE: PRT
; ORGANISM: human type VI adenylyl cyclase
US-10-201-000-2

Query Match      95.6%; Score 545; DB 9; Length 1168;
Best Local Similarity 97.1%; Pred. No. 7.5e-48;
Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSWFSGLLPVKVDERKTAWGERNGOKRSRRRTAGGCTPRYMSCLRDAPPSPTPAGP 60
Db 1 MSWFSGLLPVKVDERKTAWGERNGOKRSRRRTAGGCTPRYMSCLRDAPPSPTPAGP 60
Qy 61 PRCPWQDDAFIRRGPGXKGKELGLRAVALGFEDTEVTTTTPAG 102
Db 61 PRCPWQDDAFIRRGPGXKGKELGLRAVALGFEDTEVTTTTPAG 102

RESULT 5
US-09-750-240-11
; Sequence 11, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-750-240-6

Query Match      95.6%; Score 545; DB 10; Length 1167;
Best Local Similarity 97.1%; Pred. No. 7.5e-48;
Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSWFSGLLPVKVDERKTAWGERNGOKRSRRRTAGGCTPRYMSCLRDAPPSPTPAGP 60
Db 1 MSWFSGLLPVKVDERKTAWGERNGOKRSRRRTAGGCTPRYMSCLRDAPPSPTPAGP 60
Qy 61 PRCPWQDDAFIRRGPGXKGKELGLRAVALGFEDTEVTTTTPAG 102
Db 61 PRCPWQDDAFIRRGPGXKGKELGLRAVALGFEDTEVTTTTPAG 102

RESULT 3
US-09-750-240-13
; Sequence 13, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
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; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified AC-VI
US-09-750-240-13

Query Match      95.6%; Score 545; DB 10; Length 1167;
Best Local Similarity 97.1%; Pred. No. 7.5e-48;
Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSWFSGLLPVKVDERKTAWGERNGOKRSRRRTAGGCTPRYMSCLRDAPPSPTPAGP 60
Db 1 MSWFSGLLPVKVDERKTAWGERNGOKRSRRRTAGGCTPRYMSCLRDAPPSPTPAGP 60
Qy 61 PRCPWQDDAFIRRGPGXKGKELGLRAVALGFEDTEVTTTTPAG 102
Db 61 PRCPWQDDAFIRRGPGXKGKELGLRAVALGFEDTEVTTTTPAG 102

RESULT 4
US-10-201-000-2
; Sequence 2, Application US/10201000
; Publication No. US20020187540A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/10/201,000
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US/09/474,076
; PRIOR FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1168
; TYPE: PRT
; ORGANISM: human type VI adenylyl cyclase
US-10-201-000-2

Query Match      95.6%; Score 545; DB 9; Length 1168;
Best Local Similarity 97.1%; Pred. No. 7.5e-48;
Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSWFSGLLPVKVDERKTAWGERNGOKRSRRRTAGGCTPRYMSCLRDAPPSPTPAGP 60
Db 1 MSWFSGLLPVKVDERKTAWGERNGOKRSRRRTAGGCTPRYMSCLRDAPPSPTPAGP 60
Qy 61 PRCPWQDDAFIRRGPGXKGKELGLRAVALGFEDTEVTTTTPAG 102
Db 61 PRCPWQDDAFIRRGPGXKGKELGLRAVALGFEDTEVTTTTPAG 102

RESULT 5
US-09-750-240-11
; Sequence 11, Application US/09750240
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Search completed: February 19, 2003, 15:43:08  
Job time : 31 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 19, 2003, 15:32:53 ; Search time 15 Seconds  
(without alignments)  
203.999 Million cell updates/sec

Title: US-09-750-240-2  
Perfect score: 570  
Sequence: 1 MSWFGSLVPRKDKRTANG.....RAVALGFEDTEVTTPAGPL 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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2: /cgn2.6/ptodata/1/1aa/5B-COMB.pep:\*  
3: /cgn2.6/ptodata/1/1aa/6A-COMB.pep:\*  
4: /cgn2.6/ptodata/1/1aa/6B-COMB.pep:\*  
5: /cgn2.6/ptodata/1/1aa/PCTUS-COMB.pep:\*  
6: /cgn2.6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	568	99.6	104	US-09-008-097-2	Sequence 2, Appli
2	545	95.6	1167	US-09-008-097-6	Sequence 6, Appli
3	545	95.6	1168	US-09-474-076-2	Sequence 2, Appli
4	472.5	82.9	1165	US-08-240-357-2	Sequence 2, Appli
5	432	75.8	1180	US-08-726-214-12	Sequence 12, Appli
6	78.5	13.8	465	US-08-447-965A-2	Sequence 2, Appli
7	77.5	13.6	213	US-09-199-637A-27	Sequence 27, Appli
8	74	13.0	233	US-08-458-568A-4	Sequence 4, Appli
9	73	12.8	223	US-09-206-676C-1	Sequence 1, Appli
10	72	12.6	231	PCT-US96-09001-10	Sequence 10, Appli
11	72	12.6	232	US-08-999-811-7	Sequence 7, Appli
12	72	12.6	232	US-08-824-996-9	Sequence 9, Appli
13	72	12.6	232	US-08-807-992B-4	Sequence 4, Appli
14	72	12.6	232	US-09-042-105-7	Sequence 7, Appli
15	72	12.6	422	US-09-724-864-45	Sequence 45, Appli
16	71.5	12.5	226	US-09-206-676C-2	Sequence 2, Appli
17	70	12.3	180	US-08-483-533-29	Sequence 29, Appli
18	70	12.3	180	US-09-283-471A-29	Sequence 29, Appli
19	70	12.3	355	US-08-483-533-41	Sequence 41, Appli
20	70	12.3	355	US-09-283-471A-41	Sequence 41, Appli
21	70	12.3	355	PCT-US91-06532-3	Sequence 3, Appli
22	70	12.3	402	US-09-292-097-16	Sequence 16, Appli
23	69.5	12.2	1312	US-09-041-886-19	Sequence 19, Appli
24	69.5	12.2	2205	US-08-093-453B-2	Sequence 2, Appli
25	69	12.1	610	US-08-865-337A-6	Sequence 6, Appli
26	68	11.9	1323	US-08-026-138E-4	Sequence 4, Appli
27	67	11.8	427	US-09-199-737-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-09-008-097-2  
: Sequence 2, Application US/09008097  
: Patent No. 6306830  
: GENERAL INFORMATION:  
: APPLICANT: Hammond, H. Kirk  
: APPLICANT: Insel, Paul A.  
: APPLICANT: Ping, Peipei  
: APPLICANT: Post, Steven R.  
: APPLICANT: Gao, Meihua  
: TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE  
: TITLE OF INVENTION: HEART FAILURE  
: NUMBER OF SEQUENCES: 9  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: MORRISON & FOERSTER  
: STREET: 755 PAGE MILL ROAD  
: CITY: PALO ALTO  
: STATE: CA  
: COUNTRY: USA  
: ZIP: 94304-1018  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette  
: COMPUTER: IBM Compatible  
: OPERATING SYSTEM: DOS  
: SOFTWARE: FASTSEQ for Windows Version 2.0  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/008,097  
: FILING DATE:  
: CLASSIFICATION:  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER:  
: FILING DATE:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Dvylan, Tyler M  
: REGISTRATION NUMBER: 37,612  
: REFERENCE/DOCKET NUMBER: 22000-20567.21  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 650-813-5600  
: TELEFAX: 650-494-0792  
: TELEX: 706141  
: INFORMATION FOR SEQ ID NO: 2:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 104 amino acids  
: TYPE: amino acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: FRAGMENT TYPE: internal  
US-09-008-097-2

28	67	11.8	427	4	US-08-900-230-4	Sequence 4, Appli
29	67	11.8	427	4	US-09-058-333A-4	Sequence 4, Appli
30	66	11.6	732	1	US-08-317-522A-5	Sequence 5, Appli
31	66	11.6	778	1	US-08-439-818A-5	Sequence 5, Appli
32	66	11.6	778	2	US-08-751-965-5	Sequence 5, Appli
33	66	11.6	778	2	US-08-738-975-5	Sequence 5, Appli
34	66	11.6	778	2	US-08-728-626-5	Sequence 5, Appli
35	66	11.6	778	3	US-08-808-599A-5	Sequence 5, Appli
36	65.5	11.5	284	2	US-08-320-148B-2	Sequence 2, Appli
37	65.5	11.5	284	3	US-08-589-028-6	Sequence 6, Appli
38	65.5	11.5	284	3	US-08-784-582-6	Sequence 6, Appli
39	65.5	11.5	284	4	US-08-785-271-6	Sequence 6, Appli
40	65.5	11.5	284	4	US-09-031-898-2	Sequence 2, Appli
41	65.5	11.5	659	1	US-08-240-049B-16	Sequence 16, Appli
42	65.5	11.5	659	1	US-08-259-148A-20	Sequence 20, Appli
43	65.5	11.5	659	1	US-08-484-054-20	Sequence 20, Appli
44	65.5	11.5	659	2	US-07-876-941A-20	Sequence 20, Appli
45	65.5	11.5	659	4	US-08-477-292-14	Sequence 14, Appli



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QY      61 PRCPWDDAFIRRGPGPKXKELGLRAVALGEDTEVTTPAG 102
       !!!!!!! !! : !!!!!!! !! I
Db      74 TRCPWDDEAIFRRAGPGRGVELGRLSRVALGPDDEV-TTPMG 114

RESULT 6
US-08-447-965A-2
; Sequence 2, Application US/08447965A
; Patent No. 5776692
; GENERAL INFORMATION:
; APPLICANT: El-Zaatari, Fouad A.K.
; APPLICANT: Graham, David Y.
; APPLICANT: Naser, Saleh
; TITLE OF INVENTION: Mycobacterial Genus-Specific DNA Probe
; TITLE OF INVENTION: and its Expressed Product
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 801 Pennsylvania Ave. N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Davis, Peter J.
; REGISTRATION NUMBER: 36,119
; REFERENCE/DOCKET NUMBER: 311.019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-662-4669
; TELEFAX: 202-662-4643
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 465 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-447-965A-2

Query Match           13.8%; Score 78.5; DB 1; Length 465
Best Local Similarity 37.5%; Pred. No. 0.56;
Matches   30; Conservative    4; Mismatches   35; Indels   1

QY      13 DERKTAWGERNGQRSSRRRGTGAGCGCTPRYMSCLRDAEPFS-----BTPAGPPGP
       !: : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      99 DQDQGADARANRPAPHARRRTTRA--IAMPAS--TSAAPPESHRAALSAAGAAPP
       |: : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      68 DAFIGRGPGPKXKELGLRAV 87
       | || | |:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     153 PAAGRQQGERRRVLGLAAV 172

RESULT 7
US-09-199-637A-27
; Sequence 27, Application US/09199637A
; Patent No. 6355411
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick
; APPLICANT: Goodman, Howard M.
; APPLICANT: Rahme, Laurence G.
; APPLICANT: Mahajan-Miklos, Shalina
; APPLICANT: Tan, Man-Wah
; APPLICANT: Cao, Hui
; APPLICANT: Drenkard, Eliana

```







```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,105
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,550
; FILING DATE: 8-MAR-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,968
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TO BE ASSIGNED
; FILING DATE: 24-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ERIC K. STEFFE
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-09-042-105-7

Query Watch                12.6%; Score 72; DB 3; Length 232;
Best Local similarity      32.8%; Pred. No. 1.3;
Matches    21; Conservative   5; Mismatches 16; Indels 22; Gaps

QY   10 PKVD-----ERKTAMGRNGOKRRRGTAGGCTPRYMS-----CLRDAEPPSPT 56
     || | :| |: | |||| |:| || |
DB   132 PKDRAQRQEKSVRGKGKGRKRKK-----RYKSWSYVGACRLPWSLPGPH 181

QY   57 PAGP 60
     | ||
DB   183 PCGP 186

RESULT 15
US-09-724-864-45
; Sequence 45, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-45

Query Match                12.6%; Score 72; DB 4; Length 422;
Best Local similarity      24.6%; Pred. No. 2.7;
Matches    29; Conservative  13; Mismatches 36; Indels 40; Gaps
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PI Hammond HK, Gao M;  
 XX WPI; 2001-418260/44.  
 DR N-PSDB; AAD08561.  
 XX Novel polynucleotide encoding a modified adenylyl cyclase polypeptide  
 PT useful for enhancing cardiac function in mammalian hearts, and for  
 PT treating heart disease, especially congestive heart failure -  
 XX Example 5; Page 115; 153pp; English.  
 XX The present invention relates to methods and compositions for enhancing  
 CC cardiac function in mammalian hearts by inserting transgenes encoding  
 CC beta-adrenergic signalling proteins (beta-ASP) which increase  
 CC beta-adrenergic responsiveness within the myocardium using in vivo  
 CC gene therapy. The beta-ASPs of the invention include beta-adrenergic  
 CC receptors (beta-AR), adenylyl cyclases (also referred as adenylyl cyclase,  
 CC adenylylate cyclase and cAMP synthetase) and G-protein receptor kinase  
 CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
 CC in mammalian hearts and for treating heart disease, especially  
 CC congestive heart failure. The present sequence is a human  
 CC partial cardiac adenylyl cyclase VI (ACVI) isoform which is used for  
 CC generating a third beta-ASP transgene, used in the exemplification  
 CC of the invention.  
 XX Sequence 104 AA;  
 SQ Query Match 99.6%; Score 568; DB 22; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-55;  
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSWFSGLLVKPKVDERTKAWGERNGQKRRRGTTRAGGCTPRYMSCLRDAPPSPTPAGP 60  
 DB 1 MSWFSGLLVKPKVDERTKAWGERNGQKRRRGTTRAGGCTPRYMSCLRDAPPSPTPAGP 60  
 QY 61 PRCPWQDDAFIRRGPGPKXGKELGLRAVALGFEDTEVTTTPAGPL 104  
 DB 61 PRCPWQDDAFIRRGPGPKXGKELGLRAVALGFEDTEVTTTPAGPL 104  
 RESULT 2  
 AAW53345  
 ID AAW53345 standard; Protein; 709 AA.  
 XX AC AAW53345;  
 XX 17-JUL-1998 (first entry)  
 XX Human adenylyl cyclase isoform VI.  
 DE Human; adenylyl cyclase VI; AC-VI; beta-adrenergic signalling protein;  
 KW transgene; gene therapy; congestive heart failure; cardiac function;  
 KW adenovirus.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Misc-difference 77 /label= unknown  
 FT /note= "encoded by NGC"  
 FT Misc-difference 105 /label= unknown  
 FT /note= "encoded by AAN where N indicates a gap of 0.5 kb"  
 FT W09810085-A2.  
 PN 12-MAR-1998.  
 PD 05-SEP-1997; 97WO-US15610.  
 XX 16-JUN-1997; 97US-0048933.  
 PR 05-SEP-1996; 96US-0708661.  
 XX

PA (COLL-) COLLATERAL THERAPEUTICS.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Gao M, Hammond HK, Insel PA, Ping P, Post SR;  
 XX WPI; 1998-193633/17.  
 DR N-PSDB; AAV23246.  
 XX Vectors containing transgene(s) encoding beta-adrenergic signalling  
 PT proteins - useful for gene therapy of congestive heart failure  
 XX Claim 62; Fig 12B; 114pp; English.  
 PS The present sequence represents human adenylyl cyclase isoform VI (AC-VI)  
 CC from the present invention. The present invention describes a  
 CC recombinant replication-defective viral particle (I) comprising a gene  
 CC encoding a beta-adrenergic signalling protein (beta-ASP) operably  
 CC linked to a promoter. Also described are: (1) a recombinant pro-viral  
 CC plasmid (Ia) comprising a gene encoding a beta-ASP, as above, operably  
 CC linked to a promoter and further comprising a replication-defective  
 CC viral genome; (2) a (mammalian) cell transfected with (I) or (Ia); (3)  
 CC an isolated polynucleotide comprising a sequence encoding a human  
 CC adenylyl cyclase isoform VI (AC-VI), or a variant having AC activity;  
 CC (4) a human AC-VI encoded by (3); (5) an isolated polynucleotide  
 CC sequence which hybridises at high stringency to (3); and (6) a vector  
 CC comprising the polynucleotide of (3). (I) can be used to form a  
 CC filtered adenovirus particle preparation. (I) is used to enhance  
 CC cardiac function in mammals.  
 XX Sequence 709 AA;  
 SQ Query Match 99.6%; Score 568; DB 19; Length 709;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-54;  
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSWFSGLLVKPKVDERTKAWGERNGQKRRRGTTRAGGCTPRYMSCLRDAPPSPTPAGP 60  
 DB 1 MSWFSGLLVKPKVDERTKAWGERNGQKRRRGTTRAGGCTPRYMSCLRDAPPSPTPAGP 60  
 QY 61 PRCPWQDDAFIRRGPGPKXGKELGLRAVALGFEDTEVTTTPAGPL 104  
 DB 61 PRCPWQDDAFIRRGPGPKXGKELGLRAVALGFEDTEVTTTPAGPL 104  
 RESULT 3  
 AAE04310  
 ID AAE04310 standard; Protein; 1167 AA.  
 XX AC AAE04310;  
 XX 04-SEP-2001 (first entry)  
 XX Human cardiac adenylyl cyclase VI (ACVI) isoform #1.  
 DE Human; cardiac; beta-adrenergic signalling protein; beta-ASP;  
 KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
 KW adenylyl cyclase; adenylylate cyclase; cAMP synthetase;  
 KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
 KW cardiac adenylyl cyclase VI; ACVI isoform; beta-ASP transgene.  
 XX Homo sapiens.  
 XX WO200148164-A2.  
 PN 05-JUL-2001.  
 PD 26-DEC-2000; 2000WO-US35411.  
 XX 27-DEC-1999; 99US-0472667.  
 PR (REGC ) UNIV CALIFORNIA.  
 PA Hammond HK, Gao M;  
 PI

XX WPI; 2001-418260/44.  
 DR N-PSDB; AAD08563.  
 XX  
 PT Novel polynucleotide encoding a modified adenylyl cyclase polypeptide  
 PT useful for enhancing cardiac function in mammalian hearts, and for  
 PT treating heart disease, especially congestive heart failure -  
 XX  
 PS Example 5; Page 130-133; 153pp; English.  
 XX  
 CC The present invention relates to methods and compositions for enhancing  
 CC cardiac function in mammalian hearts by inserting transgenes encoding  
 CC beta-adrenergic signalling proteins (beta-ASP) which increase  
 CC beta-adrenergic responsiveness within the myocardium using in vivo  
 CC gene therapy. The beta-ASPs of the invention include beta-adrenergic  
 CC receptors (beta-AR), adenylyl cyclases (also referred as adenylyl cyclase,  
 CC adenylylate cyclase and cAMP synthetase) and G-protein receptor kinase  
 CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
 CC in mammalian hearts and for treating heart disease, especially  
 CC congestive heart failure. The present sequence is a human  
 CC cardiac adenylyl cyclase VI (ACVI) isoform which is used for generating  
 CC a third beta-ASP transgene, used in the exemplification  
 CC of the invention.  
 XX  
 SQ Sequence 1167 AA;  
 Query Match 95.6%; Score 545; DB 22; Length 1167;  
 Best Local Similarity 97.1%; Pred. No. 3.1e-51;  
 Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MSWFSGLLPKVDERTANGERNQKRRRRGTRAGGCTTPRYMSCLRDAEPSPPTPAG 60  
 Db 1 MSWFSGLLPKVDERTANGERNQKRRRRGTRAGGCTTPRYMSCLRDAEPSPPTPAG 60  
 QY 61 PRCPWDDAFIRRGPGKGKGLRAVALGFEDTEVTTT 102  
 Db 61 PRCPWDDAFIRRGPGKGKGLRAVALGFEDTEVTTT 102  
 RESULT 4  
 AAE04312  
 ID AAE04312 standard; Protein; 1167 AA.  
 AC AAE04312;  
 XX  
 DT 04-SEP-2001 (first entry)  
 XX  
 DE Human modified cardiac adenylyl cyclase VI (ACVI) isoform.  
 XX  
 KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;  
 KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
 KW adenylyl cyclase; adenylylate cyclase; cAMP synthetase;  
 KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
 KW cardiac adenylyl cyclase VI; ACVI isoform; beta-ASP transgene.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200148164-A2.  
 XX  
 PD 05-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000WO-US35411.  
 XX  
 PR 27-DEC-1999; 99US-0472667.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Hammond HK, Gao M;  
 XX  
 DR WPI; 2001-418260/44.  
 DR N-PSDB; AAD08568.  
 XX

PT Novel polynucleotide encoding a modified adenylyl cyclase polypeptide  
 PT useful for enhancing cardiac function in mammalian hearts, and for  
 PT treating heart disease, especially congestive heart failure -  
 XX  
 PS Claim 3; Page 150-153; 153pp; English.  
 XX  
 CC The present invention relates to methods and compositions for enhancing  
 CC cardiac function in mammalian hearts by inserting transgenes encoding  
 CC beta-adrenergic signalling proteins (beta-ASP) which increase  
 CC beta-adrenergic responsiveness within the myocardium using in vivo  
 CC gene therapy. The beta-ASPs of the invention include beta-adrenergic  
 CC receptors (beta-AR), adenylyl cyclases (also referred as adenylyl cyclase,  
 CC adenylylate cyclase and cAMP synthetase) and G-protein receptor kinase  
 CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
 CC in mammalian hearts and for treating heart disease, especially  
 CC congestive heart failure. The present sequence is a human  
 CC modified cardiac adenylyl cyclase VI (ACVI) isoform which is used for  
 CC generating a beta-ASP transgene, used in the exemplification of the  
 CC invention.  
 XX  
 SQ Sequence 1167 AA;  
 Query Match 95.6%; Score 545; DB 22; Length 1167;  
 Best Local Similarity 97.1%; Pred. No. 3.1e-51;  
 Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MSWFSGLLPKVDERTANGERNQKRRRRGTRAGGCTTPRYMSCLRDAEPSPPTPAG 60  
 Db 1 MSWFSGLLPKVDERTANGERNQKRRRRGTRAGGCTTPRYMSCLRDAEPSPPTPAG 60  
 QY 61 PRCPWDDAFIRRGPGKGKGLRAVALGFEDTEVTTT 102  
 Db 61 PRCPWDDAFIRRGPGKGKGLRAVALGFEDTEVTTT 102  
 RESULT 5  
 AAW30599  
 ID AAW30599 standard; Protein; 1168 AA.  
 XX  
 AC AAW30599;  
 XX  
 DT 21-MAY-1999 (first entry)  
 XX  
 DE Human type VI adenylyl cyclase.  
 XX  
 KW Adenylyl cyclase type VI; human; hAC6; therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9901547-A1.  
 XX  
 PD 14-JAN-1999.  
 XX  
 PF 01-JUL-1998; 98WO-US13694.  
 XX  
 PR 01-JUL-1997; 97US-0886550.  
 PR 01-JUL-1997; 97US-0070904.  
 XX  
 PA (CORP-) COR THERAPEUTICS INC.  
 XX  
 PI Tomlinson JA;  
 XX  
 DR WPI; 1999-106049/09.  
 DR N-PSDB; AAX00461.  
 XX  
 PT Newly isolated and purified human type VI adenylyl cyclase (hAC6)  
 PT polypeptide - useful for identifying potential therapeutic agents  
 PT that modulate hAC6 activity, and for the diagnosis of  
 PT hAC6-associated diseases and disorders  
 XX  
 PS Claim 1; Fig 1A-G; 42pp; English.  
 XX  
 CC This is the amino acid sequence of human type VI adenylyl cyclase

CC (hac6), as deduced from an isolated cDNA clone sequence (see  
CC AAX00461). hac6 is expressed mainly in the heart and brain. It has  
CC a similar putative structure to other adenylyl cyclase isoforms  
CC but, like type V, is distinguishable in that it has a larger  
CC N-terminus and a relatively shorter C-terminus as it lacks the C2b  
CC region. The invention relates to the hac6 gene, methods for the  
CC recombinant production of purified hac6 and the proteins made by  
CC these methods, antibodies against hac6, vectors, probes and host  
CC cells (especially HBK-293) transformed by genes encoding  
CC polypeptides having hac6 activity, along with diagnostic and  
CC therapeutic uses for these various reagents. hac6 can be used as a  
CC tool to screen for agonists and antagonists that stimulate/inhibit  
CC hac6. Such compounds have therapeutic utility in treating diseases  
CC caused by aberrant activity of this enzyme, and diseases whose  
CC symptoms can be ameliorated by stimulating or inhibiting the  
CC activity of hac6.

XX Sequence 1168 AA;  
SQ Query Match 95.6%; Score 545; DB 20; Length 1168;  
Best Local Similarity 97.1%; Pred. No. 3.1e-51;  
Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSWFGLLVPKVDERTKATWGERNGQKRRRGTRAGGCTPRYMSCLRDAPPSPTPAGP 60  
Db 1 MSWFGLLVPKVDERTKATWGERNGQKRRRGTRAGGCTPRYMSCLRDAPPSPTPAGP 60  
Qy 61 PRCPQDDAFIRRGPGKXGKGLGRAVALGFEDTEVTTTTPAG 102  
Db 61 PRCPQDDAFIRRGPGKXGKGLGRAVALGFEDTEVTTTTPAG 102

RESULT 6  
AAE04311  
ID AAE04311 standard; Protein; 1168 AA.

XX AAE04311;  
XX 04-SEP-2001 (first entry)  
XX Human cardiac adenylyl cyclase VI (ACVI) isoform #2.  
XX Human; cardiac; beta-adrenergic signalling protein; beta-ASP;  
XX myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
XX adenylyl cyclase; adenylyl cyclase; CAMP synthetase;  
XX G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
XX cardiac adenylyl cyclase VI; ACVI isoform; beta-ASP transgene.

OS Homo sapiens.  
XX WO200148164-A2.  
XX 05-JUL-2001.  
XX 26-DEC-2000; 2000WO-US35411.  
XX 27-DEC-1999; 99US-0472667.  
XX (REGC ) UNIV CALIFORNIA.

XX Hammond HK, Gao M;  
XX WPI; 2001-418260/44.  
XX N-PSDB; AAD08567.

PT Novel polynucleotide encoding a modified adenylyl cyclase polypeptide  
PT useful for enhancing cardiac function in mammalian hearts, and for  
PT treating heart disease, especially congestive heart failure -  
XX  
XX Claim 5; Page 140-143; 153pp; English.

XX The present invention relates to methods and compositions for enhancing  
XX cardiac function in mammalian hearts by inserting transgenes encoding

CC beta-adrenergic signalling proteins (beta-ASP) which increase  
CC beta-adrenergic responsiveness within the myocardium using in vivo  
CC gene therapy. The beta-ASPs of the invention include beta-adrenergic  
CC receptors (beta-AR), adenylyl cyclases (also referred as adenylyl cyclase,  
CC adenylyl cyclase and CAMP synthetase) and G-protein receptor kinase  
CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
CC in mammalian hearts and for treating heart disease, especially  
CC congestive heart failure. The present sequence is a human  
CC cardiac adenylyl cyclase VI (ACVI) isoform which is used for generating  
CC a fourth beta-ASP transgene, used in the exemplification  
CC of the invention.

XX Sequence 1168 AA;  
SQ

Query Match 95.6%; Score 545; DB 22; Length 1168;  
Best Local Similarity 97.1%; Pred. No. 3.1e-51;  
Matches 99; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSWFGLLVPKVDERTKATWGERNGQKRRRGTRAGGCTPRYMSCLRDAPPSPTPAGP 60  
Db 1 MSWFGLLVPKVDERTKATWGERNGQKRRRGTRAGGCTPRYMSCLRDAPPSPTPAGP 60  
Qy 61 PRCPQDDAFIRRGPGKXGKGLGRAVALGFEDTEVTTTTPAG 102  
Db 61 PRCPQDDAFIRRGPGKXGKGLGRAVALGFEDTEVTTTTPAG 102

RESULT 7  
AAR37309  
ID AAR37309 standard; Protein; 1165 AA.

XX AAR37309;  
XX 14-SEP-1993 (first entry)  
XX Cardiac adenylyl cyclase.  
XX Regulation; cardiac function; heart; heart failure.

XX Canis familiaris.  
XX EP543137-A.  
XX 26-MAY-1993.

XX 12-OCT-1992; 92EP-0117374.  
XX 18-NOV-1991; 91US-0793961.  
XX (AMCY ) AMERICAN CYANAMID CO.

XX Ishikawa Y;  
XX WPI; 1993-168873/21.  
XX N-PSDB; AAQ42525.

XX Purified DNA encoding cardiac adenylyl cyclase - useful to screen  
XX for cpds. which stimulate activity of the cyclase  
XX Claim 11; Fig 2; 34pp; English.

XX A canine heart cDNA library was constructed in lambda gt10 and was  
XX screened with a 970 bp AatI-HincII fragment from type I adenylyl  
XX cyclase cDNA probe (encodes the first cytoplasmic domain of adenylyl  
XX cyclase, which has significant homology to other previously known  
XX types of adenylyl cyclase). One positive clone, of 5.4 kb was obtd.  
XX Positive colonies were subcloned into pUC18 and further subcloned  
XX and sequenced bidirectionally. The 5.4 kb clone was used to  
XX rescreen the library and on overlapping clone contg. the 5' end of  
XX the gene was isolated. Together the two clones cover the complete  
XX canine cardiac adenylyl cyclase gene. The gene is suspected of  
XX being involved in the regulation of cardiac function and it is thought  
XX that decreased activity of adenylyl cyclase in the heart may be a



CC major factor in the development of heart failure. Thus the adenylyl  
CC cyclase gene is useful to screen cpds. which stimulate the activity  
CC of the cyclase.

XX Sequence 1165 AA;

SQ Query Match 82.9%; Score 472.5; DB 14; Length 1165;  
Best Local Similarity 83.2%; Pred. No. 3.1e-43;  
Matches 89; Conservative 2; Mismatches 11; Indels 5; Gaps 2;

QY 1 MSWFSGLLVPKVDERKTANGERNQKRRRGCTPRYMNSCLRDAPPSPTPAGP 60  
DB 1 MSWFSGLLVPKVDERKTANGERNQKRP-RRGTRTSGFCTPRYMNSCLRDAPPSPTPAP 59  
QY 61 PRCPWDDAFIRGGPKXKELGLRAVALGFEDTE-----VTTTPAGP 103  
DB 60 PRCPWQDEAFIRGGPKXKELGLRAVALGFEDTEAMSAVGAAGGP 106

RESULT 8

ABB57257  
ID ABB57257 standard; Protein; 1165 AA.

XX AC ABB57257;

XX DT 07-MAR-2002 (first entry)

XX DE Mouse ischaemic condition related protein sequence SEQ ID NO:717.

XX KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;  
XX KW vasospastic ischaemia; ischaemic condition; ischaemic disease.

XX OS Mus musculus.

XX PN W0200188188-A2.

XX PD 22-NOV-2001.

XX PF 18-MAY-2001; 2001WO-JP04192.

XX PR 18-MAY-2000; 2000JP-0145977.

XX PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

XX PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX DR WPI; 2002-034733/04.

XX DR N-PSDB; ABI99680.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
PT expression levels of particular genes defined in the specification or  
PT by determining the expression profile of a gene group comprising these  
PT genes -

XX Claim 2; Page 1781-1786; 2690pp; English.

XX The present invention describes a method for examining ischaemic  
CC conditions, comprising measuring the expression levels of particular  
CC genes (1) in a test sample or determining the expression profile of a  
CC gene group in the sample comprising genes selected from (1). The method  
CC is useful for examining the ischaemic condition (e.g. compressive  
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring  
CC expression levels of particular genes (ABI99202 to ABI99912, encoding  
CC the protein sequences in ABB57020 to ABB57374) or by determining the  
CC expression profile of a gene group comprising these genes. The  
CC expression levels or expression profiles produced by these genes are  
CC used as an indicator when screening for ischaemic condition-improving  
CC drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914  
CC represent PCR primers for a mouse ischaemic condition related sequence,  
CC which are used in the exemplification of the present invention.

XX Sequence 1165 AA;

Query Match 75.8%; Score 432; DB 23; Length 1165;  
Best Local Similarity 79.4%; Pred. No. 8.9e-39;  
Matches 81; Conservative 6; Mismatches 13; Indels 2; Gaps 2;

QY 1 MSWFSGLLVPKVDERKTANGERNQKRRRGCTPRYMNSCLRDAPPSPTPAGP 60  
DB 1 MSWFSGLLVPKVDERKTANGERNQKRP-RHANRASGFCAPRYMNSCLKNAEPSPPTAAH 59  
QY 61 PRCPWDDAFIRGGPKXKELGLRAVALGFEDTEVTTTPAG 102  
DB 60 TRCPWQDEAFIRAGPGRGVELGLRSVALGFDTEV-TTPMG 100

RESULT 9

AAB02010  
ID AAB02010 standard; Protein; 1180 AA.

XX AC AAB02010;

XX DT 03-JAN-2001 (first entry)

XX DE Type VI adenylyl cyclase.

XX KW Adenylyl cyclase; type I; type II; recombinant; enzyme; CAMP;  
XX KW cyclic AMP; adenosine monophosphate; screening; stimulation;  
XX KW inhibition; treatment; cholera; pituitary tumour; heart failure;  
XX KW ischaemia; endocrine disorder; cell necrosis;  
XX KW pseudohypoparathyroidism; endocrine deficiency; human.

XX OS Homo sapiens.

XX PN US6107076-A.

XX PD 22-AUG-2000.

XX PF 04-OCT-1996; 96US-0726214.

XX PR 04-OCT-1995; 95US-0005498.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Gilman AG, Tang W;

XX DR WPI; 2000-578539/54.

XX DR N-PSDB; AAA53923.

XX Novel soluble mammalian polypeptide composition comprising adenylyl  
PT cyclase activity for screening stimulators and inhibitors of adenylyl  
PT cyclase, is activated by Gsalph

XX Disclosure; Columns 79-84; 73pp; English.

XX A recombinant Adenylyl cyclase is described which lacks membrane  
CC bound domains. Separation and purification of the recombinant  
CC enzyme is much easier compared with wild type enzymes and the  
CC recombinant enzyme is more stable than the wild type enzyme which  
CC allows easier screening of compounds that stimulate and inhibit  
CC adenylyl cyclase activity. The recombinant adenylyl cyclase comprises  
CC a chimera of adenylyl cyclase C1 and C2 domains linked covalently.  
CC The domains may be linked by a linker peptide. The recombinant  
CC adenylyl cyclase is useful for screening inhibitors and stimulators  
CC of adenylyl cyclase activity. Inhibitors of the enzyme are useful for  
CC treating cholera, pituitary tumors, heart failure, ischaemia,  
CC endocrine disorders and cell necrosis. Stimulators of adenylyl  
CC cyclase are useful for treating pseudohypoparathyroidism and other  
CC endocrine deficiencies.

XX SQ Sequence 1180 AA;

Query Match 75.8%; Score 432; DB 21; Length 1180;  
Best Local Similarity 79.4%; Pred. No. 9e-39;  
Matches 81; Conservative 7; Mismatches 12; Indels 2; Gaps 2;



CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 55 AA;

Query Match 14.7%; Score 84; DB 22; Length 55;

Best Local Similarity 46.5%; Pred. No. 0.065;

Matches 20; Conservative 3; Mismatches 12; Indels 8; Gaps 1;

QY 22 RNQKSRRRGCTAGGCTPRYMSCLRDAPPSPFTAGPPRCP 64

Db 21 RHQHRTPPGTCAGPAPP-----GPPSPFTAGPVRRP 55

RESULT 12

AAG35230

ID AAG35230 standard; Protein; 370 AA.

XX AC AAG35230;

XX DT 18-OCT-2000 (first entry)

XX DE Zea mays protein fragment SEQ ID NO: 43007.

KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence; corn.

XX OS Zea mays subsp. mays.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132484.

PR 06-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 07-MAY-1999; 99US-0132487.

PR 11-MAY-1999; 99US-0132863.

PR 14-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 18-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 02-JUL-1999; 99US-0142154.  
PR 06-JUL-1999; 99US-0142055.  
PR 08-JUL-1999; 99US-0142390.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144321.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.

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PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 14.2%; Score 81; DB 21; Length 370;

Best Local Similarity 39.3%; Pred. No. 1.2;
Matches 24; Conservative 7; Mismatches 20; Indels 10; Gaps 4;
QY 39 CTPRYM-SC-LRDAPPSPPTAGP-----PRCPWODDAFIRGGPKKKGELGRAVALGF 91
DB 10 CFPLPMESCFAATAPSPFPSPSPRAPC---PILRPKPKKGKQIGVRRASGF 66
QY 92 E 92
DB 67 D 67

RESULT 13
ABP60967
ID ABP60967 standard; Protein; 782 AA.
XX
AC ABP60967;
XX
DT 10-SEP-2002 (first entry)
XX
DE Novel human protein. SEQ ID 54.
XX
KW Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian;
KW nootropic; neuroprotective; immunosuppressive; haemostatic;
KW antiinflammatory; cardiant; antiulcer; virucide; antithyroid;
KW cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
KW wound healing disorders; atherosclerosis; parkinson's disease;
KW Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
KW inflammation; neoplastic disease; nervous system disorder;
KW cardiovascular disorders; pancreatitis; respiratory disorder;
KW hyperproliferation; systemic autoimmune disease; hyper-immunity;
KW developmental abnormality; gastrointestinal ulceration; neuropathy;
KW haematological disease; metabolic disease; sperm dysfunction;
KW thyroid disorder; hypothyroidism; brain damage; colitis;
KW cone photo-transduction deficiency; neurological disease; stroke;
KW angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;
KW trachea; thymus; lymph node; muscular system; obesity; anorexia;
KW growth abnormality; precocious puberty; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200250105-A1.
XX
PD 27-JUN-2002.
XX
PF 17-DEC-2001; 2001WO-US49232.
XX
PR 19-DEC-2000; 2000US-256710P.
PR 20-DEC-2000; 2000US-257048P.
PR 09-JAN-2001; 2001US-260482P.
PR 30-JAN-2001; 2001US-264922P.
PR 06-FEB-2001; 2001US-266797P.
PR 19-MAR-2001; 2001US-276988P.
PR 04-APR-2001; 2001US-281535P.
PR 08-MAY-2001; 2001US-289622P.
XX
(SMK ) SMITHKLINE BEECHAM CORP.
PA (SMK ) SMITHKLINE BEECHAM PLC.
XX (GLAX ) GLAXO GROUP LTD.
PI Agarwal P, Birkeland M, Cogswell JP, Kabnick KF, Lai Y;
PI Martensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q;
XX
DR WPI: 2002-508784/54.
DR N-PSDB; ABQ86132.
XX
Secreted proteins and polynucleotides useful as vaccines for preventing
or treating various diseases e.g. cancer, wounds, atherosclerosis,
PT parkinson's disease, Alzheimer's disease, infection, autoimmune
PT disorder -
XX
Claim 2(a); Page 258-260; 335pp; English.
PS
XX
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GenCore version 5.1.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 20:53:24 ; Search time 4480.99 Seconds  
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Title: US-09-750-240-3  
Perfect score: 1812  
Sequence: 1 gttacgtgtgtctggcat.....gcagcttctctgaggtgttc 1812

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
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- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
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- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg\_hum.\*
- 31: em.htg\_inv.\*
- 32: em.htg\_other.\*
- 33: em.htg\_mus.\*
- 34: em.htg\_pln.\*
- 35: em.htg\_rod.\*
- 36: em.htg\_mam.\*
- 37: em.htg\_vrt.\*
- 38: em.sy.\*
- 39: em.htgo\_hum.\*
- 40: em.htgo\_mus.\*
- 41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1812	100.0	1812	6	AR174472	AR174472 Sequence
2	1812	100.0	1812	6	AX189759	AX189759 Sequence
3	1808.4	99.8	3549	6	AR174473	AR174473 Sequence
4	1808.4	99.8	3549	6	AX189761	AX189761 Sequence
5	1763.4	97.3	3552	6	AX189766	AX189766 Sequence
6	1763	97.3	6463	9	AF250226	AF250226 Homo sapi
7	1657.8	91.5	3582	6	AX189768	AX189768 Sequence
8	1604.2	88.5	5877	9	AB007882	AB007882 Homo sapi
9	1527.8	84.3	4046	4	DOGADENCYC	M94968 Canis famli
10	1519.8	83.9	4046	6	I29958	I29958 Sequence 1
11	1449.4	80.0	3465	10	MUSADNLNLCYC	M96653 Mus musculu
12	1437.2	79.3	4131	6	AR106659	AR106659 Sequence
13	1437.2	79.3	4131	10	RATADCYB	M96160 Rattus norv
14	1431.8	79.0	5841	6	AX305965	AX305965 Sequence
15	1431.8	79.0	5841	10	MUSADCYC	M93422 Mouse adeny
16	1427.6	78.8	6036	10	RATADC	L01115 Rattus norv
17	906.2	50.0	4995	4	OCMRADCYV	Z29371 O.cuniculus
18	886.6	48.9	4545	4	DOGADNCYC	M88649 Canis famli
19	858.2	47.4	3924	6	AR106658	AR106658 Sequence
20	858.2	47.4	4847	10	RATADCYA	M96159 Rattus norv
21	811	44.8	2743	9	AF497517	AF497517 Homo sapi
22	799	44.1	3137	6	AX418303	AX418303 Sequence
23	798	44.0	2554	9	AK093840	AK093840 Homo sapi
24	780	43.0	4236	5	GGA293817	AJ293817 Gallus ga
25	667.2	36.8	2429	4	DOGADCYC	M97886 Canis famli
26	436	24.1	3978	4	BOVADC	M25579 Bovine aden
27	436	24.1	3978	6	AR106654	AR106654 Sequence
28	415.2	22.9	2857	10	AF053980	AF053980 Mus muscu
29	404	22.3	3811	6	AX418306	AX418306 Sequence
30	393.2	21.7	1652	6	AR106662	AR106662 Sequence
31	362.2	20.0	7546	3	DRORAC	M81887 Drosophila
32	340	18.8	6193	4	BTAC11MR	Z49806 B.taurus mR
33	339	18.7	3563	9	AB011083	AB011083 Homo sapi
34	339	18.7	4080	9	AK027857	AK027857 Homo sapi
35	339	18.7	4142	9	AF033861	AF033861 Homo sapi
36	338.2	18.7	6005	9	HSADENCYR	Z35309 H.sapiens m
37	335.6	18.5	4533	6	AR106656	AR106656 Sequence
38	335.6	18.5	4533	10	RATADCY3	M5075 R.norvegicu
39	333.2	18.4	3674	10	AF458089	AF458089 Mus muscu
40	320.6	17.7	4601	6	AR106661	AR106661 Sequence
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42	320.6	17.7	4901	10	MM085021	U85021 Mus musculu
43	318.2	17.6	2496	9	AK093706	AK093706 Homo sapi
44	316.6	17.5	3243	6	AX463632	AX463632 Sequence
45	316.6	17.5	6196	6	AX463638	AX463638 Sequence

ALIGNMENTS

RESULT 1	AR174472	AR174472	1812 bp	DNA	linear	PAT 17-DEC-2001
LOCUS	Sequence 3	from patent US 6306830.				
DEFINITION	AR174472					
ACCESSION	AR174472					
VERSION	AR174472.1	GI:17914792				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1812)					
AUTHORS	Hammond,H.Kirk., Insel,P.A., Ping,P., Post,S.R. and Gao,M.					
TITLE	Gene therapy for congestive heart failure					
JOURNAL	Patent: US 6306830-A 3 23-OCT-2001;					
FEATURES	Location/Qualifiers					

source	1. .1812	/organism="unknown"
BASE COUNT	361 a	539 c 507 g 405 t
ORIGIN		
Query Match	100.0%	Score 1812; DB 6; Length 1812;
Best Local Similarity	100.0%	Pred. No. 0;
Matches 1812; Conservative	0; Mismatches	0; Indels 0; Gaps
Qy	1	GTTAACTGGTGTCTGGGCATCCTGGCGGCAGTCAGGTGGGGCGCTTTTCGACGACAG 60
Db	1	GTTAACTGGTGTCTGGGCATCCTGGCGGCAGTCAGGTGGGGCGCTTTTCGACGACAG 60
Qy	61	CCGCGCAGCCCTCTGTCGGGCCCTCTGGTGCCTCTGTCTTGTATATACATCGATACAG 120
Db	61	CCGCGCAGCCCTCTGTCGGGCCCTCTGGTGCCTCTGTCTTGTATATACATCGATACAG 120
Qy	121	CTCTCTCCCATCCGCATGCGGGCTGCGCTCTCAGCGGGCTGGGCTCTCCACCTTGCAT 180
Db	121	CTCTCTCCCATTCGCATGCGGGCTGCGCTCTCAGCGGGCTGGGCTCTCCACCTTGCAT 180
Qy	181	TTGATCTTGGCCTGGCAACTTAAACCGTGGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCC 240
Db	181	TTGATCTTGGCCTGGCAACTTAAACCGTGGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCC 240
Qy	241	AATGTGCTGTGTTCCTCTGCACCAAGCTCATTAGCATCTGCACACATATCCAGCAGAG 300
Db	241	AATGTGCTGTGTTCCTCTGCACCAAGCTCATTAGCATCTGCACACATATCCAGCAGAG 300
Qy	301	GTGTCTCAGCGCCAGGCGCTTTCAGGAGACCCGCGAGTTACATCAGAGCCGGCTCCACCTG 360
Db	301	GTGTCTCAGCGCCAGGCGCTTTCAGGAGACCCGCGAGTTACATCAGAGCCGGCTCCACCTG 360
Qy	361	CAGCATGAGAAATCGGCAGCAGGAGCGGCTGCTGCTGTCTGGTATTGCCCCAGACGTTGCC 420
Db	361	CAGCATGAGAAATCGGCAGCAGGAGCGGCTGCTGCTGTCTGGTATTGCCCCAGACGTTGCC 420
Qy	421	ATGAGATGAAGAAGACATCAACAAAAAAGAAGACATGTTTCCAAAGATCTACATA 480
Db	421	ATGAGATGAAGAAGACATCAACAAAAAAGAAGACATGTTTCCAAAGATCTACATA 480
Qy	481	CAGAAGCATGACAAATGCAGATCCTGTTTCAGAGACATTTAGGGCTTACCAGCCTGGCA 540
Db	481	CAGAAGCATGACAAATGCAGATCCTGTTTCAGAGACATTTAGGGCTTACCAGCCTGGCA 540
Qy	541	TCCCAGTGCATCGCGCAGGAGCTGGTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGAC 600
Db	541	TCCCAGTGCATCGCGCAGGAGCTGGTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGAC 600
Qy	601	AAGCTGGCTGGGAGAAATCACTGCCTGAGGATCAAGATCTTTGGGGACCTGTTTACTGT 660
Db	601	AAGCTGGCTGGGAGAAATCACTGCCTGAGGATCAAGATCTTTGGGGACCTGTTTACTGT 660
Qy	661	GTGTCAGGGCTGCGGAGGCCCGGGCCGACCATGCCACTGCTGTGTGAGATGGGGTA 720
Db	661	GTGTCAGGGCTGCGGAGGCCCGGGCCGACCATGCCACTGCTGTGTGAGATGGGGTA 720
Qy	721	GACATGATTGAGGCCATCTCCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATGCCG 780
Db	721	GACATGATTGAGGCCATCTCCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATGCCG 780
Qy	781	GTGGCATATCCACAGCGGGCGCTGCATCGCGGCTCCTTTGGCTTCGGAAATGGCAGTTTC 840
Db	781	GTGGCATATCCACAGCGGGCGCTGCATCGCGGCTCCTTTGGCTTCGGAAATGGCAGTTTC 840
Qy	841	GATGTGTGTTCCAAATGATGACCTTGGCCCAACCATGAGAGCAGGAAGCGGGCTGGC 900
Db	841	GATGTGTGTTCCAAATGATGACCTTGGCCCAACCATGAGAGCAGGAAGCGGGCTGGC 900
Qy	901	CGCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGACCTACGAAGTGGAGCCA 960
Db	901	CGCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGACCTACGAAGTGGAGCCA 960

Qy	961	GGCGTGGTGGCAAGCGCAACGGGTACCTCAAGAGAGACACATTGAGACGCTTTCCTCATC	1021
Db	961	GGCGTGGTGGCAAGCGCAACGGGTACCTCAAGAGAGACACATTGAGACGCTTTCCTCATC	1020
Qy	1021	CTGGGCCACGACGACAGAAACGGAAGAGGAGAAAGCATGCTGGCCAAAGCTGCACGCGACT	1080
Db	1021	CTGGGCCACGACGACAGAAACGGAAGAGGAGAAAGCATGCTGGCCAAAGCTGCACGCGACT	1080
Qy	1081	CGGGCCAACCTCCATGGAAGGGCTGATGCCCGCATGGGTTCCTGTAGTCGTCCCTTCCTCCGG	1140
Db	1081	CGGGCCAACCTCCATGGAAGGGCTGATGCCCGCATGGGTTCCTGTAGTCGTCCCTTCCTCCGG	1140
Qy	1141	ACCAAGGACTCCAAGGCCCTCCGCCAGATGGGCATTGATGATTCACAGAAAGACAACCGG	1200
Db	1141	ACCAAGGACTCCAAGGCCCTCCGCCAGATGGGCATTGATGATTCACAGAAAGACAACCGG	1200
Qy	1201	GGCACCAAGATGCCCTGAACCTCGAGGATGAGGTGGATTCCTGTAGCCGTGGCCATC	1260
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Qy	1261	GATGCCCGCAGCATTGATCAGCTGCGGGAAGACCATTGTGCGCGGCTTTTTCCTCACCTTC	1320
Db	1261	GATGCCCGCAGCATTGATCAGCTGCGGGAAGACCATTGTGCGCGGCTTTTTCCTCACCTTC	1320
Qy	1321	CAGAGAGGATTTTGAGAGAAGTACTCCCGGAAGTGGATGCCCGCTTCGGAGCCTAC	1380
Db	1321	CAGAGAGGATTTTGAGAGAAGTACTCCCGGAAGTGGATGCCCGCTTCGGAGCCTAC	1380
Qy	1381	GTGCGCTGTCGCCGTGTGGTCTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCA	1440
Db	1381	GTGCGCTGTCGCCGTGTGGTCTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCA	1440
Qy	1441	CACTCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCCCTGCTGCTGCTAATCACCGTG	1500
Db	1441	CACTCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCCCTGCTGCTGCTAATCACCGTG	1500
Qy	1501	CTGATCTGTGCTGTGACTCTGTGGTCTCTGTTCCCTAAGGCCCTGCACAGCTGTGTC	1560
Db	1501	CTGATCTGTGCTGTGACTCTGTGGTCTCTGTTCCCTAAGGCCCTGCACAGCTGTGTC	1560
Qy	1561	CGCAGCATCTGCCGCTCAGGGGCACATAGCACCGAGTTGGCATCTTTTCCGTCTCGCTT	1620
Db	1561	CGCAGCATCTGCCGCTCAGGGGCACATAGCACCGAGTTGGCATCTTTTCCGTCTCGCTT	1620
Qy	1621	GTGTTTACTTCTGCCATTCGCAACATGTTTCACTCTGTAAACCACACCCCCCATACGGAGCTGT	1680
Db	1621	GTGTTTACTTCTGCCATTCGCAACATGTTTCACTCTGTAAACCACACCCCCCATACGGAGCTGT	1680
Qy	1681	GCAGCCGGATGCTGAATTTTACACCTGTGCATCATCTGCTGCCACCTGCACAGCTC	1740
Db	1681	GCAGCCGGATGCTGAATTTTACACCTGTGCATCATCTGCTGCCACCTGCACAGCTC	1740
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AX189759			
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DEFINITION	Sequence 3 from Patent WO0148164.		linear
ACCESSION	AX189759		
VERSION	AX189759.1	GI:15149134	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1812)		



**AUTHORS** Hammond, H. K. and Gao, M.  
**TITLE** Gene therapy for congestive heart failure  
**JOURNAL** Patent: WO 0148164-A 3 05-JUL-2001;  
**FEATURES** THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
Location/Qualifiers

Query Match	100.0%	Score 1812;	DB 6;	Length 1812;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1812;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	

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Qy	61	CCGCGACGCCCTCTCGGGSCCTCTGGTGCCTGTCTCTTGTATACATCGCATACACG	120
Db	61	CCGCGAGCCCCCTCTGGGGCCCTCTGGTGCCTGTCTTGTATACATCGCATACAG	120
Qy	121	CTCTTCCCCATCGCATGCGGGTGGCGCTCTCAGCGGCTGGGGCTCTCCACCTTGCA	180
Db	121	CTCTTCCCCATCGCATGCGGGTGGCGCTCTCAGCGGCTGGGGCTCTCCACCTTGCA	180
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Qy	301	GTGTCTCAGGCCCAGGCCCTTTCAGGAGACCCGCAAGTTACATCCAGGCCCGGCTCCACCTG	360
Db	301	GTGTCTCAGGCCCAGGCCCTTTCAGGAGACCCGCAAGTTACATCCAGGCCCGGCTCCACCTG	360
Qy	361	CAGCATGAGAAATCGGCAGGAGCGGCTGCTGCTGTGGTATTGGCCCGAGCACCTTGCC	420
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Qy	541	TCCCACTGCACTCGGAGGAGCTGGTCAATGACCCCTGAATGAGCTCTTTGCCCGGTTTGAC	600
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Qy	841	GATGTGTGGTCCAATGATGTGACCCTGGCCCAACCATGGAAGCAGGAGCGGGCTGGC	900

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	Qy		901	CGACTCCACATCACTCGGGCCAACACTGCAGTAGCTAACCCTGAACGGGAGCTACGAAGTTGGAGCCA	960
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	Qy		961	GGCCGTGTGGCAAACGCGTAACCTCAAGGAGCAGCACATTGAGACTTTCCTCATC	1020
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	D	b	1081	CGGGCCAACTCCATGGAAGGGCTGATGCGCGATGGTTCCTGATGCTGCTCCCCG	1140
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	Qy		1201	GGCACCCAAAGATGCCCTGAACCCCTGAGGATGAGGTGGATGAGTTCCTGAGCCCCTGCCATC	1260
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	Qy		1261	GATGCCCGGAGCATTTGATCAGCTGCGGAAGACCATGTCGCGCGTTTTTGTGTCACTTC	1320
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	D	b	1441	CACCTCACCCCTGATGCTGGGATTTATGCCAGAGATCTCCTGCTGCTGCTAATCACCCTG	1500
	Qy		1501	CTGATCTGTGCTGTGFACCTCFCTGGTTCCTGTTCCCTAAGCCCTGCAAGCTCTGCTC	1560
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	Qy		1561	CGCAGCATTTGCCGCTCAGCGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTT	1620
	D	b	1561	CGCAGCATTTGCCGCTCAGCGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTT	1620
	Qy		1621	TGTGTTTACTTCHGCCATTGGCCAAACATGTTACCTGTGTAACACACACCCCCATACGGAGCTGT	1680
	D	b	1621	TGTGTTTACTTCHGCCATTGGCCAAACATGTTACCTGTGTAACACACACCCCCATACGGAGCTGT	1680
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	Qy		1741	AATTTACTCTCTGGGCTTGATGCTCCCTGTGTGAGGGCACCATTGCCACCTGCAGCTTT	1800
	D	b	1741	AATTTACTCTCTGGGCTTGATGCTCCCTGTGTGAGGGCACCATTGCCACCTGCAGCTTT	1800
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RESULT 3	AR174473	AR174473	Sequence 5 from patent US 6306830.	3549 bp	DNA	linear	PAT 17-DEC-2001
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DEFINITION	AR174473	AR174473					
ACCESSION	AR174473	AR174473					
VERSION	AR174473.1	AR174473.1	GI:17914793				



DEFINITION Sequence 5 from Patent WO0148164.  
ACCESSION AX189761  
VERSION AX189761.1 GI:15143135  
KEYWORDS human.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
AUTHORS 1 (bases 1 to 3549)  
TITLE Hammond, H.K. and Gao, M.  
JOURNAL Gene therapy for congestive heart failure  
Patent: WO 0148164-A 5 05-JUL-2001  
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
FEATURES Location/Qualifiers  
1..3549  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 699 a 1025 c 1061 g 764 t  
ORIGIN  
Query Match 99.8%; Score 1808.4; DB 6; Length 3549;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 3 TAACGTGGTGTGGGCAATCTGCGGGAGTGCAGGTGCGGGGCGCTTTTCGAGAGACCC 62  
Db 636 TAACGTGGTGTGGGCAATCTGCGGGAGTGCAGGTGCGGGGCGCTTTTCGAGAGACCC 695  
Qy 63 GCGAGCCCCCTCTCGGGCCCTCTGGTCCCTGTGTCTTTGTATACATCGATACAGCT 122  
Db 696 GCGAGCCCCCTCTCGGGCCCTCTGGTCCCTGTGTCTTTGTATACATCGATACAGCT 755  
Qy 123 CCTCCCATCCGATCGGGCTGCGCTCTCAGCGGCTGGGCTCTCCACCTTTCATTT 182  
Db 756 CCTCCCATCCGATCGGGCTGCGCTCTCAGCGGCTGGGCTCTCCACCTTTCATTT 815  
Qy 183 GATCTTGGCTGGCAACTTAACCTGTGTGATGCTCTCTGGAAGCAGCTCGGTGCCAA 242  
Db 816 GATCTTGGCTGGCAACTTAACCTGTGTGATGCTCTCTGGAAGCAGCTCGGTGCCAA 875  
Qy 243 TGTGCTGTCTCTGACCAACGTCATTAGCATCTGCACACACTATCCAGCAGAGGT 302  
Db 876 TGTGCTGTCTCTGACCAACGTCATTAGCATCTGCACACACTATCCAGCAGAGGT 935  
Qy 303 GTCTCAGCGCCAGGCTTTTACAGAGACCGCGAGTTATACATCCAGGCGCGCTCCACCTGCA 362  
Db 936 GTCTCAGCGCCAGGCTTTTACAGAGACCGCGAGTTATACATCCAGGCGCGCTCCACCTGCA 995  
Qy 363 GCATGAGAAATCGGAGGAGCGGCTGCTGCTGTGGTATTTGCCCGCAGCAGTTGCCAT 422  
Db 996 GCATGAGAAATCGGAGGAGCGGCTGCTGCTGTGGTATTTGCCCGCAGCAGTTGCCAT 1055  
Qy 423 GGAGTGAAGAAGACATCAACAAAAAAGAGACATGTTCCACAGATCTACATACA 482  
Db 1056 GGAGTGAAGAAGACATCAACAAAAAAGAGACATGTTCCACAGATCTACATACA 1115  
Qy 483 GAAGCATGACAATGTACAGATCTGTTTGCAGACATTTAGGCGCTTCACAGCCTGGCATC 542  
Db 1116 GAAGCATGACAATGTACAGATCTGTTTGCAGACATTTAGGCGCTTCACAGCCTGGCATC 1175  
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AF250226  
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DEFINITION Homo sapiens adenylyl cyclase type VI mRNA, complete cds.  
ACCESSION AF250226  
VERSION AF250226.1 GI:9049782  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 6463)  
Wicker, R., Catalan, A.G., Caillieux, A., Starenki, D., Stengel, D.,  
Sarasin, A. and Suarez, H.G.  
Cloning and expression of human adenylyl cyclase type VI in normal  
thyroid tissues  
Biochim. Biophys. Acta 1493 (1-2), 279-283 (2000)  
20435313  
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REFERENCE 2 (bases 1 to 6463)  
Wicker, R., Gascon Catalan, A., Caillieux, A.-F., Starenki, D.,  
Stengel, D., Sarasin, A. and Suarez, H.G.  
Direct Submission  
Submitted (28-MAR-2000) Lab Etude des Relations - Instabilite  
genetique et Cancer UPR 2169, Institut de Recherches sur le Cancer  
CNRS IFR 1221, 7 rue Guy Moquet, Villejuif 94801, France

FEATURES  
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DEFINITION Sequence 12 from Patent WO0148164.  
ACCESSION AX189768  
VERSION AX189768.1 GI:15143140  
KEYWORDS synthetic construct.  
SOURCE synthetic construct.  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 3582)  
AUTHORS Hammond,H.K. and Gao,M.  
TITLE Gene therapy for congestive heart failure

JOURNAL Patent: WO 0148164-A 12 05-JUL-2001;  
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
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ACCESSION	AB007882			
VERSION	AB007882.2	GI:20521044		
KEYWORDS	KIAA0422.			

SOURCE	Homo sapiens male brain cDNA to mRNA, clone_lib:pBluescriptII SK plus clone:hh01205sl.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 Ishikawa,K., Nagase,T., Nakajima,D., Seki,N., Ohira,M., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.		
TITLE	Prediction of the coding sequences of unidentified human genes. VIII. 78 new cDNA clones from brain which code for large proteins in vitro		
JOURNAL	DNA Res. 4 (5), 307-313 (1997)		
MEDLINE	98116655		
PUBMED	9455477		
REFERENCE	2 (bases 1 to 5877)		
AUTHORS	Ohara,O.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3914)		
COMMENT	On May 9, 2002 this sequence version replaced gi:2887418. Sequence updated (05-Jan-1998).		
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BASE COUNT	1148 a 1612 c 1782 g 1335 t		
ORIGIN			
Query Match	88.5%; Score 1604.2; DB 9; Length 5877;		
Best Local Similarity	98.7%; Pred. No. 0;		
Matches 1628; Conservative	0; Mismatches 18; Indels 3; Gaps 1;		
Qy	5	ACGTGGTGTGGGCGATCCTGGCGGCAGTGCAGGTGCGGGGGCGCTTTCGACGACGACCCGC	64
Db	774	ACGTGGTGTGGGCGATCCTGGCGGCAGTGCAGGTGCGGGGGCGCTTTCGACGACGACCCGC	833

Qy	65	GCAGCCCTCTCGGGGCTCTGTCGCCCTGTCTTTTGTATACATCGCATACAGCTCC	124
Db	834	GCAGCCCTCTCGGGGCTCTGTCGCCCTGTCTTTTGTCTACATCGCCTACAGCTCC	893
Qy	125	TCCCATCCCATCGGGCTGCGTCCTCAGCGGCTTGGGCTCTCCACCTTCATTTGA	184
Db	894	TCCCATCCGCATTCGGGCTGCGTCCTCAGCGGCTTGGGCTCTCCACCTTCATTTGA	953
Qy	185	TC TTGGCTGGCAACTTAACCGTGTGTATGCCCTTCTCTGGAAGCAGCTCGGTGCCAATG	244
Db	954	TC TTGGCTGGCAACTTAACCGTGTGTATGCCCTTCTCTGGAAGCAGCTCGGTGCCAATG	1013
Qy	245	TGCTGCTTTCCTCTGCACAAGCTCATTTAGCATCTGCACACACTATCCAGCAGAGGTGT	304
Db	1014	TGCTGCTTTCCTCTGCACAAGCTCATTTGGCATCTGCACACACTATCCAGCAGAGGTGT	1073
Qy	305	CTCAGGCCAGGCGTTTTCAGGAGACCGCAGTTACATCCAGGCCGGCTCCACCTGCAGC	364
Db	1074	CTCAGGCCAGGCGTTTTCAGGAGACCGCGGTTACATCCAGGCCGGCTCCACCTGCAGC	1133
Qy	365	ATGAAATCGGCAGCAGGAGCGGCTGCTGCTGTCGGTATTTGCCCCAGCACCTTGCCATGG	424
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Qy	425	AGATGAAGAGACATCAACACAAAAAAGAGAC---ATGTTCCACAAGATCTACATAC	481
Db	1194	AGATGAAGAGACATCAACACAAAAAAGAGACATGATGTTCCACAAGATCTACATAC	1253
Qy	482	AGAAGCATGAACATGTCAGCATCTGTTTGCAGACATTTAGGGCTTCACCAAGCTGCGAT	541
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Qy	542	CCCATGCTACTGGCGAGGAGCTGGTCATGACCCCTGAATGAGCTCTTTGCCGGTTTGACA	601
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Qy	602	AGCTGGCTGGGAGATCACTGCCTGAGGATCAAGATCTTGGGGGACTGTTTACTACTGTG	661
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Qy	662	TGTCAGGGCTGCCCGAGGCGCGGGCCAGCATGCCACTGCTGTGTGGAGATGGGGTAG	721
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Qy	722	ACATGATGAGGCCATCTCGCTGGTAGGTGACAGGTGTGAATGTGAACATGCGCG	781
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Qy	782	TGGGCATCCACAGCGGCGGCTGCACCTGGCGGCTCCTTTGGCTTCGGGAAATGGCAGTTCG	841
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Qy	842	ATGTGTGTCATGATGTGACCTTGGCCCAACCATGGAAAGCAGGAAGCCGGCTGGCC	901
Db	1614	ATGTGTGTCATGATGTGACCTTGGCCCAACCATGGAAAGCAGGAAGCCGGCTGGCC	1673
Qy	902	GCATCCACATCACTCGGGCAACACTGCAGTACCTTGAACGGGGACTTACGAAGTGGAGCCAG	961
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Qy	962	GCGTGTGTGCAAGCGCAACGCGTACCTCAAGGAGCAGCATTTGAGACTTTCTCTATCC	1021
Db	1734	GCGTGTGTGCGAGCGCAACGCGTACCTCAAGGAGCAGCATTTGAGACTTTCTCTATCC	1793
Qy	1022	TGGCGCCAGCCAGAAACGGAAGAGGAAAGGCATGCTGGCCCAAGCTGCAGCGCACTC	1081
Db	1794	TGGCGCCAGCCAGAAACGGAAGAGGAGAGGCCATGCTGGCCCAAGCTGCAGCGCACTC	1853
Qy	1082	GGCCAACTCCATGGAAGGGCTGATGCCCGATGGGTTCTTGATCTGTGCTTCTCCGGA	1141
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Qy	1142	CCAGGACTCC	AAGGCGTTC	CGGCCAGATGGG	CATTGATGATTC	CAAGAAACACCGGG	1201
Db	1914	CCAAGGACTC	CAAGGCGTTC	CGGCCAGATGGG	CATTGATGATTC	CAAGAAACACCGGG	1973
Qy	1202	GCACCCAAAG	ATGCCCTG	AAGGATGAGT	GGATGGATGCT	TGAGCGTGCCATCG	1261
Db	1974	GCACCCAAAG	ATGCCCTG	AAGGATGAGT	GGATGGATGCT	TGAGCGTGCCATCG	2033
Qy	1362	ATGCCCGCAG	CATTGATC	AGCTCGCGAAG	GACCATGTCG	CGCGGTTTTCCTCACCTTCC	1321
Db	2034	ATGCCCGCAG	CATTGATC	AGCTCGCGAAG	GACCATGTCG	CGCGGTTTTCCTCACCTTCC	2093
Qy	1322	AGAGAGAGAT	TTTGTGAG	AAGTACTCCG	GGAAGTGATCCG	CGTTCGGAGCGCTACG	1381
Db	2094	AGAGAGAGAT	TTTGTGAG	AAGTACTCCG	GGAAGTGATCCG	CGTTCGGAGCGCTACG	2153
Qy	1382	TTGGCTGTGC	CGCTTGGT	CTTCTCATCT	GCTTCATCCAG	CTTCTAATTTTCCAC	1441
Db	2154	TTGGCTGTGC	CGCTTGGT	CTTCTCATCT	GCTTCATCCAG	CTTCTAATTTTCCAC	2213
Qy	1442	ACTCCACCC	TGATGCT	TGGGATTA	TGCGCAGCATCT	TCTGCTGCTGAATCACCGTGC	1501
Db	2214	ACTCCACCC	TGATGCT	TGGGATTA	TGCGCAGCATCT	TCTGCTGCTGAATCACCGTGC	2273
Qy	1502	TGATCTGTGT	GTGTTACT	CTGTGGTTC	TCTGTTCCCT	TAAGGCCCTGCAAGCTCTGTCCC	1561
Db	2274	TGATCTGTGT	GTGTTACT	CTGTGGTTC	TCTGTTCCCT	TAAGGCCCTGCAAGCTCTGTCCC	2333
Qy	1562	GCAGCATTTG	CCGCTCAC	GGGCACAT	FAGCACCGCAG	TTGGCATCTTTTCGCTCTGCTTG	1621
Db	2334	GCAGCATTTG	CCGCTCAC	GGGCACAT	FAGCACCGCAG	TTGGCATCTTTTCGCTCTGCTTG	2393
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DOGADENCYC							
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DEFINITION		Canis familiaris		adenylyl cyclase type VI		mRNA linear	
ACCESSION		M94968		adenylyl cyclase type VI		mRNA linear	
VERSION		M94968.1		adenylyl cyclase type VI		mRNA linear	
KEYWORDS		adenylyl cyclase type VI		adenylyl cyclase type VI		mRNA linear	
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ORGANISM		Canis familiaris		adenylyl cyclase type VI		mRNA linear	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom		adenylyl cyclase type VI		mRNA linear	
AUTHORS		Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		adenylyl cyclase type VI		mRNA linear	
TITLE		Katsushika, S.; Chen, L.; Kawabe, J.; Nilakantan, R.; Hainon, N.J.,		adenylyl cyclase type VI		mRNA linear	
		Homcy, C.J., and Ishikawa, Y.		adenylyl cyclase type VI		mRNA linear	
		Cloning and characterization of a sixth adenylyl cyclase isoform		adenylyl cyclase type VI		mRNA linear	
		types V and VI constitute a subgroup within the mammalian adeny		adenylyl cyclase type VI		mRNA linear	
		cyclase family		adenylyl cyclase type VI		mRNA linear	
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 89 (18), 8774-8778 (1992)		adenylyl cyclase type VI		mRNA linear	
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ORIGIN				adenylyl cyclase type VI		mRNA linear	
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Db	762	ACGTGTGTC	GTGGGCAT	CTCGGCGCAG	TGCAGGT	TTGGGGTGCCTTCG	CAGCAGACCCCGC 821





[illegible]

Db	1839	GGGCCAACTCCATCGAAGAGCGCTGATGCCACGCTGGGTGGCGGACCGCGCTCTCTTCGCGGA	1898
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Db	1899	CCAAGGACTCCAAGGCTTCGCCACAGATGGGCATTTGATGATTCACGAAAGACAACCGGG	1958
Qy	1202	GCACCCAAAGATGCCCTGAACCCCTGAGGATGAGGTGGATGAGTTCTCGAGCCGTGCCATCG	1261
Db	1959	GTGCCAAAGATGCCCTGAACCCCGAGGATGAGGTGCGATGAGTTCTCGGCGCGTGGCATCG	2018
Qy	1262	ATGCCCGCAGCATTGATCAGCTCGCGAAGACCATGTCGCGCGGTTTTGCTCACCCTCC	1321
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Qy	1322	AGACGAGAGATTTTGAGAAGAAGTACTCTCCGGAAGGTGGATCCCGCTTCGGAGCCTACG	1381
Db	2079	AGACGAGAGATCTTGAAGAAGTACTCAAGGAAAGTGGAGCCCGCTTCGGAGCCTACG	2138
Qy	1382	TGCTCTGTCGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAAATTTTCCAC	1441
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Qy	1442	ACTCCACCTTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTTAATCACCCTGC	1501
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Qy	1502	TGATCTGCTGTGTACTCTCTGTGGTTCCTGTTCCCTAAGGCCCTGCAAGCTCTGTGCC	1561
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Qy	65	GCAGCCCTCTGCGGGCCTCTGGTGCCTGTGTCTTTGTATACATGCCATACACGCTCC 124
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Qy	125	TCCCATCGGATCGGGGTGCGCTCTCTCAGCGGCTTGGGCTCTCCACCTTCGATTGA 184
Db	734	TTCCCATTCGATCGAGCGCAGTACTCAGCGGCTGGGCTCTCTACTCTGCATTGA 793
Qy	185	TCTTGGCTGSGCACTTAACCGTGGTATGCTTCTTCTGGAAGCAGCTCGGTGCCAATG 244
Db	794	TTTTGGCTGGCAGCTCAACAGCAGCAGCCCTTCTCTTTGGAAGCAGCTCGGTCTAACG 853
Qy	245	TGCTGTCTTCTCTGACCACCAATCATATTAGCATCTGCACACACTATCCAGCAGAGTGT 304
Db	854	TGGTGTCTTCTCTGACCAATCCCATCGTGTCTGCACACACTACCTTCCTGAAGTGT 913
Qy	305	CTCAGCGCAGGCTTTTCAGAGACCCGCGAGTTACATCCAGCGCCGCTCCACCTGCGAGC 364
Db	914	CTCAGCGCAGGCTTTTCAGAGACCCGAGTTTACATCCAGCGCGGCTGCACCTGCGAGC 973
Qy	365	ATGAGATCGCAGCAGGCGGTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 424
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Qy	425	AGATGAAGAAGACATCAACACAAAAAAGAGAC---ATGTTTCCACAAGATCTACATAC 481
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Qy	542	CCCAGTGCATGCGCAGGAGCTGTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACA 601
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Qy	602	AGCTGGCTGCGGGAATCACTGCTGAGGATCAAGATCTTTGGGGGACTGTTTACTACTGTG 661
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Qy	662	TGTCAGGGCTGCCGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 721
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Db	1574	GCCGTGCTGGTGAACGCAATGCGTACCTCAAGGAGCAGTGCATTGAGACCTTCTCTCATAC 1633
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Qy	1082	GGGCAACTCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1141
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Qy	1142	CCAAAGGACTCCAAAGGCGCTTCGCGCAGATGGGCAATGATGATTTCCAGCAAGAGCAACCGGG 1201
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Qy	1202	GCACCCAAAGATGCGCTGAAACCTGAGGATGAGGTGAGTTCCTGAGCGGTGCGCATCG 1261
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Qy	1382	TTGGCTGTGCGCTGTGGTCTTTCGCTTCATCTGCTTCATCCAGTTCCTAAATTTTCCAC 1441
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Db 2487 CTGAGTACTT 2496  
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AX305965  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
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AUTHORS  
TITLE  
JOURNAL  
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Source  
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QY 65 GCAGCCCCCTCTCGGGGCCCTCTGGTGCCCTGTGTTCTTTGTATATACATCGCATACACGCTCC 124  
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QY 125 TCCCCATCCGCTGCGGGGCTGCGCTCTCAGCGGCCCTGGGCCCTTCCACCTTGCATTTGA 184  
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QY 245 TGCTGCTGTCTCTCCACCAACGCTCATTTAGCATCTGCACACACTATCCAGCAGAGGTGT 304  
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QY 1262 ATGCCCGCAGCATTTGATGAGCTGCGGAAGACCATGTGCGCGGTTTTTGTCTCACCTTCC 1321  
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Job time : 4522.99 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 20:52:08 ; Search time 334.621 Seconds  
(without alignments)  
12194.743 Million cell updates/sec

Title: US-09-750-240-3

Perfect score: 1812

Sequence: 1 gttacagtggtgctggcat.....gcagcttctcagggtgttc 1812

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1812	100.0	1812	22	AA08562 Human partial card
2	1812	100.0	2127	19	AAV23246 Human adenylylcycl
3	1808.4	99.8	3549	22	AA08563 Human cardiac aden
4	1763.4	97.3	3552	22	AA08567 Human type VI aden
5	1763	97.3	4942	20	AA00461 Human modified car
6	1657.8	91.5	3582	22	AA08568 Cardiac adenylyl c
7	1527.8	84.3	4046	14	AAQ42525 Type VI adenylyl c
8	1437.2	79.3	4131	21	AAAS3923 Mouse ischaemic co
9	1431.8	79.0	5841	24	AB199680

10	895	49.4	4523	20	AA000462	Human type V adeny
11	884.6	48.8	4356	16	AA095540	Cardiac adenylyl c
12	883.4	48.8	4356	14	AA037543	Cardiac adenylyl c
13	858.2	47.4	3924	21	AAAS3922	Type V adenylyl cy
14	799	44.1	3137	24	AA028058	Human adenylyl and
15	445.8	24.6	4827	23	AB107501	Drosophila melanog
16	436	24.1	3978	21	AAAS3918	Adenylyl cyclase t
17	404	22.3	3811	24	AA028061	Human adenylyl and
18	393.2	21.7	1652	21	AAAS3926	Adenylyl cyclase C
19	362.2	20.0	7005	23	AB115355	Drosophila melanog
20	339	18.7	4080	22	AB116647	Human cDNA sequenc
21	337.2	18.6	3505	24	AA034078	Human secreted pro
22	335.6	18.5	4533	21	AAAS3920	Type III adenylyl
23	320.6	17.7	4601	21	AAAS3925	Type VIII adenylyl
24	319.4	17.6	2601	21	AA099124	Human pancreatic c
25	311.2	17.2	5199	21	AAAS3924	Type VII adenylyl
26	301.2	16.6	4011	22	AA066820	Human adenylyl cy
27	301.2	16.6	6470	24	AA031191	Human NS cDNA sequ
28	298	16.4	4355	24	AB139754	Rat adenylyl cycla
29	286	15.8	4008	17	AA014528	Adenylyl cyclase t
30	286	15.8	4008	21	AAAS3919	Human adenylyl cy
31	284	15.7	3518	22	AA026694	Human adenylyl cy
32	280.6	15.5	5873	24	AA031190	Human polynucleoti
33	273.6	15.1	320	24	AB190026	Drosophila melanog
34	267.6	14.8	5201	23	AB129627	Type IV adenylyl c
35	256.2	14.1	3357	21	AAAS3921	Human adenylyl and
36	242.2	13.4	3769	24	AA028057	Human adenylyl and
37	241	13.3	5046	23	AB102755	Drosophila melanog
38	240.2	13.3	3312	24	AB089298	Human adenylyl cy
39	234.4	12.9	6363	23	AB116645	Drosophila melanog
40	230.8	12.7	3239	22	AA033100	Human secreted pro
41	216.8	12.0	4473	17	AA035209	Murine adenylyl c
42	209.4	11.6	4985	20	AA00463	Human type IX aden
43	189	10.4	627	22	AB142228	Human nervous syst
44	188.2	10.4	6597	23	AB114977	Drosophila melanog
45	172	9.5	1041	23	ABV25672	Human prostate exp

#### ALIGNMENTS

#### RESULT 1

AA08562

ID AA08562 standard; cDNA; 1812 BP.

XX AA08562;

AC AA08562;

DT 04-SEP-2001 (first entry)

XX Human partial cardiac adenylylase VI (ACVI) isoform #2 cDNA.

XX Human; cardiant; beta-adrenergic signalling protein; beta-ASP;

KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;

KW adenylylase; adenylylase; adenylylase; CAMP synthetase;

KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;

KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1812

FT /\*tag= a

FT /product= "Human partial cardiac ACVI isoform #2"

FT /note= "CDS does not include start and stop codon"

FT /EC\_number= "4.6.1.1"

XX WO200148164-A2.

XX 05-JUL-2001.

XX 26-DEC-2000; 2000WO-US35411.

XX 27-DEC-1999; 99US-0472667.





KW	Human; cardiant; beta-adrenergic signalling protein; beta-ASP;
KW	myocardium; gene therapy; beta-adrenergic receptor; beta-AR;
KW	adenylcyclase; adenylylate cyclase; cAMP synthetase;
KW	G-protein receptor kinase; GRK; heart disease; congestive heart failure
KW	cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ds.
XX	
OS	Homo sapiens.
XX	
FH	Location/Qualifiers
FT	1..3504
CDS	/*tag= a
FT	/product= "Human cardiac adenylylase VI isoform #1"
FT	/EC_number= "4.6.1.1"
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PN	WO200148164-A2.
XX	
PD	05-JUL-2001.
XX	
PF	26-DEC-2000; 2000WO-US35411.
XX	
PR	27-DEC-1999; 99US-0472667.
XX	
PA	(REGC ) UNIV CALIFORNIA.
XX	
PI	Hammond HK, Gao M;
XX	
DR	WPI: 2001-418260/44.
P-PSDB:	AEE04310.
XX	
PT	Novel polynucleotide encoding a modified adenylylase polypeptide
PT	useful for enhancing cardiac function in mammalian hearts, and for
PT	treating heart disease, especially congestive heart failure -
XX	
PS	Example 5; Page 122-129; 153pp; English.
XX	
CC	The present invention relates to methods and compositions for enhancing
CC	cardiac function in mammalian hearts by inserting transgenes encoding
CC	beta-adrenergic signalling proteins (beta-ASP) which increase
CC	beta-adrenergic responsiveness within the myocardium using in vivo
CC	gene therapy. The beta-ASPs of the invention include beta-adrenergic
CC	receptors (beta-AR), adenylylases (also referred as adenylylase
CC	adenylylate cyclase and cAMP synthetase) and G-protein receptor kinase
CC	(GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
CC	in mammalian hearts and for treating heart disease, especially
CC	congestive heart failure. The present DNA sequence encodes human
CC	cardiac adenylylase VI (ACVI) isoform which is used for generating
CC	a third beta-ASP transgene, used in the exemplification
CC	of the invention.
XX	
SQ	Sequence 3549 BP: 699 A; 1025 C; 1061 G; 764 T; 0 other;
	Query Match 99.8%; Score 1808.4; DB 22; Length 3549;
	Best Local Similarity 99.9%; Pred. No. 0;
	Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps
Qy	3 TAACCTGGTGTCTGGGCATCTCGGCGCAGTGTCAGTTCGGGGCGCTTTCCGACGACGCC 62
Dd	
	636 TAACCTGGTGTGGGCATCTCGGCGCAGTGTCAGTTCGGGGCGCTTTCCGACGACGCC 65
Qy	63 GCAGAGCCCCCTCTGCGGGCCCTCTGGTCCCCTGTGTCTTTGTATACATCATACACGCT 122
Dd	696 GCAGAGCCCCCTCTGCGGGCCCTCTGGTCCCCTGTGTCTTTGTATACATCATACACGCT 755
Qy	123 CCTCCCCATCGCATGCGGGCTGCCGTCCTCAGGGGCTGGGGCTCTCCACCTTGCATT 182
Dd	756 CCTCCCCATCGCATGCGGGCTGCCGTCCTCAGGGGCTGGGGCTCTCCACCTTGCATT 815
Qy	183 GATCTTGGCTGGCAACTTAACCGTGTGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAA 242
Dd	816 GATCTTGGCTGGCAACTTAACCGTGTGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAA 275
Qy	243 TGTCCTGCTGTTCCTCTGCAACACGTCATTAGCATCTGCACACACTATCCAGCAGAGT 302

Db 876 TGTCTGCTGTCTCTGTCACCAACGTCATTTAGCATCTGCACACACTATCCAGCAGAGT 935  
QY 303 GTCTCAGCGCCAGCGCTTTTCAGGAGACCGCAGTTACATCCAGGCCGCGTCCACCTGCA 362  
Db 936 GTCTCAGCGCCAGCGCTTTTCAGGAGACCGCAGTTACATCCAGGCCGCGTCCACCTGCA 995  
QY 363 GCATGAGAAATCGGCAGCAGGAGCGGCTGCTGCTGCTGGTATTTGCCCCAGCAGCTTGGCAT 422  
Db 996 GCATGAGAAATCGGCAGCAGGAGCGGCTGCTGCTGCTGGTATTTGCCCCAGCAGCTTGGCAT 1055  
QY 423 GGAGATCAAGAGACATCACACAAAAGAGAGATGTTCCACAAGATCTACATACA 482  
Db 1056 GGAGATCAAGAGACATCACACAAAAGAGAGATGTTCCACAAGATCTACATACA 1115  
QY 483 GAAGCATGACAATGTACAGCATCTCTGTTTGGACATTTGAGGGCTTACACAGCCCTGGCATC 542  
Db 1116 GAAGCATGACAATGTACAGCATCTCTGTTTGCAGACATTTGAGGGCTTACACAGCCCTGGCATC 1175  
QY 543 CCACTGCACTGCGCAGGAGCTGTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAA 602  
Db 1176 CCACTGCACTGCGCAGGAGCTGTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAA 1235  
QY 603 GCTGGCTGCGGAGAAATCACTGCTGAGGATCAAGATCTTGGGGACTGTTACTACTGT 662  
Db 1236 GCTGGCTGCGGAGAAATCACTGCTGAGGATCAAGATCTTGGGGACTGTTACTACTGT 1295  
QY 663 GTACAGGCTGCGGAGGCGCGGCGGACCATGCCCCTGCTGTTGGAGATGGGGGTAGA 722  
Db 1296 GTACAGGCTGCGGAGGCGCGGCGGACCATGCCCCTGCTGTTGGAGATGGGGGTAGA 1355  
QY 723 CATGATTGAGGCCATCTCGCTGCTGAGGTGACAGGTGACAGGTGTAATGTGAACATGCGCGT 782  
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Db 1416 GGGCATCCACAGCGCGCGTGCATCGCGCTCTTGGCTTGGGAATGGCAGTTCGA 1475  
QY 843 TGTGTGTTCCAAATGATGTACCCCTGGCCCAACCATGGAAGCAGGAGCGCGGCTGCGG 902  
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QY 1023 GGGCGCCAGCAGAAACCGGAAAGAGGAGAAAGGCATGCTGGCCAAAGCTGCAGCGGACTCG 1082  
Db 1656 GGGCGCCAGCAGAAACCGGAAAGAGGAGAAAGGCATGCTGGCCAAAGCTGCAGCGGACTCG 1715  
QY 1083 GGCCAACTCCATGGAAGGGCTGATGCCCGGATGGGTTTCCTGATCGTGCCTTCTCCCGGAC 1142  
Db 1716 GGCCAACTCCATGGAAGGGCTGATGCCCGGATGGGTTTCCTGATCGTGCCTTCTCCCGGAC 1775  
QY 1143 CAAGGACTCCAAAGCCCTCCGCCAGATGGGCATTTGATGATTCACAGCAAGACACCCGGG 1202  
Db 1776 CAAGGACTCCAAAGCCCTCCGCCAGATGGGCATTTGATGATTCACAGCAAGACACCCGGG 1835  
QY 1203 CACCAAGATGCCCTCAACCTGAGGATGAGGTGATGAGTTCTCTGAGCCGTGCCATCGA 1262  
Db 1836 CACCAAGATGCCCTCAACCTGAGGATGAGGTGATGAGTTCTCTGAGCCGTGCCATCGA 1895  
QY 1263 TGCCCGCAGCATGATCAGCTGCGGAAGGACCATGTGCGCGGTTTTTGTCTACCTTTCCA 1322  
Db 1896 TGCCCGCAGCATGATCAGCTGCGGAAGGACCATGTGCGCGGTTTTTGTCTACCTTTCCA 1955  
QY 1323 GAGAGAGATTTTGAAGAGAGTACTCCCGAAGGTGGATCCCGCTTCGGAGGCTTAGT 1382  
Db 1956 GAGAGAGATTTTGAAGAGAGTACTCCCGAAGGTGGATCCCGCTTCGGAGGCTTAGT 2015

QY 1383 TGCCTGTGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAAATTTTCCCACA 1442  
Db 2016 TGCCTGTGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAAATTTTCCCACA 2075  
QY 1443 CTCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCT 1502  
Db 2076 CTCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCT 2135  
QY 1503 GATCTGTGCTGTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1562  
Db 2136 GATCTGTGCTGTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2195  
QY 1563 CAGCATTTCTCGCTTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTTGT 1622  
Db 2196 CAGCATTTCTCGCTTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTTGT 2255  
QY 1623 GTTTACTTCTGCCAATGCGCAACATGTCACCTGTAAACACACACCCCATACAGGAGTGTGC 1682  
Db 2256 GTTTACTTCTGCCAATGCGCAACATGTCACCTGTAAACACACACCCCATACAGGAGTGTGC 2315  
QY 1683 AGCCCGGATGCTGAATTTAACACCTGCTGACATCAGTCCCTGCCACCTGCCAGCTCAA 1742  
Db 2316 AGCCCGGATGCTGAATTTAACACCTGCTGACATCAGTCCCTGCCACCTGCCAGCTCAA 2375  
QY 1743 TTACTCTTGGGCTGATGCTCCCTGCTGTGAGGGCACCCTGCCACCTGCAGCTTTCC 1802  
Db 2376 TTACTCTTGGGCTGATGCTCCCTGCTGTGAGGGCACCCTGCCACCTGCAGCTTTCC 2435  
QY 1803 TGAGGTGTT 1812  
Db 2436 TGAGGTGTT 2445  
RESULT 4  
AAD08567  
ID AAD08567 standard; DNA; 3552 BP.  
XX  
AC AAD08567;  
XX  
DT 04-SEP-2001 (first entry)  
XX  
DE Human cardiac adenylycyclase VI (ACVI) isoform #2 DNA.  
XX  
KW Human; cardiac; beta-adrenergic signalling protein; beta-ASP;  
KW myocardiium; gene therapy; beta-adrenergic receptor; beta-AR;  
KW adenylyl cyclase; adenylate cyclase; cAMP synthetase;  
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
KW cardiac adenylycyclase VI; ACVI isoform; beta-ASP transgene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..3507  
FT /product= "Human cardiac adenylycyclase VI isoform #2"  
FT /tag= a  
FT /EC\_number= "4.6.1.1"  
XX  
PN WO200148164-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US35411.  
XX  
PR 27-DEC-1999; 99US-0472667.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Hammond HK, Gao M;  
XX  
DR WPI: 2001-418260/44.  
DR P-PSDB; AAE04311.  
XX

PT Novel polynucleotide encoding a modified adenylyl cyclase polypeptide  
PT useful for enhancing cardiac function in mammalian hearts, and for  
PT treating heart disease, especially congestive heart failure -  
XX  
PS Claim 6; Page 134-140; 153pp; English.

XX The present invention relates to methods and compositions for enhancing  
CC cardiac function in mammalian hearts by inserting transgenes encoding  
CC beta-adrenergic signalling proteins (beta-ASP) which increase  
CC beta-adrenergic responsiveness within the myocardium using in vivo  
CC gene therapy. The beta-ASPs of the invention include beta-adrenergic  
CC receptors (beta-AK), adenylyl cyclases (also referred as adenylylase,  
CC adenylyl cyclase and cAMP synthetase) and G-protein receptor kinase  
CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
CC in mammalian hearts and for treating heart disease, especially  
CC congestive heart failure. The present DNA sequence encodes human  
CC cardiac adenylyl cyclase VI (ACVI) isoform which is used for generating  
CC a fourth beta-ASP transgene, used in the exemplification  
CC of the invention.

XX  
SQ Sequence 3552 BP; 686 A; 1037 C; 1068 G; 761 T; 0 other;  
Query Match 97.3%; Score 1763.4; DB 22; Length 3552;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 1789; Conservative 0; Mismatches 21; Indels 3; Gaps 1;

QY 3 TAACGTGGTGGGCATCTCGCGCAGTGCAGGTGCGGGCGCTTTCGCAGCAGACC 62  
DB TTTACGTGGTGGTGGGCATCTCGCGCAGTGCAGGTGCGGGCGCTTCGCAGCAGACC 695  
QY 63 GCGCAGCCCTCTGGGGGCTCTGGTGGCCCTGTGTTCTTTGTATACATCGATACAGCT 122  
DB GCGCAGCCCTCTGGGGGCTCTGGTGGCCCTGTGTTCTTTGTATACATCGCTACAGCT 755  
QY 123 CTCTCCCATCCGATCGCGGCTGCGTCTCTCAGCGGCTGCGGCTCTCCACCTTGCATTT 182  
DB CTCTCCCATCCGATCGCGGCTGCGTCTCTCAGCGGCTGCGGCTCTCCACCTTGCATTT 815  
QY 183 GATCTGGCTGGCACTTAACCGTGGTGTATGCTTCTTGGAGCAGCTCGGTGCCAA 242  
DB GATCTGGCTGGCACTTAACCGTGGTGTATGCTTCTTGGAGCAGCTCGGTGCCAA 875  
QY 243 TGTGCTGCTTTCCTCTGCACCAACGTGATAGCATCTGCACACATATCCAGCAGGT 302  
DB TGTGCTGCTTTCCTCTGCACCAACGTGATAGCATCTGCACACATATCCAGCAGGT 935  
QY 303 GTCTCAGCCAGGCTTTTCAGAGACCGCAGTTACATCCAGGCGGCTCCACCTGCA 362  
DB GTCTCAGCCAGGCTTTTCAGAGACCGCAGTTACATCCAGGCGGCTCCACCTGCA 995  
QY 363 GCATGAATCGGCAGCAGGCGGCTGCTGCTGGTATTTGCCCGCAGCAGTTGCCAT 422  
DB GCATGAATCGGCAGCAGGCGGCTGCTGCTGGTATTTGCCCGCAGCAGTTGCCAT 1055  
QY 423 GGAGATGAAGAGACATCAACACAAAAAAGAAC - - - ATGTTCCACAAGATCTACAT 479  
DB GGAGATGAAGAGACATCAACACAAAAAAGAACATGATTTCCACAAGATCTACAT 1115  
QY 480 ACAGAAGCATGACATGTCAGCATCTGTTTCAGACATTTAGGGCTTCACCGCTGGC 539  
DB ACAGAAGCATGACATGTCAGCATCTGTTTCAGACATTTAGGGCTTCACCGCTGGC 1175  
QY 540 ATCCAGTGCACCTGGCAGGAGCTGTATGACCTGATAGCTCTTTGGCCGGTTTCA 599  
DB ATCCAGTGCACCTGGCAGGAGCTGTATGACCTGATAGCTCTTTGGCCGGTTTCA 1235  
QY 600 CAAGTGGCTGGGAGATCACTGCTGAGATCAAGATCTTTGGGGGACTGTTTACTAC 659  
DB CAAGTGGCTGGGAGATCACTGCTGAGATCAAGATCTTTGGGGGACTGTTTACTAC 1295  
QY 660 TGTGTACGGGCTGCGGAGGCGGCGGCGCACCATGCCACTGCTGTGTGAGATGGGGT 719  
DB TGTGTACGGGCTGCGGAGGCGGCGGCGCACCATGCCACTGCTGTGTGAGATGGGGT 1355

QY 720 AGACATGATTGAGGGCCATCTCGTGTGTACGTGAGGTGACAGGTGTGAATGTGAACATGG 779  
DB AGACATGATTGAGGGCCATCTCGTGTGTACGTGAGGTGACAGGTGTGAATGTGAACATGG 1415  
QY 780 COTGGGCATCCACAGGGCGGCTGCACATGCGCGCTCTTGGCTTCGGAAATGGCAGTT 839  
DB COTGGGCATCCACAGGGCGGCTGCACATGCGCGCTCTTGGCTTCGGAAATGGCAGTT 1475  
QY 840 CGATGCTGCTCCATGATGTGACCTGCGCCACACATGGAAGCAGGAGCGGCTGG 899  
DB CGATGCTGCTCCATGATGTGACCTGCGCCACACATGGAAGCAGGAGCGGCTGG 1535  
QY 900 CGGCATCCACATCACTCGGGCAACACTGCACTACCTGAAACGGGACTACGAATGGAGCC 959  
DB CGGCATCCACATCACTCGGGCAACACTGCACTACCTGAAACGGGACTACGAATGGAGCC 1595  
QY 960 AGGCGTGTGGCAGCGCAACGCGTACCTCAAGGAGCAGACATTTGAGACTTTCCTCAT 1019  
DB AGGCGTGTGGCAGCGCAACGCGTACCTCAAGGAGCAGACATTTGAGACTTTCCTCAT 1655  
QY 1020 CTTGGCGCCAGCCAGAAAGAGAGAAAGCATGCTGGCCAAAGCTGCAGCGGAC 1079  
DB CTTGGCGCCAGCCAGAAAGAGAGAAAGCATGCTGGCCAAAGCTGCAGCGGAC 1715  
QY 1080 TCGGGCCAACTCCATGGAAGGCTGATGCCGCGATGGGTTCCTGTGATGTCGCTTCTCCCG 1139  
DB TCGGGCCAACTCCATGGAAGGCTGATGCCGCGCTGGGTTCCTGTGATGTCGCTTCTCCCG 1775  
QY 1140 GACCAAGGACTCCAAGGCTTCGGCCAGATGGGCATTTGATTTCCAGCAAGACAAACCG 1199  
DB GACCAAGGACTCCAAGGCTTCGGCCAGATGGGCATTTGATTTCCAGCAAGACAAACCG 1835  
QY 1200 GGGCACCCAAAGTGCCTCAACCTGAGGATGAGGTGGATGAGTTCTGAGCGCTGCCAT 1259  
DB GGGCACCCAAAGTGCCTCAACCTGAGGATGAGGTGGATGAGTTCTGAGCGTGCCAT 1895  
QY 1260 CGATGCCCCAGCATTTGATCAGCTGCGGAAGACCATGTCGCCCGGTTTTTGTCTACCTTT 1319  
DB CGATGCCCCAGCATTTGATCAGCTGCGGAAGACCATGTCGCCCGGTTTTTGTCTACCTTT 1955  
QY 1320 CCAGAGAGAGATTTTGAGAAGNAGTACTCCGGAGGTGGATCCCGCTTCGGAGCCCTA 1379  
DB CCAGAGAGAGATTTTGAGAAGNAGTACTCCGGAGGTGGATCCCGCTTCGGAGCCCTA 2015  
QY 1380 CGTTGGCTGTCCTGTTGTTCTTCTGCTTCTATCTGCTTCTATCCAGCTTCTAATTTCC 1439  
DB CGTTGGCTGTCCTGTTGTTCTTCTGCTTCTATCTGCTTCTATCCAGCTTCTAATTTCC 2075  
QY 1440 ACATCCACCCCTGATGCTTGGGATTTATGCCAGCATTTCTCTGCTGCTGCTGCTAATCACCT 1499  
DB ACATCCACCCCTGATGCTTGGGATTTATGCCAGCATTTCTCTGCTGCTGCTGCTAATCACCT 2135  
QY 1500 GCTGATCTGCTGCTACTCTCTGTTCTGTTCTTCCCTAAGGCCCTCAAGCTCTGTC 1559  
DB GCTGATCTGCTGCTACTCTCTGTTCTGTTCTTCCCTAAGGCCCTCAAGCTCTGTC 2195  
QY 1560 CCGCAGCATTTGTCGCTCACGGCAGCATAGCAGCGAGTTGGCATCTTTTCCGTCCTGCT 1619  
DB CCGCAGCATTTGTCGCTCACGGCAGCATAGCAGCGAGTTGGCATCTTTTCCGTCCTGCT 2255  
QY 1620 TGTGTTTACTTCTGCAATTTGCCAATGTTTACCTGTAAACACACACCCCATACGGAGCTG 1679  
DB TGTGTTTACTTCTGCAATTTGCCAATGTTTACCTGTAAACACACACCCCATACGGAGCTG 2315  
QY 1680 TGCAGCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCCACCTGCAGCAGCT 1739  
DB TGCAGCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCCACCTGCAGCAGCT 2375  
QY 1740 CAATTACTCTCTGGGCTGATGCTCCCTGTGTGAGGCGACCATGCCCCACCTGCAAGCTT 1799  
DB CAATTACTCTCTGGGCTGATGCTCCCTGTGTGAGGCGACCATGCCCCACCTGCAAGCTT 2435









Db 1077 GGAGATGAAGAAGACATCAACACAAAAAAAAGAGACATGATGTCCACAAAGATCTACAT 1136  
Qy 480 ACAGAAGCATGACAAATGTACGATCCTGTGTTGCAGACATTTGAGGGCTTTCACAGCCCTGGC 539  
Db 1137 ACAGAAGCATGACAAATGTACGATCCTGTGTTGCAGACATTTGAGGGCTTTCACAGCCCTGGC 1196  
Qy 540 ATCCAGTGCATCGGAGAGCTGTGTCATGACCCCTGAATGAGCTCTTTGGCCCGGTTTGA 599  
Db 1197 ATCCAGTGCATCGGAGAGCTGTGTCATGACCCCTGAATGAGCTCTTTGGCCCGGTTTGA 1256  
Qy 600 CAAGCTGGCTCGGAGAGCTGTGTCATGACCCCTGAATGAGCTCTTTGGCCCGGTTTGA 659  
Db 1257 CAAGCTGGCTCGGAGAGCTGTGTCATGACCCCTGAATGAGCTCTTTGGCCCGGTTTGA 1316  
Qy 660 TGTGTGAGGGCTCGGAGAGCTGTGTCATGACCCCTGAATGAGCTCTTTGGCCCGGTTTGA 719  
Db 1317 CGTGTGAGGGCTCGGAGAGCTGTGTCATGACCCCTGAATGAGCTCTTTGGCCCGGTTTGA 1376  
Qy 720 AGACATGATGAGGCCATCTGCTGTGTCATGACCCCTGAATGAGCTCTTTGGCCCGGTTTGA 779  
Db 1377 AGACATGATGAGGCCATCTGCTGTGTCATGACCCCTGAATGAGCTCTTTGGCCCGGTTTGA 1436  
Qy 780 CGTGGGATCACAGCGGGCGCTGACCTGCGGGCTCTTGGCTTGGCGAAATGGCAGTT 839  
Db 1437 TGTGGGATCACAGCGGGCGCTGACCTGCGGGCTCTTGGCTTGGCGAAATGGCAGTT 1496  
Qy 840 CGATGTGTGCTCAATGATGTGACCTGGCCCAACACACATGGAAGCAGGAGCGGGCTGG 899  
Db 1497 TGATGTCTGTGTCAAACGATGTGACCTGGCTTAACACACATGGAAGCAGGAGCGGGCTGG 1553  
Qy 900 CCGATCCACATCACTCGGGCAACACTGCACTACCTGAACGGGAGCTACGAAAGTGGAGCC 959  
Db 1554 CCGATCCACATCACTCGGGCAACACTGCACTACCTGAACGGGAGCTACGAAAGTGGAGCC 1613  
Qy 960 AGGCGCTGGTGGCAAGCGCAACGCTACCTCAAGGAGCAGCAGCATTTGACATTTCCCTCAT 1019  
Db 1614 AGGCGCTGGTGGTGAAGCAATGCGTACCTCAAGGAGCAGCAGCATTTGACATTTCCCTCAT 1673  
Qy 1020 CCGGGGCGCCAGCCAGCAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1079  
Db 1674 ACTTGGCGCCAGCCAGCAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1733  
Qy 1080 TCGGGCCAACTCCATGGAAGGCTGTATGCCCGATGGTTCCTGATGCTGCTTCTTCCCG 1139  
Db 1734 ACGGGCCAACTCCATGGAAGGCTGTATGCCCGATGGTTCCTGATGCTGCTTCTTCCCG 1793  
Qy 1140 GACCAAGGACTCCAGGCTTCCGCCAGATGGGATGATGATGATGATGATGATGATGATGATGAT 1199  
Db 1794 GACCAAGGACTCCAGGCTTCCGCCAGATGGGATGATGATGATGATGATGATGATGATGATGAT 1853  
Qy 1200 GGGCACCACAGATGCCCTGAACCTGAGGATGAGTGGATGAGTGGATGAGTGGATGAGTGGATGAGT 1259  
Db 1854 GGGTGGCCAAAGATGCTGTAACCTGAAGATGAGTGGATGAGTGGATGAGTGGATGAGTGGATGAGT 1913  
Qy 1260 CGATGCCCGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1319  
Db 1914 CGATGCCCGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1973  
Qy 1320 CCAGAGAGGATTTTGAAGAGAGTACTCCCGAAGTGGATCCCGGCTTCGAGGCTA 1379  
Db 1974 CCAGAGAGGATTTTGAAGAGAGTACTCCCGAAGTGGATCCCGGCTTCGAGGCTA 2033  
Qy 1380 CGTTGGCTGTGCCCTGTGTTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 1439  
Db 2034 CGTTGGCTGTGCCCTGTGTTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 2093  
Qy 1440 ACATCCACCCTGATGCTGGGATTTATGCGAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1499  
Db 2094 ACATCCACCCTGATGCTGGGATTTATGCGAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2153  
Qy 1500 GCTGATCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1559  
Db 2154 GCTGATCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2213

Qy 1560 CCGCAGCATTTGCTCGCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCCGCTCTGCT 1619  
Db 2214 CCGCAGCATTTGCTCGCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCCGCTCTGCT 2273  
Qy 1620 TGTGTTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1679  
Db 2274 TGTGTTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2333  
Qy 1680 TGCAGCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGACACACACACACACACACACAC 1739  
Db 2334 TGCAGCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGACACACACACACACACACACAC 2393  
Qy 1740 CAATTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1799  
Db 2394 CAATTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2453  
Qy 1800 TCCTGAGGTGTC 1812  
Db 2454 TCCTGAGTACTTC 2466  
  
RESULT 7  
AAQ42525  
ID AAQ42525 standard; DNA: 4046 BP.  
XX  
AC AAQ42525;  
XX  
DT 14-SEP-1993 (first entry)  
XX  
DE Cardiac adenylyl cyclase gene.  
XX  
KW Regulation; cardiac function; heart; heart failure; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS 131..3627  
FT /\*tag= a  
XX  
PN EP543137-A.  
XX  
PD 26-MAY-1993.  
XX  
PF 12-OCT-1992; 92EP-011737A.  
XX  
PR 18-NOV-1991; 91US-0793961.  
XX  
PA (AMCY ) AMERICAN CYANAMID CO.  
XX  
PI Ishikawa Y;  
XX  
DR WPI; 1993-168873/21.  
DR P-PSDB; AAR37309.  
XX  
PT Purified DNA encoding cardiac adenylyl cyclase - useful to screen  
PT for cpds. which stimulate activity of the cyclase  
XX  
PS Claim 1; Fig 2; 34pp; English.  
XX  
CC A canine heart cDNA library was constructed in lambda gtl0 and was  
CC screened with a 970 bp AatI-HincII fragment from type I adenylyl  
CC cyclase cDNA probe (encodes the first cytoplasmic domain of adenylyl  
CC cyclase, which has significant homology to other previously known  
CC types of adenylyl cyclase). One positive clone, of 5.4 kb was obtd.  
CC Positive colonies were subcloned into puc18 and further subcloned  
CC and sequenced bidirectionally. The 5.4 kb clone was used to  
CC rescreen the library and on overlapping clone contg. the 5' end of  
CC the gene was isolated. Together the two clones cover the complete  
CC canine cardiac adenylyl cyclase gene. The gene is suspected of  
CC being involved in the regulation of cardiac function and it is thought  
CC that decreased activity of adenylyl cyclase in the heart may be a  
CC major factor in the development of heart failure. Thus the adenylyl







Qy	842	ATGTGTTGCTCCAATGATGTGACCCCTGGCGAACACCACATGGGAAGCAGGAAAGCGGGCTGC	901
Db	1567	ATGTCGTGTAACAACATGTGACCCCTGGCTTAAACCAATAGAGAGCGCGGGGC---GGCCGCGC	1623
Qy	902	GCATCACACATCACTCGGGCAACACTGCAGTAGTACCTGAACGGGGAGCTACGAAGTGAGGACG	961
Db	1624	GCATCACACATCACTCGGGCTACACTGCGAGTACTTGAACGGGGAGCTATGAGGTGGAGCGAG	1683
Qy	962	GCGTGTGGCAAGGCCAACGCGTACCTCAAGGAGCAGCATTGAGACTTTTCCCTCATCC	1021
Db	1684	GCGTGTGTGTAACGCAATGCGTACCTCAAGGAGCAGTGCATTGAGACCTTCTCTATAC	1743
Qy	1022	TGGGCGCCAGCAGAAACGGAAGAAGAGGAAAGGAGTCTCTGGCAAAGTGCAGCGGACTC	1081
Db	1744	TTGGCGCCAGCCAAAACGGAAGAAGAGGAAAGCCATCTCTGGCCAAGCTTCAGCGGACAC	1803
Qy	1082	GGCCCAACTCCATGGAAGGCTGATGCCGCGATGGGTTCCTGATGCTGTCGCTTCNC	1141
Db	1804	GGCCCAACTCCATGGAAGGACTGATGCCCGCTGGGTTCTTGACCGGTGCTTCFCCC	1863
Qy	1142	CCAAGGACTCCAAGGCTTCCTCCGCCAGATGGGCATTGATGATTCAGCAAAAGACAACCGGG	1201
Db	1864	CBAAGGACTCTAAGGACTTCGCCAGATGGGCATTGATGATTCAGCAAAAGACAACCGGG	1923
Qy	1202	GCACCAAGATGCCCTGAACCTGAGGATGAGGTGGATGAGTTCCTGAGCGGTGCCATCG	1261
Db	1924	GTCCCCAAGATGCTCTGAACCTGAACTGAGGTGATGAGTGGATGAGTTCCTGGCGGAGCCATCG	1983
Qy	1262	ATGCCCGCAGCATTGATCAGCTGCGGAGGAGGACCATGTCGGCGCGTTTTTGTCTACACCTTC	1321
Db	1984	ATGCCCGCAGCATTCGACCAACTTCGCTAAGGACCAATGTCGGCGGTTCTGTCTACACCTTC	2043
Qy	1322	AGAGAGAGGATTTTGAGAAGAAGTACTCCCGGAAGGTGGATCCCGGTTCTCGGAGCCTACG	1381
Db	2044	AGAGAGAGGATCTTGAGAAGAAGTATTCAAGGAAGTAGATCCCTCGTTCGGAGCCTACG	2103
Qy	1382	TTGCCGTGCCCCGTGTTGCTCTCTCTCATCTGCTTCATCCAGCTTCATAATFTTCCAC	1441
Db	2104	TCGCCGTGCCCCGTGTTGCTCTCTCTCATCTGCTTTTATCCAGCTCCTGTGTGTTCCCAT	2163
Qy	1442	ACTCCACCCTGATCTTGGGATTTATGCCAGCATCTTCCTGCTGCTGAATCACCGTGC	1501
Db	2164	ACTCCACCCTGATCTCGGGATTTATGCCGCTATCTTCCTGCTGTGCTGCTCACTGTC	2223
Qy	1502	TGATCTGTGCTGTGACTCTCTGTGTCTCTGTTCCCTAAGGCCCTGCAAGCTCTGTCCC	1561
Db	2224	TGATCTGTGCGGTGCTCTCTCGGTTCTTCTTCCCCAAGGCCCTGCAAGCCTGTCCC	2283
Qy	1562	GCAGATTTGCCGCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCOGTCTGCTTG	1621
Db	2284	GCAATATTGCCGCTCACGGGTGCACAGCACCGCGGTTGGAATCTTCTCGGTTCTGCTTG	2343
Qy	1622	TGTTACTTCTGCGCATTGCCACATGTTTCACCTGTAACCAACACCCCATACGGAGCTGTG	1681
Db	2344	TGTTACTTCTGCGCATTCGCCACATGTTTACGTGTAATCACACCCCATTAAGGACCTGCG	2403
Qy	1682	CAGCCCGGATGCTGAATTTAAACACCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCA	1741
Db	2404	CGCCCGGATGCTGAATTTAAACACCAAGCGGATGTCACCGCTGCACCTTACAACAGCTCA	2463
Qy	1742	ATTACTCTCTGGSCCTGGATGCTCCCTCTGTGTGAGGGCACCATTGCCACCTGCAGCTTC	1801
Db	2464	ATTACTCTCTGGSACTGGATGCTCCCTCTGTGTGAGGGCAACCGCACCTTGCAGCTTC	2523
Qy	1802	CTGAGGTGTC 1812	
Db	2524	CTGAGTACTTC 2534	
RESULT 10			
AA00462			
ID	AA00462 standard; DNA; 4523 bp.		
XX			

AC	AAX00462;	
XX		
DT	25-MAY-1999	(first entry)
XX		
DE	Human type V adenylyl cyclase coding sequence.	
XX		
KW	Type V adenylyl cyclase; human; hAC5; heart disease; brain;	
KW	therapy; diagnosis; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	W09901546-A1.	
XX		
PD	14-JAN-1999.	
XX		
PF	01-JUL-1998;	98WO-US13540.
XX		
PR	01-JUL-1997;	97US-0886362.
XX		
PR	01-JUL-1997;	97US-0070901.
XX		
PA	(CORT-) COR THERAPEUTICS INC.	
XX		
PI	Tomlinson JA;	
XX		
DR	WPI; 1999-106048/09.	
DR	P-PSDB; AAW30600.	
XX		
XX		
PT	Newly isolated and purified human type V adenylyl cyclase (hAC5)	
PT	polypeptide - useful for identifying potential therapeutic agents	
PT	that modulate hAC5 activity, and for the diagnosis of	
PT	hAC5-associated diseases and disorders	
XX		
PS	Claim 3; Fig 1a-h; 40pp; English.	
XX		
CC	This sequence encodes the human type V adenylyl cyclase (hAC5) of the	
CC	invention. hAC5 has a similar putative structure to other adenylyl	
CC	cyclase isoforms but, like type VI, is distinguishable in that it has a	
CC	larger N-terminus and a relatively shorter C-terminus as it lacks the	
CC	C2b region. The hAC5 polypeptides are useful in assays that screen for	
CC	potential therapeutic agents, which modulate hAC5 activity. These	
CC	polypeptides are also useful in assays for the diagnosis of diseases and	
CC	disorders. Agonists of hAC5 are useful control agents in such assays, and	
CC	they may have useful effects in vivo for treating disease. Antibodies	
CC	acting as (ant)agonists have diagnostic and therapeutic effects, and are	
CC	useful in immunoassays for hAC5. (Ant)agonists are particularly useful in	
CC	treating diseases caused by abnormal hAC5 activity (e.g. in the heart and	
CC	brain), and in diseases, which are alleviated by modulating hAC5	
CC	activity. The oligonucleotides are useful in methods that inhibit or	
CC	regulate hAC5 expression in vivo and in vitro. The cloning of the human	
CC	isotype of AC5 enables the development of tissue-specific and selective	
CC	pharmacological agents for use in treating particular human diseases	
CC	associated with hAC5.	
XX		
SQ	Sequence 4523 BP; 840 A; 1419 C; 1428 G; 836 T; 0 other;	
	Query Match	49.4%; Score 895; DB 20; Length 4523;
	Best Local Similarity	69.8%; Pred. No. 5.7e-229;
	Matches 1277; Conservative	0; Mismatches 525; Indels 27; Gaps
QY	5	ACGTGGTGCTGGGCATCTCGCGGCAGTCAGGTGGGGGCGCTTTCGCAGCAGACCCGC 64
DB	1046	ATGCGCTCATCGCGTGTGTGTCGGCCGTCAGGTGGTGGGCGTCTGCTGCTGCCGACGCCAC 1105
QY	65	GCAGCCCTCTGCGGGCCCTCTGGTGCCCTCTGTTGTATATCATCGCATACACGCTCC 124
DB	1106	GCAGCGCCTCTGAGGGGCATCTGGTGGACCGGTCTTTCATCTACACCATCTACACGCTGC 1165
QY	125	TCCCATCCGCATCGGGGCTGCGGTCCTCAGCGGCTGGGCGCTCTCCACCTTGCAATTGA 184
DB	1166	TGCCGTGCGCATCGGGCCGCGAGTGCACGCGGGGTGCTCTGCTGCCGCCCTCCACCTGG 1225
QY	185	TCTTGGCCTGCACACTTAACCGTGTGTATGCCCTCTCTGGAAGCAGAGCTCGGTGGCAATG 244

RESULT 10  
AAX00462  
ID AAX0  
XX



xx AAQ95540 encodes AAR78519, the novel effector enzyme cardiac adenylyl  
CC cyclase.  
XX  
SQ Sequence 4356 BP; 836 A; 1372 C; 1373 G; 775 T; 0 other;  
3;  
Query Match 48.8%; Score 884.6; DB 16; Length 4356;  
Best Local Similarity 69.1%; Pred. No. 3.4e-226;  
Matches 1259; Conservative 0; Mismatches 549; Indels 15; Gaps  
3;  
QY 5 ACGTGGTCTGGGCATCTCGCGCAGTGCAGGTGCGGGGGCTTTGCGAGCACACCCGC 64  
DB 821 ACGCGCTCATCGCGGTGTCGCGCTGCGAGTGGTGGCGCTCTGTCGCCAGCGC 880  
QY 65 GCAGCCCTCTGCGGGCTCTGGTCCCTGTTGTTTGTATACATCGATACAGCTCC 124  
DB 881 GCAGCGCTCGAGGGCATCTGGTGGACCGTGTCTTCATCTACCCATCTACAGCTGC 940  
QY 125 TCCCATCCGATCGCGGCTGCGTCTCTGAGCGCCCTGGCCCTCTCCACCTTGCATTGA 184  
DB 941 TGCCTGCGCATCGCGGCGCGCTCTGAGCGAGTGTCTCTGCGCCCTGCACTGG 1000  
QY 185 TCCTGGCTGGCACTTAACCGTGGTGTATGCTTCTCTGAGCAGCTCGGTGCCAATG 244  
DB 1001 CCATCGCCCTGCGCGCAACGCCAGCAGCGGTTCCTGCTCAAGCAGCTGCTCTCCA 1080  
QY 245 TGTGCTGTTCTCTGCACCAAGCTCATTAGCATCTGCACACATATCCAGCAGAGTGT 304  
DB 1061 TCCTCATTTCTCTGACCAACATCTGTGGTGTCTGTACCCATCTACCGGCTGACGTCT 1120  
QY 305 CTCAGCCCGAGGCTTTTCAGGACACCGCGATATACATCCAGCGCCGCTCCACCTGCGAGC 364  
DB 1121 CCCAGAGACAGGCTTCCAGAGACCGCGGAGTGCATCCAGGCAGCGCTCCACTCGCAAC 1180  
QY 365 ATGAGATCGGCAGCAGGCGGTGCTGCTGTCGGTATGCCCCAGCAGCTTGCCATGG 424  
DB 1181 GGGAGACCAACAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1240  
QY 425 AGATGAAGAGAGATCAACACAAAGAAAGA- --CATGTTCACAAAGATCTACATAC 481  
DB 1241 AGATGAAGAGAGATCAATGCCAGGAGGATATGATGTTCCATTAAGATTTACATCC 1300  
QY 482 AGAAGCATGAATGTGAGCATCTGTTTGCAGACATGAGGGCTTCACCAAGCCTGCGAT 541  
DB 1301 AGAAACATGACACGTGAGCATCTGTTTGTGACATGAGGGCTTCACCAAGCTTGGCAT 1360  
QY 542 CCCAGTCCATGCGCAGGAGCTGTCATGATGACCCCTGATGAGCTTTTGGCCGGTTGACA 601  
DB 1361 CCCAGTCCATGCGCAGGAGCTGTCATGATGAGCTTCAATGAGCTTTCGCCGCTTCGACA 1420  
QY 602 AGCTGGCTGCGGAGATCACTGCTGAGATCAAGATCTTGGGGGACTGTTACTACTGTG 661  
DB 1421 AGCTGGCTGCGGAGATCACTGTTTACGTATTAAGATCTTGGGGGATGTTTACTACTGTG 1480  
QY 662 TGTGAGGCTGCGGAGGCGCGGCGCAGCATGCCCCACTGCTGTGTGAGATGGGGTAG 721  
DB 1481 TCTGCGCTGCTGTAAGCAGGAGGCGCCAGCACGCCACTGCTGCTGAGATGGGCATGG 1540  
QY 722 ACATGATGAGGCCATCTCGTGTAGTGCAGGTGACAGGTGTAATGTGNACATGCGCG 781  
DB 1541 ACATGATGAGGCCATCTCGTGTGTCGGGAGGTGACAGGGGTGAACGTGAACATGCGCG 1600  
QY 782 TGGCATCCACAGCGGCGGTGCTGCTGCGCGCTTGGCTTGGGAAATGGCAGTTGCG 841  
DB 1601 TGGGAATTCACAGCGGCGAGTACACTGCGGTGTCTTGGTCTCAGGAAGTGGCAGTTGCG 1660  
QY 842 ATGTGTGTCOAATGATGTGACCTGGCCACCAACATGGAAGCAGGAGCGGCTGGCC 901  
DB 1661 ACCTGTGCTTAATGAGCTACCGTGGCCCAACCATATGGAAGCTGGAGGCAAGCTGGGC 1720  
QY 902 GCATCCACATCATCTCGGCGACATGTCAGTACCTTGACGGGGACTACGAAGTGAGCCAG 961  
DB 1721 GCATCCACATCAACCAAGCCACATCTAGCTACCTGAACGGTGAAGTACGAGGTGAGCCAG 1780

QY 962 GCCGTGTCGCAAGCGCAACGCGTACCTCAAGGAGCAGCACATTGAGACTTTTCTCATCC 1021  
DB 1781 GCTCGGGGGGAGCGCAACGCGTACCTCAAGGAGCAGCATGATGAGACCTTCTCATCC 1840  
QY 1022 TGGCGCCAGCCAGAAACGGAAGAGAGGAGCATGCTGGCCAAAGTGCAGCGGACTC 1081  
DB 1841 TGCCTGTCACCCAGAACGGAAGAAAGAAAGGCGCATGATCGCCAAAGATGAATCGCCAGA 1900  
QY 1082 GGGCCAACTCCATGGAAGGCTGATGCGCGGATGGGTTCCTGTGATCGTGCCTTCTCCCGGA 1141  
DB 1901 GAACCAACTCCATTGGGCACAACCCGCCACTGGGGGCGAAGCTGCCCTTCTACAAC 1960  
QY 1142 CCAAGGACTCCAAAGCGCTTCGCCAGATGGGCATTGATTCCAGAGAAAGCAACACGGG 1201  
DB 1961 ACCTAGAGGCAACCAAGGTGTCGAAGGAGATGAAGCGCATGGGCTTCGAAGACCCCAAGG 2020  
QY 1202 GCA-----CCCAAGATGCCCTGAACCCCTGAGGATGAGGTGATGTTCTGAGCCGTG 1255  
DB 2021 ACAAGAAGCGCCAGGAAGTGCGAACCTGAGGATGAAGTGAATGAATTTCTGGCGCG 2080  
QY 1256 CCATCGATGCGCGCAGCATTCATCAGCTGCGGAAGGACCATGTGGCGGTTTTTGTCTCA 1315  
DB 2081 CCATTGACGCCAGGATCGACAGGTGCGGTGCGGACGCTCCGCAAGTTCCTCTGA 2140  
QY 1316 CTTTCCAGAGAGAGATTTCGAGAAAGTACTCCCGGAAGGTGATCCCGCTTCGGAG 1375  
DB 2141 CCTTCAGGAGCCCTGACTTAGAAAAGAGTACTCAAGCAGGTGATGACCGATTCGGTG 2200  
QY 1376 CCTACGTGTCCTGTCCTGTTCTGCTTCATCTGCTTCATCCAGCTTCTTAATTT 1435  
DB 2201 CCTACGTGGGATGTCCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2260  
QY 1436 TCCACACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTAATCA 1495  
DB 2261 TACCCCACTCGGTTCATGTTGATTTCTACTTGAACCTGTTTCTGCTGCTGCTGCTGCTG 2320  
QY 1496 CCGTGTGATCTGTGCTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1555  
DB 2321 TGGTATTGTGTCGTGATCTATTCCTGCGTGAAGCTTCCCGGGGCGGCTCCAGAGCC 2380  
QY 1556 TGTCCCGCAGCATGTCGCTCAGCGGCACATAGCAGCGAGTTGGCATCTTTTCCGTC 1615  
DB 2381 TCTCGAGGAAGATGTCGCTTCCAAAGCAACAGCACCCCTGTCGGGGTGTTCACCATCA 2440  
QY 1616 TGTCTGTGTTTACTTCTGCCATTGCCACATGTTCACTGTAAACACACACCCCATACGGA 1675  
DB 2441 CCCTGGTGTCTGCTGCGCTTTCGTCAACATGTTTCACTGTGTAACCTCGAGGACCTGTTGG 2500  
QY 1676 GCTGTGAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCTGCTGCTGCTGCTG 1730  
DB 2501 GCTGCTGCGGAGCAGCACAACATCAGCACCGCGGTCACGCGTGCACGCTGGCGG 2560  
QY 1731 -GCAGAGCTCAATTACTTCTGCGGCTGGATGTCCCTGTGTGAGGGCACCATGCCCCA 1789  
DB 2561 CGTGGCGGCAACCTCAGCCTGGCGCAGCAGGAGGCTTCTGCGGCACGCGCTGGCCCCA 2620  
QY 1790 CCTGCACTTCTTCAGGTGTTTC 1812  
DB 2621 CCTGCAACTTCCCGAGTACTTC 2643

RESULT 12  
AAQ37543  
ID: AAQ37543 standard; cDNA; 4356 BP.  
XX  
AC AAQ37543;  
XX  
DT 17-JUN-1993 (first entry)  
XX  
DE Cardiac adenylyl cyclase type V gene.  
XX  
KW CACV; therapy; diagnostic; cardiac function; cyclic AMP; cAMP; heart;



failure; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS 148..3702  
FT /\*tag= a  
XX  
XX EP529622-A.  
XX  
XX 03-MAR-1993.  
PD  
XX 27-AUG-1992; 92EP-0114637.  
PF  
XX 29-AUG-1991; 91US-0751460.  
PR  
XX (AMCY ) AMERICAN CYANAMID CO.  
PA  
XX  
XX Ishikawa Y, Konski AF;  
PI WPI; 1993-068688/09.  
DR P-PSDB; AAR32882.  
XX  
XX Isolated nucleic acid mol. encoding Cardiac adenylyl cyclase type  
PT V - useful for determining and modifying cardiac function  
XX  
XX Claim 1; Page 15-27; 38pp; English.  
XX  
XX Left ventricular tissue of canine heart was used as a source of mRNA.  
CC A cDNA library was prepd. in lambda gt10 phage. A 970 bp Aat-HincII  
CC fragment from type I adenylyl cyclase cDNA was used as probe. The  
CC clones isolated were used to obtain cDNA encoding CACV. This probe  
CC may also be used to screen a human cardiac cDNA library to obtain  
CC the cDNA encoding human CACV. CACV, its analogues and antibodies  
CC are useful in therapy or diagnostic assays, e.g. in modifying and  
CC determining cardiac function. A decrease in CACV content of the  
CC heart contributes to impaired cAMP prodn. and in heart failure. The  
CC CACV can also be used to screen for cpds. which stimulate or inhibit  
CC the activity of the cyclase.  
XX  
SQ Sequence 4356 BP; 837 A; 1367 C; 1377 G; 775 T; 0 other;  
  
Query Match 48.8%; Score 883.4; DB 14; Length 4356;  
Best Local Similarity 68.9%; Pred. No. 7.2e-226;  
Matches 1243; Conservative 0; Mismatches 551; Indels 9; Gaps 2;  
  
QY 5 ACCTGGTGTGGCATCTCTGGCGGAGTCAGGTGCGGGGCGCTTTTCGACGAGACCCGC 64  
DB 821 ACGCGCTCATCGCGGTGTGCTGGCGGTGCAGGTGGTGGGCGCTGTGCTGCCACGCCG 880  
  
QY 65 GCAGGCCCTCTCGGGGCCCTCTGGTGCCTGTGTCTTTGTATACATCGCATACAGCTCC 124  
DB 881 GCAGGCCCTCCGAGGCGCATCTGGTGACCGTGTCTTCATCTACACCATCTACAGCTCC 940  
  
QY 125 TCCCATTCGCATGGGGGTGCGGCTCTCAGCGGCTGGGCGCTCTCCACCTTTGCATTGA 184  
DB 941 TGCCTGTGGCATGGGGGCGCGCTCTCAGCGGAGTGTCTCTGCGGCCCTGCACCTGG 1000  
  
QY 185 TCTTGGCTGGCACTTACCTGGTGTGATGCCCTCTCTGGAAGCAGCTCGGTGCCAATG 244  
DB 1001 CCATCGCTTGGCGGCAACGCCCGGAGTGTCTCTCAAGCAGCTCGTCTCCAAATG 1060  
  
QY 245 TGCTGTGTCTCTGCACCAACGTCATTAGCATCTGCACACACTATCCAGCAGAGGTGT 304  
DB 1061 TCTCATTTTCTCTGCACCAACATCGTGGGTGTCTGTACCCACTACCGGGCTGAGTCT 1120  
  
QY 305 CTCAGGCGCAGGCTTTTCAGAGACCCGAGTGTACATCAGCGCGGCTCCACCTTCAGC 364  
DB 1121 CCAGAGACAGGCTTCCCAAGAGACCCGGGAGTGCATCAGGACGCGGTCCACTCGCAAC 1180  
  
QY 365 ATGAGAATCGGACGAGGAGGCGTCTCTGCTGCTGATTTGCCAGACAGTTCGCATG 424  
DB 1181 GGGAAACACGACACAGGAGGCGGCTCTCTGTCTCTGCCCGACACAGTTGCCATGG 1240

QY 425 AGATGAAGAAGACATCAACACAAAAAAGAAC----ATGTTCCACAAGATCTACATAC 481  
DB 1241 AGATGAAGACAGACATCAATGCCAAGCAGAGGATGATGTTCCATAGATTTATATCC 1300  
  
QY 482 AGAAGCATGACAATGTACAGTCTCTGTTTTCAGACATTTAGGGCTTTCACAGGCTGGCAT 541  
DB 1301 AGAAACATGACAAAGTGTAGCATCTCTTTGCTGACATCGAGGCTTTCACAGCTGGCAT 1360  
  
QY 542 CCCAGTGCACCTGGCAGGAGCTGGTCAATGACCTGATGAGCTTTTGGCCGGTTTGACA 601  
DB 1361 CCCAGTGCACCTGCCAGGAGCTGGTCAATGACCTGATGAGCTTTTGGCCGGCTTCGACA 1420  
  
QY 602 AGCTGGCTCGGAGATCACTGCTGAGGATCAAGATCTTGGGGGAGCTTTACTACTGTG 661  
DB 1421 AGCTGGCTCGGAGATCACTGTTTACGTATTAAAGATCTCGGGGATTTGTTACTGTG 1480  
  
QY 662 TGTAGGGCTGCCGGAGGCCCGGCGACCATGCTGCTGCTGTGTGTGGAGATGGGGTAG 721  
DB 1481 TCTCTGGCTGCTGAAGCGAGGCGGCGACACGCCCACTGCTGCTGGAGATGGGCATGG 1540  
  
QY 722 ACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATCGCG 781  
DB 1541 ACATGATTGAGGCCATCTCGTTGGTCCGGGAGGTGACAGGGGTGAACGTGAACATCGCGG 1600  
  
QY 782 TGGCATCCACAGCGGGCGCTGCTGCTGCGGGCTTCTTGGCTTTCGCGAAATGCGAGTTCC 841  
DB 1601 TGGGAATTCACAGCGGGCGGAGTACACTGCGGTCTCTCAGGAAGTGCAGTTTCG 1660  
  
QY 842 ATGTGTGTTCATGATGATGACCTTGGCCAAACCATGGAAGCAGGAAGCGGGCTGGCC 901  
DB 1661 AGCTGTGTGTTAATGACGTGACGCTGCGGCAACCATATGGAAGCTGGAGGCAAGCTGGGC 1720  
  
QY 902 GCATCCACATCACTCGGGCAACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 961  
DB 1721 GCATCCCATCAACAGGCGCACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1780  
  
QY 962 GCGTGTGTGGCAAGCGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1021  
DB 1781 GCTGCGGGGCGGCGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1840  
  
QY 1022 TGGGCGCCAGCCAGAAAG 1081  
DB 1841 TCGGCTGCAACCCAGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1900  
  
QY 1082 GGGCCCAACTCCATGGAAGGCTGATGCGCGGATGGTGTCTGCTGCTGCTGCTGCTGCTG 1141  
DB 1901 GAACCAACTCCATGCGGCACACACCCCGCCACTGGGGGCGGCAACGCTCCTCTACAAC 1960  
  
QY 1142 CCAAGGACTCCAAGGCTTCCGCCAGATGGCATTTGATGATTTCCAGCAAGACAAACCGGG 1201  
DB 1961 ACCTAGGAGCAACAGGTGTCCAAGGAGATGAAGCGCATGGCTTCGAAGACCCCAAGG 2020  
  
QY 1202 GCA-----CCCAAGATGCCCTGACCCCTGAGATGAGTGGATGATTTCTTGAGCCGTG 1255  
DB 2021 ACAAGAACCCAGGAAAGTGGCAACCTGAGATGAAGTGAATGATTTCTTGGGCGCG 2080  
  
QY 1256 CCATCGATCCCGCAGCATTTGATGCTGCGGAAGACCATGTCGCGCGGTTTTCCTCA 1315  
DB 2081 CCATTCACCCAGGAGCATTCGAGCGCTGCGGTGCGGAGCAGCTGCCCAAGATTCCTCCTGA 2140  
  
QY 1316 CTTTCCAGAGAGAGGATTTTGAAGAGAGTACTCCCGGAGGTGGATCCCGGCTTCGGAG 1375  
DB 2141 CCTTCAGGAGGCTGACTTTAGAAAAGAGTACTCCAAAGCAGGTGGATGACCGGATTCGGTG 2200  
  
QY 1376 CTTAGTTCGCTGTGCCCTGTGGTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 1435  
DB 2201 CTTAGTTCGCTGTGCCCTGTGGTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 2260  
  
QY 1436 TCCACACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCT 1495  
DB 2261 TACCCACCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2320







Best Local Similarity 73.5%; Pred. No. 2.4e-203;  
Matches 1069; Conservative 0; Mismatches 365;

QY	5	ACGTGCTGGGCATCTCTGGCGGCAGTGCAGGTGGGGGCGCTTTTCGCACAGACACCCG	64
Db	1064	ATGCGCTCATCCCTGTGCTTGGCCGTGCCAAGTGGTGGGCTGCTGCTGCCGAGGCAC	1123
QY	65	GCAGCCCTCTCGGGGCTCTGGTCCCTGTGTTCTTTGTATACATCGCATACACGCTCC	124
Db	1124	GCAGCCCTCTGAGGGCATCTGGTGGACCGTGTCTTCATCTACACCATCTACACGCTGC	1183
QY	125	TCCCCATCCGATATGGGGCTGCCGCTCTCAGCGGCTTGGGCTCTCCACCTTGCATTTGA	184
Db	1184	TGCCCCGTGCATCTGGGCGCAGTGCTCAGCGGGTGCTCTCTGCCGCCCTCCACCTGG	1243
QY	185	TCTTGGCCTGGCAACTTAACTGCTGATGCTTCCCTCTGGAAGCAGCTCGGTGCCAATG	244
Db	1244	CCATGCCCTCTGGCACCAAGCCGCCAGGACAGTTCCTGCTGAAGCAGCTTGTCTCCAATG	1303
QY	245	TGCTGTGTTCTCTGCACCAACGTCATTAGCATCTGCACACACTATCCAGCAGAGTGT	304
Db	1304	TTCTCATTTTCTCTGCACCAACATCGTGGTGTCTGCACCCACTATCCGGCTGAGGTCT	1363
QY	305	CTCAGGGCCGCTTTCAGGAGACCCGAGTTACATCCAGGCCGGCTCCACCTGCAGC	364
Db	1364	CCAGAGACAGGCTTTCAGGAGACCCGAGAGTGCATCCAGGCGGGCTCCACTCCGAGC	1423
QY	365	ATCAGAACTCGGACGAGGAGCGGCTGCTGCTGTCGGTATTGCCCCAGCAGCTTGGCCATGG	424
Db	1424	GGGAGAACTCAGCAGAGGAACGGCTCTGCTGCTGTCTCTCCCGCTCATGTGTGCCATGG	1483
QY	425	AGATGAAAGAACATCAACACAAAAAAGAGA- --CATGTTCCACAAGATCTACATAC	481
Db	1484	AGATGAAACGACATCAACGCCAAGCAGGAGGATATGATCTCCATAAGATTTTACATCC	1543
QY	482	AGAACTGACAAATGTACGATCTCTGTTTGCAGACATTTGAGGGCTTCACAGCCTGGCAT	541
Db	1544	AGAAATGACAACTGTAGCATCTCTGTTGTGATCGAGGGCTTCACAGCCTGGCGT	1603
QY	542	CCAGTGTCACTCGCAGAGGCTGGTCATGACCTCAATGAGCTCTTTGCCGGTTTGACA	601
Db	1604	CCAGTGTCACTGCACAGGAACCTGTGCATGACCTCAACGAGCTCTTCCGCCGTGTACA	1663
QY	602	AGTGTGTCGGGAATCACTGCCTGAGGATCAAGATCTTGGGGAGCTGTTACTACTGTG	661
Db	1664	AGTGTGTCGAGAAATCACTGTTTACGTATTATAGATCCTTTGGGATGTTTATTACTGCG	1723
QY	662	TGTCAGGCTCGGAGGCCCGGGCCAGCATGCCACTGCTGTGTGGAGATGGGGGTAG	721
Db	1724	TCTCGGGGCTGCTGAAGCAAGGGCTGACCAGCCCACTGCTGTGTGGAGATGGGCATGG	1783
QY	722	ACATGATTGAGGCCATCTCGCTGGTACGTGAGTGCACAGGTGTGAATCTGAACATGCGCG	781
Db	1784	ACATGATCAGGCCATCTCGTTGGTCCGGAGGTGACAGGGTGAACTGAACTGACATGCGTG	1843
QY	782	TGGGCATCACAGCGGCGCTGCATCGCGCGTCTTTGGCTTGGGAAATGGCAGTTCCG	841
Db	1844	TGGGAATTCACAGCGGCGAGTACACTGCGGTGTCTTTGGTCTCAGGAAGTGGCAGTTCCG	1903
QY	842	ATGTGTGTCGAATGATGTGACCTTGGCCCAACCATGGAAGCAGGAAGCCGGGCTGGCC	901
Db	1904	ACGTCTGTCTAACGATGTACGGCTAGCCAGCAACCATGGAGGCTGGCGGCAAGCAGGAC	1963
QY	902	GCATCCACATCACTCGGCAACACTTGCAGTACCTGAAACGGGGACTACCAAGTGGAGCCAG	961
Db	1964	GCATCCACATCAACAAAGGCTACACTCAACTGAAATGGGGACTACGAGTGGAGCCAG	2023
QY	962	GCCGTGTTGGCAAGCGCAACCGTACCTCAAGGACGACATTTGAGACTTTCTCTCATCC	1021
Db	2024	GCTGTGGGGCGGCGCAACGGCTACCTCAAGGACGACAGTATGAGACCTTTCTCTCATCC	2083
QY	1022	TGGGCCCAAGCCAGAAACGGAAGGAGAAAGGACTGCTGGCCAAAGCTGCAGCGCACTC	1081

Db	2084	TGCGCTGCACCCAGAAAGCGGAAAGAAAGAGAGAGAGCCCATGATCCCAAGATGAACCGCCAGA	2144
Qy	1082	GGGCAACTCCATGGGAAGGGCTGATGCGCGGATGGGTTCTCTGATCGTGCCTTCTCC	1137
Db	2144	GAACCAACTCCATCGGGCACAAACCCACACACTGGGGGCTCAGCGCCCTTCTACAACC	2203
Qy	1138	-----CGAGACCAAGACTCCAAAGCGCTTCCGGCCAGATGGGCATTGATGATTCAGCA	1189
Db	2204	ACCTGGGTGGCAACACAGGTGTCCAAGGAGATGAAGCGGATGGGCTTTGAAGACCCCA	2260
Qy	1190	AAGCAACCCGGGGCACCCAAAGATGCCCTGAACCCCTGAGGATCAGGTGGATGAGTTCCITCA	1249
Db	2261	---AGGACAAGACCCCGAGAGATGGCAACCCCTGAGGATGAAGTGATGATTTCTCG	2317
Qy	1250	GCCGTGCATCGATGCCCGCAGCATTTGATCAGCTCGGAAGACCATGTGCGCCGGTTTT	1309
Db	2318	GCCGTGCATTTGACGCCAGGAGCATTTGATAGGCTTCGGTCTCAGCACGTCGCCAAGTTC	2377
Qy	1310	TGCTCACCTTCAGAGAGAGATTTTGAAGAAGTACTCCCGGAGGTGGATCCCGCT	1369
Db	2378	TCCTGACCTTCAGGAGAGCTGACTTTAGAGAAGAAGTACTCCAAGCAGGTAGACGACCGAT	2437
Qy	1370	TCGAGAGCTAGCTTCGCTGTGCCCTGTTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTC	1429
Db	2438	TGGTGCCTATGTGGCGTATGCCCTCGCTGCTTCTCCTCTTCATCTGCTTTGCCAGATCA	2497
Qy	1430	TAATTTTCCACACT	1444
Db	2498	CCATCGTGCCCACT	2512
RESULT	15		
ABL07501	ID	ABL07501 standard; cDNA: 4827 BP.	
XX	AC	ABL07501;	
XX	DT	26-MAR-2002 (first entry)	
XX	DE	Drosophila melanogaster expressed polynucleotide SEQ ID NO 16985.	
XX	KW	Drosophila; developmental biology; cell signalling; insecticide;	
XX	KW	pharmaceutical; gene; ss.	
XX	OS	Drosophila melanogaster.	
XX	PN	WO200171042-A2.	
XX	PD	27-SEP-2001.	
XX	PF	23-MAR-2001; 2001WO-US09231.	
XX	PR	23-MAR-2000; 2000US-191637P.	
XX	PR	11-JUL-2000; 2000US-0614150.	
XX	FA	(PEKE ) PE CORP NY.	
XX	PI	Venter JC, Adams M, Li PWD, Myers EW;	
XX	DR	WPI; 2001-656860/75.	
XX	DR	P-PSDB; ABB63398.	
PT	PT	New isolated nucleic acid detection reagent for detecting 1000 or more	
PT	PT	genes from Drosophila and for elucidating cell signalling and cell-cell	
PT	PT	interactions -	
XX	PS	Claim 1; SEQ ID NO 16985; 21pp + Sequence Listing; English.	
XX	CC	The invention relates to an isolated nucleic acid detection reagent	
XX	CC	capable of detecting 1000 or more genes from Drosophila. The invention	
XX	CC	useful in developmental biology and in elucidating cell signalling and	
XX	CC	cell-cell interactions in higher eukaryotes for the development of	
XX	CC	insecticides, therapeutics and pharmaceutical drugs. The invention	

CC discloses genomic DNA sequences (AB161176-AB130511), expressed DNA  
CC sequences (AB101840-AB161175) and the encoded proteins  
CC (AB57737-AB572072).

CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX  
SQ Sequence 4827 BP; 1115 A; 1377 C; 1340 G; 995 T; 0 other;

```

Query Match          24.6%; Score 445.8; DB 23; Length 4827;
Best Local Similarity 57.7%; Pred. No. 1.2e-108;
Matches 913; Conservative 0; Mismatches 607; Indels 63; Gaps 4;

QY 5 ACCTGTCTGGGCATCTTGGCGGCGAGTGCAGGTGGGGGGCGCTTTCGAGCAGACCCCGC 64
DB 1187 ACCTCATCTTGGGCACCTTCTTGGCCATCGAAGTGGCCGTAGCTATGCCATGCAACCCA 1246
QY 65 GCAGCCCTCTCTGGGGGCTCTGGTGGCCCTGTGTTCTTTGTATACATCGCATACAGCTCC 124
DB 1247 GCAAAATCTTCAACGGCAGCGCTGCTGCTATGCTCATCTACATGAGCTACACGATGC 1306
QY 125 TCCTCCATCCGCATGCGGGCTGC-----CGTCTCAGCGGCTGGGGCTCT 169
DB 1307 TGGCCCTTGGCTTGGGGAGGCTCTGATCGGGGAATCTCTTGAGCGCTGCTCCATCTGT 1366
QY 170 CCACCTTGGCATTTTGCTTGGCTGGCAACTTAACCGTGGTGATGCTTTCCTCTGGAAGC 229
DB 1367 ACACCTGCCTGAGGCTCAACGGATGATGAGTGCAGCGGTGATGATGATGATGATGATG 1426
QY 230 AGCTCGGTGCCAATGCTGTGCTTCTTCTGCAACACGCTCATTTAGCATCTGACACACT 289
DB 1427 AGCTCTCTGCACTTTGGTGGCCCTACTCTGGCCCACTCTCACTGGCGCTACACCACT 1486
QY 290 ATCCACACAGGTGCTCAGCGCCAGCGCTTTCAGAGACCCGCGTACATCCAGGCC 349
DB 1487 GGCCTAAGGAGAGGCGCCAGCGAAGCGGTTCATCAGAGACGAGCGATGATCGAGGCCA 1546
QY 350 GGCTCCACCTGACGATGAGATCGCAGCAGGAGCGGTGCTGTGCTGGGTATTCGCC 409
DB 1547 GCTGAGGACGACGCGCAACCAACAGCAGGAGCGCTTGTGCTGCTGGTCTCGCG 1606
QY 410 AGCAGCTTCCCATGGAGATGAAGAGACATCAACACAAAAGAGACAT---GTTCC 466
DB 1607 GTCATGGCCATGGAGATGAAGGAGCATATTGCGGGCCAGCCACGTGACACCCAGTTCC 1666
QY 467 ACAAGATCTACATACAGAGCATGACAATGTCTAGCATCTGTTTGCAGACATTTAGGGCT 526
DB 1667 ATAAGATATACATCCAAACGCGCAGAGATGTCAGCATCTTTTGGGACATCTGCGGT 1726
QY 527 TCACCACTGGCATCCCATGCTGACATGCGCAGGAGCTGCTATGACCCCTGAATGAGCTCT 586
DB 1727 TCACCACTGCTCTCGGATCATGTCAGCCGCGAGGAATTGGTGGCTCTGCTGAACGAGCTCT 1786
QY 587 TTGCGCGGTTTGACAGCTGGCTGGCGGAGAACTACCTGCTGAGGATCAAGATCTTGGGG 646
DB 1787 TTGCGCGCTTTGATGCTGGCTGGGAGCATCTATGCTGGGCAATTAAGCTGCTGGGG 1846
QY 647 ACTGTTACTACTGTGTGTCAGGGCTCGCGGAGCGCCGCGGACCATGCGCACTGCTGTG 706
DB 1847 ATTGCTACTACTGCTCTCGGACTCCCGAACCCTCGGATCAGCCCATTTGCGCG 1906
QY 707 TGGAGATGGGGTAGACATGATTTAGGCCATCTCGCTGCTGCTAGGTGACAGGTGTGA 766
DB 1907 TCGAAATGGGATCGCATATGATTGACGCCATCGCATGTTTCGCGAAGTATGCGCGGTGA 1966
QY 767 ATGTGAACATGCGCGTGGCATCCAGCGGGCGCTGACATCGCGGCTCTTGGCTTGC 826
DB 1967 ACGTGAACATGCGAGTGGGATCCATACGCGCGCTGTGACATCGCGCGCTTTGGCGCTG 2026
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Search completed: February 22, 2003, 22:28:44  
Job time : 377.621 secs

GenCore version 5.1.3  
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# OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 22:08:18 ; Search time 59,7082 Seconds  
(without alignments)  
9306.902 Million cell updates/sec

Title: US-09-750-240-3

Perfect score: 1812

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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3	1763	97.3	4942	4	US-09-474-076-1
4	1519.8	83.9	4046	1	US-07-793-961A-1
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8	858.2	47.4	3924	3	US-08-726-214-9
9	436	24.1	3978	3	US-08-726-214-1
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12	320.6	17.7	4601	3	US-08-726-214-15
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19	216.8	12.0	4473	3	US-08-894-173-1
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44	39.2	2.2	2734	3	US-09-135-021-79	Sequence 79, Appl
45	39.2	2.2	2821	4	US-09-135-010A-115	Sequence 115, Appl

## ALIGNMENTS

RESULT 1  
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; Sequence 3, Application US/09008097  
; Patent No. 6306830  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. Kirk  
; APPLICANT: Insel, Paul A.  
; APPLICANT: Ping, Peipei  
; APPLICANT: Post, Steven R.  
; APPLICANT: Gao, Meihua  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE  
; TITLE OF INVENTION: HEART FAILURE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/008,097  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dylan, Tyler M  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 22000-20567.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1812 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1...1812  
; OTHER INFORMATION:

0:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Disquette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Fastseq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/008,097  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Dylan, Tyler M  
REGISTRATION NUMBER: 37,612  
REFERENCE/DOCKET NUMBER: 20000-20567.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-813-5600  
TELEFAX: 650-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3549 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...3501  
OTHER INFORMATION:  
US-09-008-097-5

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; Sequence 1, Application US/09474076  
; Patent No. 6465237  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, James E.  
; APPLICANT: COR Therapeutics, Inc.  
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL  
; TITLE OF INVENTION: CYCLASE  
; FILE REFERENCE: 44481-5028-01-US  
; CURRENT APPLICATION NUMBER: US/09/474, 076  
; CURRENT FILING DATE: 1999-12-12  
; PRIOR APPLICATION NUMBER: PCT/US98/13694  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/070, 904  
; PRIOR FILING DATE: 1997-07-01  
; PRIOR APPLICATION NUMBER: 08/886, 550  
; PRIOR FILING DATE: 1997-07-01  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4942  
; TYPE: DNA  
; ORGANISM: human type VI adenylyl cyclase  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (145)..(3648)  
US-09-474-076-1

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DB 1779 TGGGAGCCAGCAGAAACGGAAGAGGAGAAAGGAGATGCTGGCCAAAGCTGCGAGCGGAGC 1838
QY 1082 GGCCCAACTCCATGGAAGGCTGATGCGCGGATGCGGCTTCTCATCGTGCCTTCCCGGA 1141
DB 1839 GGCCCAACTCCATGGAAGGCTGATGCGCGGATGCGGCTTCTCATCGTGCCTTCCCGGA 1898
QY 1142 CCAAGGACTCCAAGGCTTCCGCCAGATGGGATGATGATGATGATGATGATGATGATGATGAT 1201
DB 1899 CCAAGGACTCCAAGGCTTCCGCCAGATGGGATGATGATGATGATGATGATGATGATGATGAT 1958
QY 1202 GCACCCAAAGATGCCCTGAACCTCAGGATGAGTGATGATGATGATGATGATGATGATGATG 1261
DB 1959 GTGCCCAAGATGCCCTGAACCTCAGGATGAGTGATGATGATGATGATGATGATGATGATG 2018
QY 1262 ATGCCCGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1321
DB 2019 ATGCCCGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2078
QY 1322 AGAGAGGAGATTTTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1381
DB 2079 AGAGAGGAGATTTTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2138
QY 1382 TTGCCCTGTCGCCCTGTTGGTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 1441
DB 2139 TTGCCCTGTCGCCCTGTTGGTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 2198
QY 1442 ACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTG 1501
DB 2199 ACTCAACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTG 2258
QY 1502 TGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1561
DB 2259 TGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2318
QY 1562 GCAGCATTTCCGCTCAGCGGCATAGCAGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1621
DB 2319 GCAGCATTTCCGCTCAGCGGCATAGCAGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2378
QY 1622 TGTTTACTTCTGCCATTCGCAACATGTTTCACTGTAACACACACCCCATACGAGCTGTG 1681
DB 2379 TGTTCACCTCTGCCATTCGCAACATGTTTCACTGTAACACACACCCCATACGAGCTGTG 2438
QY 1682 CAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTG 1741
DB 2439 CAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTG 2498
QY 1742 ATTACTCTCGGCCCTGGATGCTCCCTGTGTGAGGGCACCATTGCCACCTCGAGCTTTC 1801
DB 2499 ATTACTCTCGGCCCTGGATGCTCCCTGTGTGAGGGCACCATTGCCACCTCGAGCTTTC 2558
QY 1802 CTGAGGTGTT 1812
DB 2559 CTGAGGTACTTC 2569
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RESULT 5
US-08-240-357-1
; Sequence 1, Application US/08240357
; Patent No. 5578481
; GENERAL INFORMATION:
; APPLICANT: Ishikawa, Yoshihiro
; TITLE OF INVENTION: Cloning and Characterization of a
; TITLE OF INVENTION: Cardiac Adenylyl Cyclase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
```

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; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,357
; FILING DATE: 10-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,705-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4046 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 131..3625
; US-08-240-357-1
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Query Match 83.9%; Score 1519.8; DB 1: Length 4046;
Best Local Similarity 90.7%; Pred. No. 0;
Matches 1643; Conservative 0; Mismatches 162; Indels 6; Gaps 2;

QY 5 ACGTGTGTGTGGGCTCCTGGGCGCAGTCAGGTGGGGGCGCTTTTCGACGACAGACCCCG 64
DB 762 ACGTGTGTGTGGGCTCCTGGGCGCAGTCAGGTGGGGGCGCTTTTCGACGACAGACCCCG 821
QY 65 GCAGCCCCCTCGGGGCCCTCTGGTGGCCCTGTCTTGTATATACATCGCATACACCTCC 124
DB 822 GCAGCCCCCTCTGGTGGCCCTCTGGTGGCCCTGTCTTGTATATACATCGCATACACCTCC 881
QY 125 TCCCCATCCGATCGCGGCTCGCTCTCAGCGCCCTGGGCCCTTCACACTTGCATTGTA 184
DB 882 TACCCATCCGATCGCGGCGAGCTGTCTTCACTGGCCCTGGCCCTGTCACCTTGCATTGTA 941
QY 185 TCTTGGCCCTGGCAACTTAACCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 244
DB 942 TCTTGGCCCTGGCAACTTAACCGCGGTGAGCCCTTCCCTCTGGAAGCAGCTCGGTGCAACA 1001
QY 245 TGTGCTGTCTCTCGACCAACAGTCATTAGCATCTGCACACACTATCCAGCAGAGGTGT 304
DB 1002 TGTGCTGTCTCTCGACCAACAGTCATTGGCATCTGCACACACTATCCAGCTGAGGTCT 1061
QY 305 CTCAGCGCCAGGCTTTTCAGGAGACCCGAGTTTACATCCAGGCCCGGCTCCACCTGCAGC 364
DB 1062 CTCAGCGCCAGGCTTTTCAGGAGACCCGCGGTTTACATTCAGGCCCGGCTGCACCTGCCAG 1121
QY 365 ATGAGAATCGGACGAGGCGCTGCTGCTGTGGTATTTGCCCGCCAGCAGTGTGCCATGG 424
DB 1122 ATGAGAATCGGACGAGGCGCTGCTGCTGTGGTATTTGCCCGCCAGCAGTGTGCCATGG 1181
QY 425 AGATGAAGAAGACATCAACACAAAAAAGAGAC---ATGTTCCACAGATCTACATAC 481
DB 1182 AGATGAAGAAGATATCAACACAAAAAAGAGACATGATGTTTCCAAAGATCTACATCC 1241
QY 482 AGAAGCATGACATGTCAGCATCTCTTTGCAGACATTTGAGGGCTTCCAGCAGCTGGCAT 541
DB 1242 AGAAGCATGACATGTCAGCATCTCTTTGCAGACATTTGAGGGCTTCCAGCAGCTGGCAT 1301
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Db	2066	TGCGCTGCACCCAGAAGACGGGAAGARAGAGAGGCCATCATGCCAAGATGAACCGCCACA	2121
Qy	1082	GGGCCCAACTCCATGGAAGGGCTGATGCCCGCATGGTGTTCCTGATCGTGCCCTTCCTCC	1137
Db	2126	GAACCAACTCATTGCGGCACAACCCACCACACTGGGGGCTGAGCGCCCTTCTACAACC	2185
Qy	1138	-----CGGACCAAGGACTCCAAGGCCTTCCGCCAGATGGGCAATGATGATTTCCAGCA	1189
Db	2186	ACCTGGGTGGCAACCAAGTGTCCAAGGAGATGAACGCGATGGGCTTTGAAGACCCCA	2242
Qy	1190	AAGACAACCGGGGACCCAAAGATGCCCTGAACCCCTGAGGATGAGGTGSATCAGTTCTCTGA	1249
Db	2243	---AGACAAGAACGCCCGAGGAGATGGCAACCCCTGAGGATGAAGTGGATGAGTTCCTGG	2299
Qy	1250	GCCGTGCCATTCGATGCCCGCACGATTCATGACTGCGGAAGGACCATGTGCGCGCGTTTT	1309
Db	2300	GCCGTGCCATTCGACGCCAGGACATTCATAGGCTTCGGTCTTGAGCAGCTCGCAAGTTCC	2359
Qy	1310	TGCTCACTTCCAGAGAGAGGATTTTGAGAAGAAGTACTCCCGAAGGTGGATNCCCCTG	1369
Db	2360	TCCTGACCTTCAGGGAGCCTGACTTTAGAGAAGAAGTACTCCAAGCAGGTAGACGACCGAT	2419
Qy	1370	TCCGAGCTACGTTGCCTGCGCCTGTGGCTTCTGTCCTTCTGCTTATCTGCTTATCCAGCTTC	1429
Db	2420	TTGGTGCCATGTTGGGGTGTGCTCGCTCGCTCTTCTCTTCTTCTGCTTTGTCCAGATCA	2479
Qy	1430	TAATTTTCCACACTCCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTG	1489
Db	2480	CCATCGTCCCCACTCCATTCATGCTCAGCTTCTACTGACCTGTTCCCTGCTGCTGCTGA	2539
Qy	1490	TAATCACTGCTGCTGATCTGCTGTGTACTCTCTGTGGTCTCTGTTCCTTAAGGCCCTGC	1549
Db	2540	CCTTGGTGGTGTGTGTGTGTGATCTACTCTCGTAAAGCTCTTCCCTCCCACTGC	2599
Qy	1550	AAGCTGTGCCCCACGACATTCGCGTCACGGGCACATAGCACCGCAGTTGGCATCTTTT	1609
Db	2600	AGACCTCTCCAGGAAGATCGTGGGTCCAAGATGAACAGACACCTGGTTGGGGTGTCA	2659
Qy	1610	CCGTCTGCTGTGTTTACTTCTGCGATTGCCAACATGTTCCACTGTAAACACACCCCA	1669
Db	2660	CCATACCCTGGTGTCTTGGCGGCTTTGTCAACATGTTTACGTGCACTCCAGGACCC	2719
Qy	1670	TACGAGCTGTGCAGCCGGATGCTGAATTTAACACCTGCTGACATCACTGCGTGCACCC	1729
Db	2720	TGCTGGGTGCTTGGCACAGGAGCAACATCAGCGCGAGCGAGGTCAACCGTGTCAAG	2779
Qy	1730	TGCAGAG-----CTCAATTACTCTGGGCGCTGGATGCTCCCTCTGTGAGGGGCACCA	1783
Db	2780	TGCGGAGTGGCCGCTCACTACAGCCTGGCGGATGAGCAGGGCTTCTGTGGCAGCCCT	2839
Qy	1784	TGCCCACTGSCAGCTTTCCTGAGGTCTC	1812
Db	2840	GGCCCAACTGCACATTCGCCGAGTACTTC	2868
RESULT 8			
US-08-726-214-9			
; Sequence 9, Application US/08726214			
; Patent No. 6107076			
; GENERAL INFORMATION:			
; APPLICANT: Tang, Wei-Jen			
; APPLICANT: Gilman, Alfred G.			
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE			
; TITLE OF INVENTION: AND USES THEREOF			
; NUMBER OF SEQUENCES: 31			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Arnold, White & Durkee			
; STREET: P.O. Box 4433			
; CITY: Houston			
; STATE: Texas			
; COUNTRY: United States of America			
; ZIP: 77210			
; COMPUTER READABLE FORM:			

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,214  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/005,498  
FILING DATE: 04-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: UTSD:450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3924 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-726-214-9

Query Match 47.4%; Score 858.2; DB 3; Length 3924;  
Best Local Similarity 68.6%; Pred. No. 1.5e-219;  
Matches 1254; Conservative 0; Mismatches 548; Indels 27; Gaps 4;

QY 5 ACCTGGTCTGGGCATCTCTGGGGAGTGCAGTGGGGGGCGCTTTTCGAGCAGACCCGC 64  
DB 421 ATCGCTCATTTGACGTGGTCTGGCGCTCCAGGTAGTGGGCGCTTGTGCTGCCACGCCAC 480

QY 65 GCAGCCCTCTGGGGCTCTGGTGGCTGGTCTTTGTATACATCGCATACACCTCC 124  
DB 481 CGAGCCCTCCGAGGGCATCTGGTGAGCGGTCTTCTCATACCATCTACACCCCTGC 540

QY 125 TCCCATCCGCATCGGGCTGCGCTCTCAGCGGCTGGGCGCTCTCCACCTTGCATTTGA 184  
DB 541 TGCTGTGCGCATGAGGGCTGCGGTCTCAGGGGGTGTCTCTGTCGGCTCTCCACTTGG 600

QY 185 TCTTGGCCTGGCACTTACCGTGGTGTGATGCCCTTCTCTGGAAGAGCTGGTGGCCATG 244  
DB 601 CCATCTCTCTGACACCAACGCCAGCCAGGTCTTCTGTGAAACAGCTTGTCTCCACG 660

QY 245 TGCTGTGTCTCTGCACCACTTATAGCATCTGCACACATATCCAGCAGAGGTGT 304  
DB 661 TCTCATCTCTCTGACCAACATCGTGGTGTGTGCTACTACTACCCAGCGAGGTCT 720

QY 305 CTCAGCCGAGCGCTTTCAGGAGACCCGAGTTACATCCAGGCGCGGCTCCACCTGCAGC 364  
DB 721 CCCAGACAAAGCTTCCAGGAGACCCGGAGTGCATCCAAAGCTCGGCTCCACTCACAGC 780

QY 365 ATGAGAAATCGGAGCAGGAGCGGCTGCTGCTGCTGATTTGCCAGCAGAGTTGCCATGG 424  
DB 781 GGGAGAACCGACGACAGAGCGCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840

QY 425 AGATGAAGAAGACATCAACACAAAAAGAGA---CATGTTCCACAGATCTACATAC 481  
DB 841 AGATGAAGACGACATCAACGCCAACAGAGGATATGATTTCCACAGATTTATACCC 900

QY 482 AGAAGCATGACATGTGACATCTCTGTTGACACATTTGAGGCGCTTCCAGCGCTGGCAT 541  
DB 901 AGAAACATGACATGTGACATCTCTGTTGCTGACATCGAAGGCTTCACTAGCGCTGGCAT 960

QY 542 CCCAGTGCATCGGAGGAGCTGGTGCATGACCGCTGAATGAGCTCTTGGCCGGTTTGACA 601  
DB 961 CCCAGTGTACTGCCCAAGAACTGGTGCATGACCGCTCAACGAGCTCTTTCGCCCGCTTTGACA 1020

QY 602 AGCTGGCTGGGAGATCACTGCTCAGGATCAAGATCTTGGGGGACTGTTACTACTGTG 661  
DB 1021 AGTTGGCTGGGAGATCACTGCTTACGATTAAGATCTCCGGGGATTTGTTACTACTGTG 1080

QY 662 TGTCAAGGCTGCCGAGAGCCGGCGGCGAGCATGCCCACTGCTGTGTGGAGATGGGGTAG 721  
DB 1081 TCTCGGGGCTGCTGAAGCCAGAGCTGACACGCCCACTGCTGCTGAGATGGGAATGG 1140

QY 722 ACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTAATGTGAACATGCGCG 781  
DB 1141 ACATGATCGAGGCCATCTCGTGGTCCGGAGGTGACAGGTTGAACATCGGTG 1200

QY 782 TGGGCATCCACAGCGGCGGTGCTGCTGCGGCGTCTTGGCTTGGCGAAATGCACTGTCG 841  
DB 1201 TGGGAATTCACAGCGGAGAGTACACTGCGGTGCTTGGCTCAGAAAGTGCAATTCG 1260

QY 842 ATGTGTGGTCCAATGATGTGACCTTGGCCCAACACATGGAAGCAGGAAGCGCGCTGGCC 901  
DB 1261 ACGTGTGGTCTAACGATGTACACTGGCCAAACCATGGAAGCTGCGCGCAAGCGAGCC 1320

QY 902 GCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGACTACGAAGTGGAGCCAG 961  
DB 1321 GCATCCACATCAACCAAGGCCACACTCACTGTAACGGGACTATGAGGTGGAGCCAG 1380

QY 962 GCGTGTGGCAAGCGCAACGCTACCTCAAGGAGCAGACATTTGAGACTTTCTCTCATCC 1021  
DB 1381 GCTGTGTGTGAGCGCAATGCTTACTCTCAAGGAGCAGCAGCTCGAGACCTTCTCTCATCC 1440

QY 1022 TGGGCCGCCAGCCAGAAACGGAAGAGGAGAAAGGCTGTGCGCAAGCTGCAAGCGGACTC 1081  
DB 1441 TGGCGTGTATCCCAAGAGCGGAAGAGAGAGGCCATGATCGCAAGATGAACCGCCAGA 1500

QY 1082 GGGCCAACTCCATGGAAGGGCTGATGCCGGATGGGTTCTGTATGCTGCTTCTCTCC---- 1137  
DB 1501 GAACCAACTCCATTTGACACAACTCGCCCTCACTGGGGAGCTGAGCGCCCTTCTTACAACC 1560

QY 1138 -----CGGACCAAGGACTCCAAAGGCTTCCGCGAGATGGGCAATGATGATTCACGCA 1189  
DB 1561 ACTTGGGTGCAACACAGTGTCCAAAGAAATGAAGAGGATGGCTTTGAGGAGCCCA--- 1617

QY 1190 AAGACAACCGGGGCAACCAAGATGCCCCGCTGAGGATGAGGTGGATGATGATTCCTGA 1249  
DB 1618 ---AGCACAAAGATGCCAGGAAAGTGCCAAACCTCAGGATGAAGTGGACGAGTTCTCTGG 1674

QY 1250 GCGCTGCCATCGATGCCCGCAGCATTTGATCAGCTGCGGAAGGACCATGTGCGCGGCTTT 1309  
DB 1675 GTGAGGCCATCGATGCCAGGATTTTGAAGACTCCGAGACTCCGAAACGCTCCGAAAGTTC 1734

QY 1310 TGCTCACTTCCAGAGAGAGGATTTTGAAGAAAGTACTCCCGGAAAGGTGGATCCCGCT 1369  
DB 1735 TCTTGACCTTTAGGGAGCGCGACTTAGAGAGAAAGTACTCCAAGCAGGTGGATGCGGAT 1794

QY 1370 TCGGAGCCTTACGTTGCTGTGCGCTGTGGTCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 1429  
DB 1795 TTTGGTGCCTATGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1854

QY 1430 TAATTTTCCACACTCCACCTGATGCTTGGGATTTATGCCACATCTTCTGCTGCTGCTGCT 1489  
DB 1855 CCATGTGCGCCACTCCCTGTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1914

QY 1490 TAATACCGTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1549  
DB 1915 CCTTGGTGTGTTTATATCTGTGATCTAGCCCTGTGAGACTCTTCCCTACTCTCCCTGCT 1974

QY 1550 AAGCTGTGTCGCGCAGCATTTGCCGCTCAGGGGCACATAGCACCGCAGTGGCATCTTTT 1609  
DB 1975 AGACACTCTCCAGGAAGATGCGGATCCAAAGAAAGAACAGCACCCCTGGTGGGGTGTTC 2034

QY 1610 CCGTCTGCTGTTGTTTACTTCTGCCAATGTTTCCACTGTTTCCACTGTTTCCACTGTTTCC 1669  
DB 2035 CCATCACTGTTGTTTCTCTCGGCTTTTGTCAACATGTTTCTGTTTCTGTTTCTGTTTCT 2094

QY 1670 TACGAGCTGTGCGAGCGCGGATGCTCAATTTAAACACTGCTGACATCACTGCTGCTGCTGCT 1729  
DB 2095 TGGTGGGTTGCCGAGAGGAGCACAAATCAGGTTGAACCGGTTGACGCGATGTCATG 2154









Db 1270 AAGGACGAGCAGTCTCAACACCATGTACATGTACCGCATGAGATGTTCAGCATCCTG 1329  
Qy 508 TTTCGACACATTGAGGCTTACCAGCCTGGCATCCAGTGCATCGCCAGGAGCTGGTC 567  
Db 1330 TTTTCAGATATTGGGCTTTACCCAGCTGCTCTGCTGAGTGGCCAGGAGCTCGTG 1389  
Qy 568 ATGACCTGATGAGCTCTTTGGCCGCTTGACAAAGCTGGCTGGGAGATCACTGCTG 627  
Db 1390 AAGCTACTCAAGAGCTCTTTGGCCGCTTTGACAAGCTGGGGCCAAATACCACAGCTG 1449  
Qy 628 AGGATCAAGATCTTTGGGGAGCTGTACTACTGTGTGTCAGGCTGCGGAGGCCGCCGCC 687  
Db 1450 AGGATCAAGATCTTACGCGAGCTGTACTACTGTGTGTCAGGCTGCGGAGCTGCTG 1509  
Qy 688 GACCATGCCACTGCTGTGGAGATGGGGTACACATGATTGAGGCGCATCTCGTACGTG 747  
Db 1510 GACCACCGCTGTCTCCATCTCTGATGGGCTTGCCATGGTGGAGGCGCATCTCGTACGTG 1569  
Qy 748 CGTGAGGTGACAGGTGTGAATGTGAACATGCGCTGGGCGATCCACAGCGGCGCTGCAC 807  
Db 1570 CGGGAGAAGACCAAGACCGGAGTGCACATCGTGTGGGGTGCACACAGGCACTGTGCTA 1629  
Qy 808 TGGCGCTCTTGGCTTGGGAAATGGCAGTTGCATGTGTGGTCCAATGATGTGACCCCTG 867  
Db 1630 GGTGGCTCTTGGGCCAAGAGCGCTGGCAGTATGATGTGTACCGATGTCTACTGTG 1689  
Qy 868 GCCAACACATGGAAGCAGGAGCGCGGCTGGCGCATCCACATCACTTCGGGCAACACTG 927  
Db 1690 GCAACAAAGATGGAGGCTGGCGGCATCCAGGGCGGCTGGACATTTCCAGAGCACCATG 1749  
Qy 928 CAGTACCTGAACGGGAGTACGAAGTGGAGCGGCGCTGGTGGCAAGCGCAAGCGGTAC 987  
Db 1750 GACTGCCTGAAAGGGAGTTCGATGTGGAACCTGGTGTGATGTGTCAGTGGTGGACTAC 1809  
Qy 988 CTCAGGAGCAGCAGATGTAGACTTTCTCATCTCTGGGCGCCAGCAGCAAGAAAGAG 1047  
Db 1810 CTAGATGAGAAGGCGCATCGAAACCTACCTCATCTATCTGCTCCAAAGCAGAGGTGAAGAAG 1869

RESULT 12

US-08-726-214-15  
; Sequence 15, Application US/08726214  
; Patent No. 610706  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Wei-Jen  
; APPLICANT: Gilman, Alfred G.  
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYL CYCLASE  
; TITLE OF INVENTION: AND USES THEREFOR  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,214  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/005,498  
; FILING DATE: 04-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L.  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: UTSD:450

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4601 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-726-214-15

Query Match 17.7%; Score 320.6; DB 3; Length 4601;  
Best Local Similarity 59.5%; Pred. No. 7.8e-76;  
Matches 567; Conservative 0; Mismatches 374; Indels 12; Gaps 1;

Qy 79 GGCCTCTGGTGGCCCTGTGCTCTTTGTATACATCGCATACAGCTCCTCCCATCGGCATG 138  
Db 1575 GGCATAGCTACGTGCTTTTACACTCTTCGCCACCTTCACAGCATGCTTCCGCTGCCCTC 1634  
Qy 139 CGGCTGCGGTCCTCAGCGGCTGGCCCTCTCCACCTTGCATTTGATCTTGGCCTGGCAA 198  
Db 1635 ACCTGGGCCATCTTGGCGGCTGGGCACATCCTTGTGCAAGTCACACTTCAAGTGTGTC 1694  
Qy 199 CTTAACCGTGTGTGATGCTTCCCTGTGGAAGCAGCTCGGTGCCAATGTGCTGTCTC 258  
Db 1695 ATACCCAGACTAGCGGTCTTTTCCATCAACCAGGTCTCTGGCCAGGTGCTGCTTCTCATG 1754  
Qy 259 TGCACCAACGTCATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCC 318  
Db 1755 TGCATGAATCAGCAGGCACTTTCATCAGTTACCTTTCAGACCGCGCCAGCGGAGGCC 1814  
Qy 319 TTTCAGGAGAGCCCGCAGTTTACATCAGGCGGCTTCCACCTGCAGCATGAGAATCGGCAG 378  
Db 1815 TTCTGGAGAGCCCGAGGTGTGTGGAGCCAGGCTCCGCTGGAGCAGAGAACCAAGA 1874  
Qy 379 CAGGAGCGGTGTGCTGTCTGCTGATGTGCCCAGCAGCTTGGCCATGGAGATGAAAGAGAC 438  
Db 1875 CAGGAGCGGTGTGCTGTCTGCTGCTCCAGGTTTGTGCTTCTAGAAAATGATCAATGAC 1934  
Qy 439 ATCAACACAAAAAAGAG-----ACATGTTCCACAGATCTACATACAGAG 486  
Db 1935 ATGACCAATGTGGAGGAGCAGCAGCTGCAGCATCAGTTCCACCGCATCTACATCCATCGC 1994  
Qy 487 CATGACAATGTGAGCATCTCTGTTGCAGACATTTGAGGCTTCCAGCAGCTGGCATCCAG 546  
Db 1995 TACGAGACGTGAGTATCTTTTGCAGATGTCAAGGATTTACCAACTCTCTACGACC 2054  
Qy 547 TGCAGTGGCAGGAGCTGGTGCATGACCTGAATGAGCTCTTTGGCCGCTTTGACAAGCTG 606  
Db 2055 TTGTCTGCTCAGGAGCTTGTCAAGATGCTCAACAGGCTCTTTGCCAGATTTGATCGGCTG 2114  
Qy 607 GCTGGGAGATCACTGCTGCTGAGGATCAAGATCTTGGGGAGCTGTACTACTGTGTGCA 666  
Db 2115 GCCATGAGCATCACTGCTTTCGCATTTAAATTCCTGGGGAGCTGCTACTACTGTGTGCA 2174  
Qy 667 GGGCTGCGGAGGCGCGGCGGAGCAGCATGCCACCTGCTGTGTGGAGATGGGGTAGACATG 726  
Db 2175 GGACTGCTGAGCCCGCAGGACCATGCTCATGCTGTGTGAATGGGCTCAGCATG 2234  
Qy 727 ATTGAGGCCATCTCGCTGGTGTGAGGTGACAGGTGTGAATGTGAACATCGCGCTGGGC 786  
Db 2235 ATCAAAATATCAGGTTTGTGAGGTCCAGAACAGCATGATGTTCATATGCAATTTGA 2294  
Qy 787 ATCCACAGCGGCGGCTGCACTGCGGCTCTTGGCTTGGGAAATGCAAGTTCAGTGTG 846  
Db 2295 ATCCATTCAGGCTCTGCTGTGTGTGTGGGCTTGAGAAAATGCAAGTTCAGTGTG 2354  
Qy 847 TGGTCCAATGATGTCAACCTGGCCAAACCATGGAAGCAGGAGCGGCTGGCGCATC 906  
Db 2355 TGGTCTTGGGATGTGGACATCGAAACAAACTTGAATCTGGAGGAATCCCTGGGAGAA 2414  
Qy 907 CACATCACTCGGCAACACTCAGTACCTGAACGGGAGTACGAAGTGGAGCCAGGCGGT 966

[illegible]

	Query Match	15.8%	Score 286;	DB 3;	Length 4008;
	Best Local Similarity	60.7%	Pred. No. 1.3e-66;		
	Matches 503;	Conservative	0;	Mismatches 295;	Indels 30; Gaps 1;
QY	219	CCTCTGGAAGCAGCTGCGTGCCAAATGTGCTGCTGTTCTCTCTGCACCAACGTCATTAGCAT	278		
Db	624	CCTCTTCTGCGCAGATCTGCGCAATGTGATCATTTTCTGTGGAACTTGGCGGGAGC	683		
QY	279	CTGCACACATATCCACGACAGAGGTGTCTCAGCGCCGAGGCCCTTCAGGAGACCCCGCAGTTA	338		
Db	684	CTACCAACAGCACCCTATGAGGCTTGCTCTCAGCAACACCTATCGGACACGCTGTAATTG	743		

	Query Match	15.8%	Score 286;	DB 3;	Length 4008;
	Best Local Similarity	60.7%;	Pred. No. 1.3e-66;		
	Matches 503;	Conservative 0;	Mismatches 295;	Indels 30;	Gaps
219	CCTCTGGAGCAGCTCGGTGCCAATGTGCTGCTGTTCCTCTGCACCAACGTCATTAGCA <sup>1</sup>				278
624	CCTGTTCTGGCAGATAC <sup>2</sup> TGCGCAATGTGATCATTTTCATTGTGGAACTTGGCGGGAGC				683
279	CTGCACACATATCCAGCAGAGGTTGTTCTACGGCGCCAGCGCTTTCAGAGACACCGCATTTA				338
684	CTACCAACAGCACCTCATGGAGCTTGGCTTGCACAAACCTATTCGGACACAGTGTAAATGG				743





GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 23, 2003, 02:25:49 ; Search time 95.15 Seconds  
(without alignments)  
10695.650 Million cell updates/sec

Title: US-09-750-240-3  
Perfect score: 1812  
Sequence: 1 gttacagtgtgtctggcat.....gcagcttctcgtggttc 1812

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 442118 seqs, 280819700 residues  
Total number of hits satisfying chosen parameters: 884236

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1812	100.0	1812	10	US-09-750-240-3
2	1808.4	99.8	3549	10	US-09-750-240-5
3	1763.4	97.3	3552	10	US-09-750-240-10
4	1763	97.3	4942	9	US-10-201-000-1
5	1657.8	91.5	3582	10	US-09-750-240-12
6	895	49.4	4523	9	US-10-175-158-1
7	319.4	17.6	2601	10	US-09-925-297-352
8	284	15.7	3518	9	US-10-121-911-2
9	216.8	12.0	4473	10	US-09-751-1008-1
10	209.4	11.6	4985	12	US-10-071-223-1
11	207.8	11.5	5515	10	US-09-751-1008-98
12	124.4	6.9	330	9	US-09-764-868-182
13	124.4	6.9	330	9	US-09-989-442-71
14	124.4	6.9	330	10	US-09-764-869-445
15	79.2	4.4	11881	9	US-09-764-868-1351
16	79.2	4.4	11881	9	US-09-764-868-1353
17	79.2	4.4	11881	10	US-09-764-869-2124
18	64.4	3.6	1259	9	US-10-051-643-123
19	64.4	3.6	1259	9	US-09-880-505-123

20	64.4	3.6	2013	9	US-10-051-643-176	Sequence 176, App
21	64.4	3.6	2013	9	US-09-880-505-176	Sequence 176, App
22	64.4	3.6	2172	9	US-10-051-643-173	Sequence 173, App
23	64.4	3.6	2172	9	US-09-880-505-173	Sequence 173, App
24	46.6	2.6	837	9	US-09-989-442-23	Sequence 23, Appl
25	46.6	2.6	915	9	US-09-764-868-181	Sequence 181, App
26	46.6	2.6	915	9	US-09-989-442-69	Sequence 69, Appl
27	42.2	2.3	923	9	US-09-989-442-20	Sequence 20, Appl
28	42.2	2.3	1180	10	US-09-915-582-11	Sequence 11, Appl
29	39.4	2.2	2602	10	US-09-866-582-19	Sequence 19, Appl
30	39.2	2.2	2028	10	US-09-840-125-1	Sequence 1, Appl
31	39.2	2.2	2821	10	US-09-880-107-3358	Sequence 3358, Ap
32	38.6	2.1	434	10	US-09-960-352-2292	Sequence 2292, Ap
33	38.4	2.1	455	9	US-09-954-531-848	Sequence 848, App
34	38	2.1	3121	9	US-10-033-245-6	Sequence 6, Appli
35	38	2.1	3121	9	US-10-033-223-6	Sequence 6, Appli
36	38	2.1	3121	9	US-10-033-167-8	Sequence 6, Appli
37	38	2.1	3121	9	US-10-033-244-6	Sequence 6, Appli
38	38	2.1	3121	9	US-10-033-435-6	Sequence 6, Appli
39	38	2.1	3121	9	US-10-032-990-6	Sequence 6, Appli
40	38	2.1	3121	12	US-10-033-246-6	Sequence 6, Appli
41	38	2.1	3121	12	US-10-033-301-6	Sequence 6, Appli
42	38	2.1	3121	12	US-10-033-326-6	Sequence 6, Appli
43	37.6	2.1	397	10	US-09-960-352-14458	Sequence 14458, A
44	37.6	2.1	1041	9	US-09-738-626-349	Sequence 349, App
45	37.4	2.1	1759	9	US-10-227-884-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1  
US-09-750-240-3  
; Sequence 3, Application US/09750240  
; Patent No. US20020103147A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammon, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
; FILE OF INVENTION: FAILURE  
; FILE REFERENCE: 220002056723  
; CURRENT APPLICATION NUMBER: US/09/750,240  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/472,667  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1812  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-750-240-3

Query Match	100.0%;	Score	1812;	DB	10;	Length	1812;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	1812;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Oy	1	GTTAACGTTGGTCTGGGCATCTGGCGCAGTGCAGGTCGGGGCGCTTTTCGACGAC	60				
Db	1	GTTAACGTTGGTCTGGGCATCTGGCGCAGTGCAGGTCGGGGCGCTTTTCGACGAC	60				
Oy	61	CCGCGCAGCCCTCTCTGGCGGCTCTGGTGCCTGTGTCTTTGTATACATCGCATACG	120				

Db 61 CCGCGAGCCCTCTCGGGCCCTCTGGTGCCCTGTGTCTTTGATATACATCGCATACCG 120  
QY 121 CTCCTCCCATCCGCATCGGGCTGCGCTCCTCAGCGGCTGGGCTCTCCACCTTGCAT 180  
Db 121 CTCCTCCCATCCGCATCGGGCTGCGCTCCTCAGCGGCTGGGCTCTCCACCTTGCAT 180  
QY 181 TTGATCTTGCGCTTGGCAACTTAACCGTGGTGATGCGCTTCTCTGGAAGCAGCTCGGTGCC 240  
Db 181 TTGATCTTGCGCTTGGCAACTTAACCGTGGTGATGCGCTTCTCTGGAAGCAGCTCGGTGCC 240  
QY 241 AATGTGCTGCTTCTCTGACCAACAGCTCAITAGCATCTGCACACACTATCCAGCAGAG 300  
Db 241 AATGTGCTGCTTCTCTGACCAACAGCTCAITAGCATCTGCACACACTATCCAGCAGAG 300  
QY 301 GTGCTCAGCGCCAGCGCTTTTCAGGAGACCGCAGTTACATCCAGGCCCGGCTCCACCTG 360  
Db 301 GTGCTCAGCGCCAGCGCTTTTCAGGAGACCGCAGTTACATCCAGGCCCGGCTCCACCTG 360  
QY 361 CAGCATGAGAAATCGGACGAGCGGCTGCTGCTGCGGTATTGCCCCCAGCAGCTTGCC 420  
Db 361 CAGCATGAGAAATCGGACGAGCGGCTGCTGCTGCGGTATTGCCCCCAGCAGCTTGCC 420  
QY 421 ATGAGATGAAAGACATCAACAAAAAGAAAGACATGTTCCACAGATCTACATA 480  
Db 421 ATGAGATGAAAGACATCAACAAAAAGAAAGACATGTTCCACAGATCTACATA 480  
QY 481 CAGAAGCATGACAAATGTCAGCATCTGTTTTCAGACATTCAGGSGCTTCACAGCCTGGCA 540  
Db 481 CAGAAGCATGACAAATGTCAGCATCTGTTTTCAGACATTCAGGSGCTTCACAGCCTGGCA 540  
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QY 661 GTGTCAGGGCTCGGAGGCGCGGCGGACATGCCACTGCTGTGTGGAGATGGGGTA 720  
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QY 721 GACATGATTGAGCCATCTCGCTGGTGACGTGAGGTGACAGGTGTAATGTGAACATGCGC 780  
Db 721 GACATGATTGAGCCATCTCGCTGGTGACGTGAGGTGACAGGTGTAATGTGAACATGCGC 780  
QY 781 GTGGGATCCACAGCGGCGGTGCACCTGGGCGCTCTTGGCTTGGGAATGGCAGTTTC 840  
Db 781 GTGGGATCCACAGCGGCGGTGCACCTGGGCGCTCTTGGCTTGGGAATGGCAGTTTC 840  
QY 841 GATGTGTGTCCAAATGATGTACCCCTGGCCAAACCACATGGAAGCAGGAGCCGGCTGGC 900  
Db 841 GATGTGTGTCCAAATGATGTACCCCTGGCCAAACCACATGGAAGCAGGAGCCGGCTGGC 900  
QY 901 CGCATCCATCACTCGGGCAACACTGCAGTACCTGAAAGGGGACTACGAAAGTGGAGCCA 960  
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QY 961 GGCCTGTGGCAGCGCAACGCTACCTCAAGGAGCAGCAGATTCAGACTTTCCTCATC 1020  
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QY 1021 CTGGGCGCCAGCAAAACGGAAGAGGAAAGGATGCTGGCCAAAGTTCAGCGGACT 1080  
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QY 1081 CGGGCAACTCCATGGAAGGCTGTATCCGCGATGGGTTCCTGATCGTCTTCCCGG 1140  
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QY 1141 ACCAAGGACTCCAGGCTTCCCGCAGATGGGATTTGATGATTTCCAGCAAGACACCGG 1200  
Db 1141 ACCAAGGACTCCAGGCTTCCCGCAGATGGGATTTGATGATTTCCAGCAAGACACCGG 1200

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QY 1201 GGCAACCAAGATGCCCTGAACCTGAGGATGAGTGSATGAGTTCCTGAGCCGTGCCATC 1260  
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QY 1261 GATGCCCGCAGCATTTGATCAGCTGCGGAGGAGCAGTGTGCGCGGTTTTTGTCTCACCTTC 1320  
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QY 1321 CAGAGAGAGATTTTGAAGAAGTACTCCGGAAGTGGATCCCGCTTCGAGGCTAC 1380  
Db 1321 CAGAGAGAGATTTTGAAGAAGTACTCCGGAAGTGGATCCCGCTTCGAGGCTAC 1380  
QY 1381 GTTGCTGTGCCCTGTTGCTTCTCATCTGCTTCTCATCTGCTTCTTAATTTCCCA 1440  
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QY 1441 CACTCCACCTGATGCTGGGATTTATGCCAGCATCTTCTGCTGTGCTTAATCACCGTG 1500  
Db 1441 CACTCCACCTGATGCTGGGATTTATGCCAGCATCTTCTGCTGTGCTTAATCACCGTG 1500  
QY 1501 CTGATCTGTGCTGTACTCTCTGCTTCTGCTTCCCTAAGGCCCTGCAACGCTGTCC 1560  
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QY 1621 GTGTTTACTTCTGCCATTTGCCAATGTTTCACTGTAACACACACCCCATACGAGCTGT 1680  
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QY 1681 GCAGCCGGATGCTGAATTTAACACCTGCTGACATCAGTCCCTGCCACCTGCGAGCTC 1740  
Db 1681 GCAGCCGGATGCTGAATTTAACACCTGCTGACATCAGTCCCTGCCACCTGCGAGCTC 1740  
QY 1741 AATTACTCTCTGGGCTGGATGCTCCCTGTGTGAGGGCAGCACCATGCGCCACTTCAGCTTT 1800  
Db 1741 AATTACTCTCTGGGCTGGATGCTCCCTGTGTGAGGGCAGCACCATGCGCCACTTCAGCTTT 1800  
QY 1801 CCTGAGGTGTTT 1812  
Db 1801 CCTGAGGTGTTT 1812

RESULT 2  
US-09-750-240-5  
; Sequence 5, Application US/09750240  
; Patent No. US20020103147A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
; FILE OF INVENTION: FAILURE  
; FILE REFERENCE: 220002056723  
; CURRENT APPLICATION NUMBER: US/09/750,240  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/472,667  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05  
; NUMBER OF SEQ ID NOS: 13

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; APPLICANT: Gao, M.

RESULT 3  
US-09-750-240-10  
: Sequence 10, Application US/09750240  
: Patent No. US20020103147A1  
: GENERAL INFORMATION:  
: APPLICANT: Hammon, H. K.  
: APPLICANT: Insel, P. A.  
: APPLICANT: Ping, P.  
: APPLICANT: Post, S. R.  
: APPLICANT: Gao, M.

; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE OF INVENTION: FAILURE
; FILE REFERENCE: 22002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 3552
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-750-240-10

Query Match 97.3%; Score 1763.4; DB 10; Length 3552;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 21; Indels 3; Gaps 1;

QY 3 TACGTGGTGGGCATCTCGCGCAGTGCAGGTGCGGGGCGCTTCGCGACGACCC 62
DB 636 TTACGTGGTGGGCATCTCGCGCAGTGCAGGTGCGGGGCGCTTCGCGACGACCC 695
QY 63 GCGACGCCCTCTGCGGGCCTCTGSGCCCTGTGTTCTTTATACATCGCATACACGCT 122
DB 696 GCGACGCCCTCTGCGGGCCTCTGSGCCCTGTGTTCTTTGTTCTACATCGCTACACGCT 755
QY 123 CCTCCCATCCGCGGCGCTCGCTCTCAGCGCCCTGGGCCCTTCACCTTGCATTT 182
DB 756 CCTCCCATCCGCGGCGCTCGCTCTCAGCGCCCTGGGCCCTTCACCTTGCATTT 815
QY 183 GATCTTGGCTGGCACTTAACCGTGGTGTGATGCTTCTTGAAGCAGCTGGTGCCAA 242
DB 816 GATCTTGGCTGGCACTTAACCGTGGTGTGATGCTTCTTGAAGCAGCTGGTGCCAA 875
QY 243 TGTGCTGTGTTCTCTGCACCAACGTCATTAGCATCTGCACACATATCCAGCAGGT 302
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QY 303 GTCTCAGCGCCAGGCGCTTTCAGAGACCCGCGATTACATCCAGCGCGGCTCCACCTGCA 362
DB 936 GTCTCAGCGCCAGGCGCTTTCAGAGACCCGCGATTACATCCAGCGCGGCTCCACCTGCA 995
QY 363 GCATGAGATCGGCACGAGGCGGCTGCTGTGTCGGTATTGCCCGCAGCAGCTTGCCAT 422
DB 996 GCATGAGATCGGCACGAGGCGGCTGCTGTGTCGGTATTGCCCGCAGCAGCTTGCCAT 1055
QY 423 GGAGATGAAGAGACATCAACACAAAAAAGAGAC---ATGTTCCAAAGATCTACAT 479
DB 1056 GGAGATGAAGAGACATCAACACAAAAAAGAGACATGATTCCACAAGATCTACAT 1115
QY 480 ACAGAAGCATGACAATGTCAGATCTCTGTTTCAGACATTTGAGGGCTTCACGAGCCTGGC 539
DB 1116 ACAGAAGCATGACAATGTCAGATCTCTGTTTCAGACATTTGAGGGCTTCACGAGCCTGGC 1175
QY 540 ATCCCATGTCATGCGCAGGAGCTGTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGA 599
DB 1176 ATCCCATGTCATGCGCAGGAGCTGTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGA 1235
QY 600 CAAGCTGGCTGGGGAATCACTGCGCTGAGGATCAAGATCTTGGGGGATGTTTACTACTG 659
DB 1236 CAAGCTGGCTGGGGAATCACTGCGCTGAGGATCAAGATCTTGGGGGACTGTTTACTACTG 1295
QY 660 TGTGTCAGGCGCTGCGGAGGCGCGGCCGACCATGCCACTGCTGTGTGAGATGGGGCT 719

DB 1296 TGTGTCAGGCGTCCCGAGGCGCCGGCCGACCATGCCACTGCTGTGTGAGATGGGGT 1355
QY 720 AGACATGATTGAGGCCATCTCGCTGTAGTGTGAGGTGACAGGTGTAATGTGAACATGCG 779
DB 1356 AGACATGATTGAGGCCATCTCGCTGTAGTGTGAGGTGACAGGTGTAATGTGAACATGCG 1415
QY 780 CTTGGGCATCCACAGCGGCGCTGCACCTGCGGCGCTTGGCTTGGGAAATGGCAGTT 839
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QY 840 CGATGTGTGTCATGATGTGACCTTGGCCAAACACATGGAAGCAGGAGCGGCGTGG 899
DB 1476 CGATGTGTGTCATGATGTGACCTTGGCCAAACACATGGAAGCAGGAGCGGCGTGG 1535
QY 900 CCGCATCCACATCACTCGGCGACACTGCAGTACCTGAAGGGGACTACGAGGTGGAGCC 959
DB 1536 CCGCATCCACATCACTCGGCGACACTGCAGTACCTGAAGGGGACTACGAGGTGGAGCC 1595
QY 960 AGGCCGTGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGCACATTTGAGACTTTCCTCAT 1019
DB 1596 AGGCCGTGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGCACATTTGAGACTTTCCTCAT 1655
QY 1020 CTTGGCGCCAGCCAGAAAG 1079
DB 1656 CTTGGCGCCAGCCAGAAACGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1715
QY 1080 TCGGGGCAACTCATGGAAGGCGTGTGCGGCGATGGTTCCTGTATCGTCCCTTCTCCCG 1139
DB 1716 TCGGGGCAACTCATGGAAGGCGTGTGCGGCGTGTGCGGCTGGTTCCTGTATCGTCCCTTCTCCCG 1775
QY 1140 GACCAAGGACTCCAGGCGCTTCGCGCAGATGGGCATTTGATGATTTCCAGCAAAAGACAACCG 1199
DB 1776 GACCAAGGACTCCAGGCGCTTCGCGCAGATGGGCATTTGATGATTTCCAGCAAAAGACAACCG 1835
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DB 1836 GGGCACCCAGATGCGCCTGAACCCCTGAGGATGAGGTGGATGAGTTCTGAGCGCTGCCAT 1895
QY 1260 CGATGCGCCGAGCATTTGATGCGGAGGAGACCATGTCGCGCGGTTTTTGTGCTACCTTT 1319
DB 1896 CGATGCGCCGAGCATTTGATGCGGAGGAGACCATGTCGCGCGGTTTTTGTGCTACCTTT 1955
QY 1320 CCAGAGAGAGGATTTTGAAGAAGTACTCCCGGAAGGTGGATCCCGCGTTCCGAGGCGCTA 1379
DB 1956 CCAGAGAGAGGATTTTGAAGAAGTACTCCCGGAAGGTGGATCCCGCGTTCCGAGGCGCTA 2015
QY 1380 CGTTGCTGTGCGCTGTGTTCTGCTTCATCTGCTTCATCCAGCTCTTAATTTTCCC 1439
DB 2016 CGTTGCTGTGCGCTGTGTTCTGCTTCATCTGCTTCATCCAGCTCTCTCATCTTCCC 2075
QY 1440 ACACCTCCACCCCTGANGCTTTGGGATTTATGCCAGCATTTCTCTGCTGCTGCTAATACCGT 1499
DB 2076 ACACCTCCACCCCTGANGCTTTGGGATTTATGCCAGCATTTCTCTGCTGCTGCTAATACCGT 2135
QY 1500 GCTGATCTGTGCTGTACTCTGTTGTTCTCTGTTCCCTAAGGCCCTGCAAGCTGTGTC 1559
DB 2136 GCTGATCTGTGCTGTACTCTGTTGTTCTCTGTTCCCTAAGGCCCTGCAAGCTGTGTC 2195
QY 1560 CCGCAGCATTTGTCGCTCACGGCAGCATAGCACCGCAGTTGGCATCTTTTCCCTCTGCT 1619
DB 2196 CCGCAGCATTTGTCGCTCACGGCAGCATAGCACCGCAGTTGGCATCTTTTCCCTCTGCT 2255
QY 1620 TGTGTTTACTTCTGCAATTTGCCAACATGTTTCACTGTAACACACACCCCATACGAGCTG 1679
DB 2256 TGTGTTTACTTCTGCAATTTGCCAACATGTTTCACTGTAACACACACCCCATACGAGCTG 2315
QY 1680 TCGAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCCACTGCGAGCAGCT 1739
DB 2316 TCGAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCCACTGCGAGCAGCT 2375
QY 1740 CAATTACTCTGCGGCTGATGCTCCCTGTGTGAGGCGACCATGCCACCTGCGAGCTT 1799
DB 2376 CAATTACTCTGCGGCTGATGCTCCCTGTGTGAGGCGACCATGCCACCTGCGAGCTT 2435





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Db 2342 GCAGCATTTGCCGCTCACGGGCACATAGCACCGAGTTGGCATCTTTTCCGTCCTGCTTG 2401
QY 1622 TGTFTTACTTCTGCATTGGCCATTGCCAATCTTCACTGTAAACACACCCCCCATACGGAGCTGTG 1681
Db 2402 TGTFTTACTTCTGCCATTGCCAATCTTCACTGTAAACACACCCCCCATACGGAGCTGTG 2461
QY 1682 CAGCCCGGATGCTGAATTTAAACACCTTGCCTGACATCACTGCCTGCCACCTGCAGCAGCTCA 1741
Db 2462 CAGCCCGGATGCTGAATTTAAACACCTTGCCTGACATCACTGCCTGCCACCTGCAGCAGCTCA 2521
QY 1742 ATTACTCTCTGGGCCCTGGATGCTCCCTGTGTGAGGGCACCATGCCCACCTGCAGGCTTTC 1801
Db 2522 ATTACTCTCTGGGCCCTGGATGCTCCCTGTGTGAGGGCACCATGCCCACCTGCAGGCTTTC 2581
QY 1802 CTGAGGTGTTTC 1812
Db 2582 CTGAGTACTTTC 2592

RESULT 5
US-09-750-240-12
; Sequence 12, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3582
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified AC-VI
US-09-750-240-12
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Query Match 91.5%; Score 1657.8; DB 10; Length 3582;  
Best Local Similarity 95.4%; Pred. No. 0;  
Matches 1730; Conservative 0; Mismatches 77; Indels 6; Gaps 2;

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QY 3 TAACGTGGTCTGGGGCATCTGCGGCAGTGCAGGTGCGGGGGCGCTTTGCGACGACCC 62
Db 657 TTACGTGGTCTGGGGCATCTGCGGCAGTGCAGGTGCGGGGGCGCTTCTGCGACGACCC 716
QY 63 GCGCAGCCCTCTGCGGGCTCTGGTCCCTGTGTGTATACATCGCATACACGCT 122
Db 717 GCGCAGCCCTCTGCGGGCTCTGGTCCCTGTGTGTATACATCGCATACACGCT 776
QY 123 CTCCCCATCCGATCGGGCTGCCCTCTCTCAGCGCCCTGGGCTCTCCACCTTGCATTT 182
Db 777 CTCCCCATCCGATCGGGCTGCCCTCTCTCAGCGCCCTGGGCTCTCCACCTTGCATTT 836
QY 183 GATCTTTGGCTGGCACTTAAACGTGGTGTATGCTTCTTGAAGCAGCTCGGTGCCAA 242
Db |||||
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Db 837 GATCTTTGGCTTGCACAACTTTAAACGTTGGTGTATGCTTCTCTGGAAGCAGCTCGGTGCCAA 896
QY 243 TGTGCTGCTGTTCTCTCTGCACCAACGTCATTAGCATCTGCACACACTATCCACGAGGT 302
Db 897 TGTGCTGCTGTTCTCTCTGCACCAACGTCATTGGCATCTGCACACACTATCCACGAGGT 956
QY 303 GTCTCAGCCCGAGGCCCTTTTCAGGAGACCCGCGAGTTACATCCAGGCCCGGCTCCACCTGCA 362
Db 957 GTCTCAGCCCGAGGCCCTTTTCAGGAGACCCGCGAGTTACATCCAGGCCCGGCTCCACCTGCA 1016
QY 363 GCATGAGATTCGCGCAGCAGAGGCGCTGTGCTGTGCGTATTCGCCCAGCAGCTTGGCAT 422
Db 1017 GCATGAGATTCGCGCAGCAGGCGCTGTGCTGTGCGTATTCGCCCAGCAGCTTGGCAT 1076
QY 423 GGAGATGAAGAAGACATCAACACAAAAAAGAACAC --- ATGTTCCACAAGATCTACAT 479
Db 1077 GGAGATGAAGAAGACATCAACACAAAAAAGAACATGATGTTCCACAAGATCTACAT 1136
QY 480 ACAGAAGCATGACAATCTCAGCATCTCTGTTTGACAGACATTTAGGGGCTTCCACGACCTGGC 539
Db 1137 ACAGAAGCATGACAATCTCAGCATCTCTGTTTGACAGACATTTAGGGGCTTCCACGACCTGGC 1196
QY 540 ATCCAGTGCATGCGCAGCAGAGCTGTGTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGA 599
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QY 660 TGTGTCAGGGCTGCCGGAGGCCCGGCGACCATGCCACTGCTGTGTGGAGATGGGGT 719
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QY 960 AGGCCGTGTGGCAAGCGCAACCGCTACCTCAAGAGCAGCAGCATTTGAGACTTTCTCTCAT 1019
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QY 1020 CTTGGCGCCAGCCAGAAACGGAAAGAGGAGAAAGCATGCTGGCCAAAGTGCAGCGGAC 1079
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QY 1260 CGATGCCCGCAGCATTTGATCAGCTGCGGGAAGACCATGTGCGCCGGTTTTGTGCTACCTT 1319
Db 1914 CGATGCCCGCAGCATTTGATCAGCTGCGGGAAGACCATGTGCGCCGGTTTTGTGCTACCTT 1973
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Db 2126 GAACCAACTCCATCGGGCACAACCCACACACTGGGGGGCTGAGCGCCCTTCTACAAAC 2185
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QY 1190 AAGACAACCGGGCACCACAGATGCCCTGAACCTTGAGGATGAGGTGGATGATTCCTGA 1249
Db 2243 ---AGGACAAGACGCCAGAGAGTGCGAACCTTGAGGATGAAGTGGATGATGTTCTGG 2299
QY 1250 GCCGTGCCATCGATGCCCGCAGCATGATCAGCTGCGGAAGGACCATGTCGCGCGGTTTT 1309
Db 2300 GCCGTGCCATGACGCCAGGAGCATGATAGGCTTCGGTCTGAGCAGCTCCGCAAGTTC 2359
QY 1310 TGCTACCTTCCAGAGAGAGATTTTGAAGAAGTACTCCCGAAGGTGGATCCCGGCT 1369
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QY 1490 TAATACCGCTGATGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1549
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RESULT 7

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US-09-925-297-352
; Sequence 352, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 352
; LENGTH: 2601
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: misc feature
; LOCATION: (2520)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2572)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-352
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Query Match 17.6%; Score 319.4; DB 10; Length 2601;
Best Local Similarity 64.5%; Pred. No. 3.6e-76;
Matches 515; Conservative 0; Mismatches 271; Indels 13; Gaps 2;
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QY 294 AGCAGAGGTGTCAGCGCCAGGCGCTTTTCAGGAGACCCGAGTTACATCCAGGCCCGCT 353
Db 34 AACAGCCGCAAGCACCGCAAGGCTTCTCTGGAGGCCCGCAGTCGCTGGAGTGAAGAT 93
QY 354 CCACCTGCACATCAGAAATCGGCAGCAGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 413
Db 94 GAACCTGGAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 153
QY 414 CGTTGCCATGGAGATGAAGAAGACATCAACACA-----AAAAAAGAGACAT 461
Db 154 CGTGGCTGACGAGATGCTGAAGACATGAAGAAGACAGAGCAGAGCAGAGCAGCAGCAGCA 213
QY 462 GTTCCACAAGATCTACATACAGAAGCATACATGTGTCAGCATCTCTTTGAGACATGTA 521
Db 214 GTTCAACACCATGTACATGTACCGTACAGAGACGTGAGCATCTCTTTGCCGACATCGT 273
QY 522 GGGCTTCCACAGCTGTCATCCCATCCAGTGCCTGCGCAGAGCTGTCATGACCTGATGATGA 581
Db 274 GGGCTTTACCCAGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 333
QY 582 GCTCTTTTCCCGGCTTTCACAAGCTGGCTGGCGGAGCAATCACTGCTGAGGATCAAGATCTT 641
Db 334 GCTCTTTTCCCGGCTTTCACAAGCTGGCGAGCTAAATACCAACAGCTGCGGATTAAGATCT 393
QY 642 GGGGAGCTGTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 701
Db 394 GGGGAGCTGTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 453
QY 702 CTGTGTGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTGCTGCTGCTGCTGCTGCTGCT 761
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QY 762 TGTGAATGTGAACATGCGCGTGGSCATCCACAGCGGCGCTGCACATGCTGCTGCTGCTGCT 821
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QY 822 CTTGCGGAATGGCAGTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 881
Db 574 CCAGAAGCGTGGCAGTACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 633
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QY 1002 CATTGAGCTTTTCTCATCTCTGGCGCC-AGCCAGAAACGGAAGAGAGAGAGGATGCT 1060
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RESULT 8

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US-10-121-911-2
; Sequence 2, Application US/10121911
; Patent No. US20020164632A1
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; GENERAL INFORMATION:  
; APPLICANT: Kapeller-Libermann, Rosana  
; TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE  
; FILE REFERENCE: 5800-47  
; CURRENT APPLICATION NUMBER: US/10/121,911  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US/09/412,210  
; PRIOR FILING DATE: 1999-10-05  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 3518  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: 21529 adenylate cyclase  
; NAME/KEY: CDS  
; LOCATION: (247)...(3480)  
US-10-121-911-2

Query Match 15.7%; Score 284; DB 9; Length 3518;  
Best Local Similarity 56.4%; Pred. No. 1.5e-66;  
Matches 617; Conservative 0; Mismatches 435; Indels 42; Gaps 3;

Qy 6 CQTGCTGCTGGGCATCCTGGCGCAGTGCAGGTGCGGGGCGCTTTCGAGCAGACCCGCG 65  
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Qy 234 CGGTGCCATGTGCTGTTCTCTGCTGCACCAAGCTCATATTAGCATCTGCACACATGCC 293  
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Db 888 CGGCTGGACACCGAGAGAGACCAAGACACCTTCTTGTCTCATCTCTCTGCTA 947  
Qy 414 CGTTGCCATGGAGATGAAGAGACATCAACACAAAAAAG----- 457  
Db 948 CTGCGCCGAGAGATGAAGGACAGAGATCATGCAAGCGGCTGCGAGGAGGCGTCAAG 1007  
Qy 458 -----ACATGTTCCACAAGATCTACATACAGAGCATGACAATGTACGAT 503  
Db 1008 GCCAGAGACCTAACAATTTCCAGACGCTTATGTCAGAGGACACAGGAGTCAAGGT 1067  
Qy 504 COTGTTTGCAGACATTGAGGGCTTCCAGCGCTTCCAGTCCCATCCAGTGCAGCGAGGT 563  
Db 1068 GCTGTATGCTGACATCGTGGCTTTCACGCGCTGCGGAGTGTTCCTTAAGAGCT 1127  
Qy 564 GGTATGACCTGAATGAGCTTTTGGCGGTTTGCAGAGCTGCTGGGAGAACTACTG 623  
Db 1128 GGTGCTCATGCTCAATGAGCTTTTGGCAAGTTTCAGCAGATTTGCAAGGAGCATGAATG 1187  
Qy 624 COTGAGGATCAAGATCTTGGGGAGCTGTACTACTGTGTGTCAGGGCTGCCGGCGCG 683  
Db 1188 CATCGGGATCAAGATCTTGGGGAGCTGTACTACTGTGTCTCTGGGCTGCCACTCTCACT 1247

Qy 684 GGCCGACCATGCCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGCCATCTCGCT 743  
Db 1248 GCCAGACCATGCCCACTCAACTGCTGCGCATGGCCCTGGACATGTGCCGGCCATCAGAA 1307  
Qy 744 GGTACTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCT 803  
Db 1308 ACTGGCGGACGCACTGGCGTGGACATCAACATGGCTGTGGCGTGCACCTCAGGCGCT 1367  
Qy 804 GCACCTGCGGCTTGTGCTTGGCGAATGGCAGTTCGATGTGTGTCATGATGATGATGAC 863  
Db 1368 ACTGTGTGAGTGCATCGGCTCGAAGTGGCAGTACGAGCTTGTGTACATGATGTAC 1427  
Qy 864 CCGTCCCAACACATCGAAGCAGGAGCGCGCTGCCGCATCCACATCACCTCGGCGAAC 923  
Db 1428 ACTGCTTAACACATGAGGACGCGGTGTACAGGGCGAGTGCACATCACAGGGCTAC 1487  
Qy 924 ACTGAGTACCTGAACGGGACTACGAAGTGGAGCGGCGCTGTGGCAAGCGCAACGC 983  
Db 1488 CCGGCGCTGCTGGCAGGGCTTATGCTGTGGAGGACGAGCATGGAGCATCGGAGCC 1547  
Qy 984 GTACCTCAAGGAGCAGCATTTGAGACTTTCCTCATCTCCTGGCGGCGCAGCAAGCGAA 1043  
Db 1548 CTACCTTCGGGAGCTAGGGAGCCCTACCTATCTGTCATCGATCCAGGGCAGAGGA 1607  
Qy 1044 AGAGGAGAAAGCA 1057  
Db 1608 GGATGAGAGGCA 1621

RESULT 9  
US-09-751-100B-1  
; Sequence 1, Application US/09751100B  
; Patent No. US20020142436A1  
; GENERAL INFORMATION:  
; APPLICANT: Medical Research Council  
; TITLE OF INVENTION: Human Adenylate Cyclase and Use Therefor  
; FILE REFERENCE: P27948A  
; CURRENT APPLICATION NUMBER: US/09/751,100B  
; CURRENT FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 4473  
; TYPE: DNA  
; ORGANISM: Mouse  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (43)...(4101)  
; OTHER INFORMATION: Adenylate cyclase coding region  
US-09-751-100B-1

Query Match 12.0%; Score 216.8; DB 10; Length 4473;  
Best Local Similarity 63.8%; Pred. No. 2.2e-48;  
Matches 329; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

Qy 463 TTCCACAAGATCTACATACAGAAGCATGACAATGTGTCAGCATCTGTTGCAACATGAG 522  
Db 1186 TTCCGCCCTTTAAGATGCAGCATTTGAAGAAGTCAGTATTTATTTCACACATG 1245  
Qy 523 GCGTTACACAGCTGGCATCCAGTGCACATGCGCAGGAGCTGTGTATGACCTGAAATGAG 582  
Db 1246 GGTTCACCAAGATAGCGCCCAAAATCTGGCATCTGTTGTTAGGCTTACTCAATGAC 1305  
Qy 583 CTCCTTGGCGCTTTGACAAAGCTGGCTGCGGAGATCACTGCTGAGGATCAAGTCTTG 642  
Db 1306 CTGTTGCGTCTGTTGACCGCTGTGTGAGCAGACCAAGTGTGAGAAGATCAGACTCTG 1365  
Qy 643 GGGGACTGTTTACTACTGTGTGTCAGGCTGCGGAGGCGCGCGGCGGCGGCGGCGGCGG 702  
Db 1366 GGGGACTGTTTACTACTGTGTGTCAGGCTGCGGAGGCGGCTGCGGAGCGGCGGCGGCGG 1425  
Qy 703 TGTGTGAGATGGGGTAGACATGATTGAGGCCATCTCTGCTGCTGATGAGGTGAGGT 762

Db 1426 TGCATTGAATGGCTTAGGCATGATAAAGCCATCAGAGAGTCTGCCAGGAGAGAAA 1485  
QY 763 GTGAATCTGAACATGCGCGTGGGATCCACAGCGGGCGGTGCACTCGCGCGTCTTGGC 822  
Db 1486 GAGATGGTGAACATGCGGTGGGGTTCAACACGGGACTCTCTGTGTGCGCATCCTGGC 1545  
QY 823 TTGCGGAAATGGCAGTTGTCATGTGTGTCCTCAATGATGTGACCTGGCCCAACACATGAA 882  
Db 1546 ATGAGGAGGTTTAAATTTGATGTGTGTCCTCAACGATGTGAATTTGGCTAATCTCATGAG 1605  
QY 883 GCAGGAGCGCGGTGCGCGCATCCACATCCTCGGGCAACACTGCACTGCAAGCGG 942  
Db 1606 CAGCTGGGAGTGGCGTGGCAAGTTCAATATCTGAGGCCACTGCAAAATACTTAGACG 1665  
QY 943 GACTTACCAAGTCAGCCAGCGGTGTGGCAAGCG 978  
Db 1666 AGGTATGAATGAAGATGGAGAGTATTGAGCGC 1701

## RESULT 10

US-10-071-223-1  
; Sequence 1, Application US/10071223  
; Patent No. US20020137174A1  
; GENERAL INFORMATION:  
; APPLICANT: Storm, Daniel R.  
; APPLICANT: Hacker, Beth  
; APPLICANT: Tomlinson, James E.  
; APPLICANT: COR Therapeutics, Inc.  
; APPLICANT: University of Washington  
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLIVL  
; TITLE OF INVENTION: CYCLASE  
; FILE REFERENCE: 44481-5029-02-US  
; CURRENT APPLICATION NUMBER: US/10/071,223  
; CURRENT FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: 09/473,717  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: PCT/US98/13541  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/098,559  
; PRIOR FILING DATE: 1997-07-01  
; PRIOR APPLICATION NUMBER: 08/886,440  
; PRIOR FILING DATE: 1997-07-01  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; TYPE: DNA  
; ORGANISM: human type IX adenylyl cyclase  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (17)..(3898)  
US-10-071-223-1

Query Match 11.6%; Score 209.4; DB 12; Length 4985;  
Best Local Similarity 62.1%; Pred. No. 2.3e-46;  
Matches 330; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

QY 426 GATGAAGAAGACATCAACACAAAAAAGAGACATGCTCCACAAAGATCTACATACAGAA 485  
Db 1123 GAAGAAAAGCTTCCATCCAAAAGCTCTCTATAGCCTTCGCCCTTTTAAAGATGCAGCA 1182  
QY 486 GCATGACAATGTCAGCATCTGTTTGCAGACATTTAGGGCTTCACCAAGCCTGGCATCCCA 545  
Db 1183 GATCGAAGAAGTCAGTATTTTATTTCAGATATCGTGGGCTTCACCAAGATGAGTGCAC 1242  
QY 546 GTCACATGCGCAGAGCTGCTCATGACCTGAAATGAGCTCTTTGCCCGGTTTGACAAGCT 605  
Db 1243 CAAGTCTGCCACGCCCTTGCTGGGTCTCTCTGAACGATCTGTCGGTGCCTTCGACCGCCT 1302  
QY 606 GCGTCGGGAGAATCACTGCCTCAGGATCAAGATCTTGGGGGACTGTTTACTACTGTGTGTC 665  
Db 1303 GTGTGAGGAGCAACAGTGTGAGAAAATCAGCACCCCTGGGAGACTGTTTACTACTGCGTGGC 1362

QY 666 AGGCTGCCGAGGCGCGGCCACCATGCCACTGCTGTGTGGAGATGGGGGTAGACAT 725  
Db 1363 GGGCTGTCCGAGCGCGGCCGACCATGCTACTGCTGCATCAGATGGCCTGGGCAT 1422  
QY 726 GATTGAGGCATCTCGCTGTGTAGTGTGAGTGTGACAGTGTGAAATGTGAACATGCGCGTGGG 785  
Db 1423 GATCAAGGCCATCGAGCAGTTCTGCCAGAGAAGAGAGATGCTGAACATGAGAGTCGG 1482  
QY 786 CATCCACAGCGCGCGGTGCACTCGCGGTCCTTGGCTTCGGGAAATGGCAGTTCGATGT 845  
Db 1483 GGTGCACACAGGCCACCGTCTTTCGGGCATCTGGGCATGAGGAGTTTAAATTTGACGT 1542  
QY 846 GTGGTCCAATGATGTGTACCTTGCCCAACACATCGAAGACAGGAGCGCGCTGGCCGCAT 905  
Db 1543 GTGGTCCAACGATGTGAACCTGGCCCATCTCTGAGCAGCTGGGAGTGGCCGCAAGT 1602  
QY 906 CCACATCACTCGGGCAACACTGCACTGACCTGACCTGGAACGGGAGCTACGAAGTGA 956  
Db 1603 TCACATTTCTGAGGCCACCGCAAAATACTTAGATGACCGGTACGAAATGGA 1653

## RESULT 11

US-09-751-100B-98  
; Sequence 98, Application US/09751100B  
; Patent No. US20020142436A1  
; GENERAL INFORMATION:  
; APPLICANT: Medical Research Council  
; TITLE OF INVENTION: Human Adenylylate Cyclase and Use Therefor  
; FILE REFERENCE: P27948A  
; CURRENT APPLICATION NUMBER: US/09/751,100B  
; CURRENT FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 98  
; LENGTH: 5515  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (539)..(4600)  
; OTHER INFORMATION:  
US-09-751-100B-98

Query Match 11.5%; Score 207.8; DB 10; Length 5515;  
Best Local Similarity 62.0%; Pred. No. 6.6e-46;  
Matches 329; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

QY 426 GATGAAGAAGACATCAACACAAAAAAGAGACATGCTCCACAAAGATCTACATACAGAA 485  
Db 1645 GAAGAAAAGCTTCCATCCAAAAGCTCTATAGCCTTCGCCCTTTTAAAGATGCAGCA 1704  
QY 486 GCATGACAATGTCAGCATCTGTTTGCAGACATTTAGGGCTTCACCAAGCCTGGCATCCCA 545  
Db 1705 GATCGAAGAAGTCAGTATTTTATTTCAGATATCGTGGGCTTCACCAAGATGAGTGCAC 1764  
QY 546 GTGCACTGCCAGAGCTGCTCATGACCTGAAATGAGCTCTTTGCCCGGTTTGACAAGCT 605  
Db 1765 CAAGTCTGCCACGCCCTGCTGGGTCTCTCTGAACGATCTGTCGGTGCCTTCGACCCGCT 1824  
QY 606 GCGTCGGGAGAATCACTGCTGAGGATCAAGATCTTTGGGGACTGTTTACTACTGTGTGTC 665  
Db 1825 GTGTGAGGAGACCAAGTGTGAGAAAATCAGCACCCCTGGGAGCTGTTTACTACTGCGTGGC 1884  
QY 666 AGGCTGCCGAGGCGCGGCCGACCATGCCACTGCTGTGTGAGATGGGGGTAGACAT 725  
Db 1885 GGCTGTGTCGAGCGCGCGGCCCATGCTCTGCTGCTGAGATGGGCTGGGCTGGGAT 1944  
QY 726 GATTGAGGCCATCTCGCTGCTGAGTGTGAGTGTGACAGTGTGAAATGTGAACATGCGCGTGGG 785  
Db 1945 GATCAAGGCCATCGAGCAGTCTCTGCCAGGAGAGAGGAGATGCTGAACATGAGAGTCGG 2004  
QY 786 CATCCACAGCGCGGCTGCACTGCGGCGTCTTGGCTTCGGGAAATGGCAGTTCGATGT 845





2	PRIOR FILING DATE:	2000-11-17	
3	PRIOR APPLICATION NUMBER:	60/249,217	
4	PRIOR FILING DATE:	2000-11-17	
5	PRIOR APPLICATION NUMBER:	60/249,211	
6	PRIOR FILING DATE:	2000-11-17	
7	PRIOR APPLICATION NUMBER:	60/249,215	
8	PRIOR FILING DATE:	2000-11-17	
9	PRIOR APPLICATION NUMBER:	60/249,264	
10	PRIOR FILING DATE:	2000-11-17	
11	PRIOR APPLICATION NUMBER:	60/249,214	
12	PRIOR FILING DATE:	2000-11-17	
13	PRIOR APPLICATION NUMBER:	60/249,297	
14	PRIOR FILING DATE:	2000-11-17	
15	PRIOR APPLICATION NUMBER:	60/232,400	
16	PRIOR FILING DATE:	2000-09-14	
17	PRIOR APPLICATION NUMBER:	60/231,242	
18	PRIOR FILING DATE:	2000-09-08	
19	PRIOR APPLICATION NUMBER:	60/232,081	
20	PRIOR FILING DATE:	2000-09-08	
21	PRIOR APPLICATION NUMBER:	60/232,080	
22	PRIOR FILING DATE:	2000-09-08	
23	PRIOR APPLICATION NUMBER:	60/231,414	
24	PRIOR FILING DATE:	2000-09-08	
25	PRIOR APPLICATION NUMBER:	60/231,244	
26	PRIOR FILING DATE:	2000-09-08	
27	PRIOR APPLICATION NUMBER:	60/233,054	
28	PRIOR FILING DATE:	2000-09-14	
29	PRIOR APPLICATION NUMBER:	60/233,063	
30	PRIOR FILING DATE:	2000-09-14	
31	PRIOR APPLICATION NUMBER:	60/232,397	
32	PRIOR FILING DATE:	2000-09-14	
33	PRIOR APPLICATION NUMBER:	60/232,399	
34	PRIOR FILING DATE:	2000-09-14	
35	PRIOR APPLICATION NUMBER:	60/232,401	
36	PRIOR FILING DATE:	2000-09-14	
37	PRIOR APPLICATION NUMBER:	60/241,808	
38	PRIOR FILING DATE:	2000-10-20	
39	PRIOR APPLICATION NUMBER:	60/241,826	
40	PRIOR FILING DATE:	2000-10-20	
41	PRIOR APPLICATION NUMBER:	60/246,475	
42	PRIOR FILING DATE:	2000-11-08	
43	PRIOR APPLICATION NUMBER:	60/241,786	
44	PRIOR FILING DATE:	2000-10-20	
45	PRIOR APPLICATION NUMBER:	60/241,221	
46	PRIOR FILING DATE:	2000-10-20	
47	PRIOR APPLICATION NUMBER:	60/246,475	
48	PRIOR FILING DATE:	2000-11-08	
49	PRIOR APPLICATION NUMBER:	60/231,243	
50	PRIOR FILING DATE:	2000-09-08	
51	PRIOR APPLICATION NUMBER:	60/233,065	
52	PRIOR FILING DATE:	2000-09-14	

Qy	569	GCTGCGGAGGCCCGGGCCGACCATGCCACTGCTGTGTGGAGATGGGGTAGACATGAT	728
Db	1	GCTGCCACTCTCACTGCCAGACATGCCATCAACTCGCTCGCATGGGCTGSCATATGG	60
Qy	729	TGAGGCGCATCTCCGCTGGTAGCTGAGGTGCACAGTGTGAATGTGAACATCGCGCTGGGCAT	788
Db	61	CKKGGCCATCAGGAACACTGGGCGCACCCACTGCGGTGGACATCAACATGCGTGTGGCGT	120
Qy	789	CCACAGCGGCGCGTGCATGCGGCGCTCTTGCTTTCGCGAAATGSCATTCGATGTGTG	848
Db	121	GCACCTCAGGCAGCGGTACTGTGTGGAGTCACTCGGGCTGCAGAAAGTGCAGCTAGCACCTTTG	180
Qy	849	GTCCAATGATGTACCCCTGSCCAACACATGGAGCAGGAACCGCGCTGGCGGCATCCA	908
Db	181	GTCCATGATGTCCACACTGCTGTAAACCACATGTGAGGCGAGCGGTGTACCAAGGCGAGTGCA	240
Qy	909	CATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTSGA	956
Db	241	CATCACAGGGCTTACCTCTGCTGCCCTGTGCGANGGCTTATGCTGNNGA	288



RESULT 14

US-09-764-869-445  
; Sequence 445, Application US/09764869  
; Patent No. US20020061521A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC007  
; CURRENT APPLICATION NUMBER: US/09/764,869  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 2442  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 445  
; LENGTH: 330  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (272)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (285)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (289)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-869-445

Query Match 6.9%; Score 124.4; DB 10; Length 330;  
Best Local Similarity 64.2%; Pred. No. 5.2e-24;  
Matches 185; Conservative 0; Mismatches 103; Indels 0; Gaps 0;  
QY 669 GCTGCCGGAGGCGCGGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGAT 728  
Db 1 GCTGCCACTCTCACTGCCAGACCATGCCATCACTGCTGCGCATGGCGCTGGACATGTG 60  
QY 729 TGAGAGCCATCTCGTGTGAGTGAGGTGACAGGTGTAATGTAACATGCGCGTGGCAT 788  
Db 61 CCKGCCATCAGAAACTGCGGGGAGCCACTGGCGTGACATCAACATGCGTGTGGCGT 120  
QY 789 CCACAGCGGCGCGTGCACACTGCGGCGCTCTTGGCTTGGGAAATGGCAGTTGATGTGTG 848  
Db 121 GCACTCAGGCGAGCTACTGTGTGGAGTCACTCGGCGCTGCAGAAAGTGGCAGTACGACGTTTG 180  
QY 849 GTCCAAATGATGTGACCTTGGCCAAACACATGGAAGCAGGAAGCGGCTGGCCGCATCCA 908  
Db 181 GTCAATGATGTACACTGGCTTAACACATGGAGGAGCGCGGTGTACCAGGCGAGTGCA 240  
QY 909 CATCACTCGGGCAACACTGCAGTACCTGAAACGGGACTACGAAGTGA 956  
Db 241 CATCACAGGGGCTACCCCTGGCCCTGCTGGCANGGGCTTATGCTGNNGA 288

RESULT 15

US-09-764-868-1351  
; Sequence 1351, Application US/09764868  
; Patent No. US20020168711A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT232  
; CURRENT APPLICATION NUMBER: US/09/764,868  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1510  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1351  
; LENGTH: 11881  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-09-764-868-1351

Query Match 4.4%; Score 79.2; DB 9; Length 11881;  
Best Local Similarity 63.4%; Pred. No. 4.8e-11;  
Matches 137; Conservative 0; Mismatches 78; Indels 1; Gaps 1;  
QY 746 TACGTGAGGTGACAGGTGTGAATGTGAACATGCGGTGGGCATCCACAGCGGCGGTGC 805  
Db 227 TCGCGGCAGCCCACTGCGCTGGACATCAACATGCGTGTGGCGTGCACCTCAGGCAGCGTAC 286  
QY 806 ACTGCGGCGTCTTGGCTTGGCGAAATGCCAGTTGATGTGTGGTCCCAATGATGTGACCC 865  
Db 287 TGTGTGGAGTCACTCGGGCTGCAGAAAGTGGCAGTACGACGTTTGGTCACATGATGTACAC 346  
QY 866 TGGCCAAACACATGGAAGCAGGAAGCGGGCTGGCGG-CATCCACATCACTCGGGCAACA 924  
Db 347 TGGCTAACACATGGAGGCGAGCGGTGTACCAGGGTGAGACCTAGGGCCCTAGGCAGCTA 406  
QY 925 CTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCA 960  
Db 407 CAGCAGAAAGGCCAACCCAGGCCTFACCACAGGCTGCCA 442

Search completed: February 23, 2003, 07:53:15  
Job time : 127.15 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 22:19:04 ; Search time 3575.79 Seconds  
(without alignments)  
12740.746 Million cell updates/sec

Title: US-09-750-240-3

Perfect score: 1812

Sequence: 1 gttacaagtgtgctgggcat.....gcagcttctcagggtgttc 1812

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Pending\_Patents\_NA\_Main:\*
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  - 2: /cgn2\_6/ptodata/1/pna/US06\_COMB.seq:\*
  - 3: /cgn2\_6/ptodata/1/pna/US07\_COMB.seq:\*
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  - 5: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq:\*
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  - 30: /cgn2\_6/ptodata/1/pna/US097C\_COMB.seq:\*
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  - 33: /cgn2\_6/ptodata/1/pna/US098C\_COMB.seq:\*
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  - 36: /cgn2\_6/ptodata/1/pna/US099C\_COMB.seq:\*
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  - 38: /cgn2\_6/ptodata/1/pna/US100A\_COMB.seq:\*
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  - 40: /cgn2\_6/ptodata/1/pna/US101A\_COMB.seq:\*
  - 41: /cgn2\_6/ptodata/1/pna/US101B\_COMB.seq:\*
  - 42: /cgn2\_6/ptodata/1/pna/US102A\_COMB.seq:\*
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- 44: /cgn2\_6/ptodata/1/pna/US6000\_COMB.seq:\*
- 45: /cgn2\_6/ptodata/1/pna/US6001\_COMB.seq:\*
- 46: /cgn2\_6/ptodata/1/pna/US6002\_COMB.seq:\*
- 47: /cgn2\_6/ptodata/1/pna/US6003\_COMB.seq:\*
- 48: /cgn2\_6/ptodata/1/pna/US6004\_COMB.seq:\*
- 49: /cgn2\_6/ptodata/1/pna/US6005\_COMB.seq:\*
- 50: /cgn2\_6/ptodata/1/pna/US6006\_COMB.seq:\*
- 51: /cgn2\_6/ptodata/1/pna/US6007\_COMB.seq:\*
- 52: /cgn2\_6/ptodata/1/pna/US6008\_COMB.seq:\*
- 53: /cgn2\_6/ptodata/1/pna/US6009\_COMB.seq:\*
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- 55: /cgn2\_6/ptodata/1/pna/US6011\_COMB.seq:\*
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- 58: /cgn2\_6/ptodata/1/pna/US6014\_COMB.seq:\*
- 59: /cgn2\_6/ptodata/1/pna/US6015\_COMB.seq:\*
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- 62: /cgn2\_6/ptodata/1/pna/US6018\_COMB.seq:\*
- 63: /cgn2\_6/ptodata/1/pna/US6019\_COMB.seq:\*
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- 66: /cgn2\_6/ptodata/1/pna/US6022\_COMB.seq:\*
- 67: /cgn2\_6/ptodata/1/pna/US6023\_COMB.seq:\*
- 68: /cgn2\_6/ptodata/1/pna/US6024\_COMB.seq:\*
- 69: /cgn2\_6/ptodata/1/pna/US6025\_COMB.seq:\*
- 70: /cgn2\_6/ptodata/1/pna/US6026\_COMB.seq:\*
- 71: /cgn2\_6/ptodata/1/pna/US6027\_COMB.seq:\*
- 72: /cgn2\_6/ptodata/1/pna/US6028\_COMB.seq:\*
- 73: /cgn2\_6/ptodata/1/pna/US6029\_COMB.seq:\*
- 74: /cgn2\_6/ptodata/1/pna/US6030\_COMB.seq:\*
- 75: /cgn2\_6/ptodata/1/pna/US6031\_COMB.seq:\*
- 76: /cgn2\_6/ptodata/1/pna/US6032\_COMB.seq:\*
- 77: /cgn2\_6/ptodata/1/pna/US6033\_COMB.seq:\*
- 78: /cgn2\_6/ptodata/1/pna/US6034\_COMB.seq:\*
- 79: /cgn2\_6/ptodata/1/pna/US6035\_COMB.seq:\*
- 80: /cgn2\_6/ptodata/1/pna/US6036\_COMB.seq:\*
- 81: /cgn2\_6/ptodata/1/pna/US6037\_COMB.seq:\*
- 82: /cgn2\_6/ptodata/1/pna/US6038\_COMB.seq:\*
- 83: /cgn2\_6/ptodata/1/pna/US6039\_COMB.seq:\*
- 84: /cgn2\_6/ptodata/1/pna/US6040\_COMB.seq:\*
- 85: /cgn2\_6/ptodata/1/pna/US6041\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1812	100.0	1812	18	US-09-472-667-3	Sequence 3, Appli
2	1812	100.0	1812	29	US-09-750-240-3	Sequence 3, Appli
3	1808.4	99.8	3549	18	US-09-472-667-5	Sequence 5, Appli
4	1808.4	99.8	3549	29	US-09-750-240-5	Sequence 10, Appli
5	1763.4	97.3	3552	18	US-09-472-667-10	Sequence 10, Appli
6	1763.4	97.3	3552	29	US-09-750-240-10	Sequence 10, Appli
7	1763	97.3	3356	68	US-60-245-228-549	Sequence 549, App
8	1763	97.3	3706	68	US-60-248-592-183	Sequence 183, App
9	1763	97.3	4942	42	US-10-201-000-1	Sequence 1, Appli
10	1657.8	91.5	3582	29	US-09-750-240-12	Sequence 12, Appli
11	1599.6	87.7	5353	18	US-09-491-404-837	Sequence 837, App
12	1599.6	87.7	5353	34	US-09-922-279-837	Sequence 837, App
13	1599.6	87.7	5353	34	US-09-922-279A-837	Sequence 837, App
14	1454.2	80.3	5826	80	US-60-360-207-5921	Sequence 5921, Ap
15	1437.2	79.3	4131	9	US-08-538-815-11	Sequence 11, Appli
16	895	49.4	4523	41	US-10-175-158-1	Sequence 1, Appli
17	886.6	48.9	3969	3	US-07-751-460-1	Sequence 1, Appli
18	886.6	48.9	4356	3	US-07-899-058-1	Sequence 1, Appli
19	886.2	47.4	3924	9	US-08-538-815-9	Sequence 9, Appli
20	829.8	45.8	4349	80	US-60-360-207-19529	Sequence 19529, A
21	799	44.1	3137	66	US-60-223-545-2	Sequence 2, Appli



Db	1021	CTGGCGCCAGCCAGAAACGGAAGAGAGAAAGCATCTGGCCAAAGCTGCACGGACT	1080
Qy	1081	CGGGCCAACTCCATGGAAGGCTGATGCGCGATGGGTTCCTGATCGTGCTTCTCCCGG	1140
Db	1081	CGGGCCAACTCCATGGAAGGCTGATGCGCGATGGGTTCCTGATCGTGCTTCTCCCGG	1140
Qy	1141	ACCAAGACTTCCAAGGCCCTCCGCCAGATGGGCATGTGATTCACGACAAGACAACCGG	1200
Db	1141	ACCAAGACTTCCAAGGCCCTCCGCCAGATGGGCATGTGATTCACGACAAGACAACCGG	1200
Qy	1201	GGCACCCAGATGCCCTGAACCCCTGAGATGAGGTGGATGAGTTCCTGAGCCGTGCCATC	1260
Db	1201	GGCACCCAGATGCCCTGAACCCCTGAGATGAGGTGGATGAGTTCCTGAGCCGTGCCATC	1260
Qy	1261	GATGCCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCGCCGTTTTGCTCACCTTC	1320
Db	1261	GATGCCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCGCCGTTTTGCTCACCTTC	1320
Qy	1321	CAGAGAGAGATTTTGAGAAGAAGTACTCCCGGAAGTGGATCCCGCTTCGGAGCCATC	1380
Db	1321	CAGAGAGAGATTTTGAGAAGAAGTACTCCCGGAAGTGGATCCCGCTTCGGAGCCATC	1380
Qy	1381	GTTGCCCTGTGCCCTGPTGGTCTTCTGCTTCACTGCTTCATCCAGCTTCTAATTTTCCCA	1440
Db	1381	GTTGCCCTGTGCCCTGPTGGTCTTCTGCTTCACTGCTTCATCCAGCTTCTAATTTTCCCA	1440
Qy	1441	CACCTCCACCCGTGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTAATCACCGTG	1500
Db	1441	CACCTCCACCCGTGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTAATCACCGTG	1500
Qy	1501	CTGATCTGTGCTGTACTCCCTGCTGCTGCTGCTGCTTCCCTAAGGCCCTGCAACGCTGTCC	1560
Db	1501	CTGATCTGTGCTGTACTCCCTGCTGCTGCTGCTGCTTCCCTAAGGCCCTGCAACGCTGTCC	1560
Qy	1561	CGCAGCATTTGTCGCTACGGGCACATAGCACCCAGTTGGCATCTTTTCGTCCTGCTT	1620
Db	1561	CGCAGCATTTGTCGCTACGGGCACATAGCACCCAGTTGGCATCTTTTCGTCCTGCTT	1620
Qy	1621	GTGTTTACTTCTGCCATTCGCCAATGTTTCACTGTACACACACCCCGCATACGGAGCTGT	1680
Db	1621	GTGTTTACTTCTGCCATTCGCCAATGTTTCACTGTACACACACCCCGCATACGGAGCTGT	1680
Qy	1681	GCAGCCGGATGCTGAATTTAAACCTGCTGACATCACTGCTGCCACCTGCGACAGCTC	1740
Db	1681	GCAGCCGGATGCTGAATTTAAACCTGCTGACATCACTGCTGCCACCTGCGACAGCTC	1740
Qy	1741	AATTACTCTGTGGCCTGGATGCTCCCTGTGTGAGGGCACCATGCCACCTGCAGCTTT	1800
Db	1741	AATTACTCTGTGGCCTGGATGCTCCCTGTGTGAGGGCACCATGCCACCTGCAGCTTT	1800
Qy	1801	CCTGAGGTGTC 1812	
Db	1801	CCTGAGGTGTC 1812	

## RESULT 2

US-09-750-240-3

00 03 750 240 3  
; Sequence 3, Application US/09750240

; GENERAL INFORMATION:

APPLICANT: HAMMON, H. K.

APPLICANT: Insel, P. A.

; APPLICANT: ping, p.

; APPLICANT: Post, S. R.

APPLICANT: Gao, M.

; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART

; TITLE OF INVENTION: FAILURE

FILE REFERENCE: 220002056723

; CURRENT APPLICATION NUMBER: US/09/750,240

; CURRENT FILING DATE: 2001-10-12

;; PRIOR APPLICATION NUMBER: US 09/472,667

;; PRIOR FILING DATE: 1999-12-27

; PRIOR APPLICATION NUMBER: US 09/008,097

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, PRIOR FILING DATE: 1998-01-16
, PRIOR APPLICATION NUMBER: US 08/924,757
, PRIOR FILING DATE: 1997-09-05
, PRIOR APPLICATION NUMBER: US 60/048,933
, PRIOR FILING DATE: 1997-08-16
, PRIOR APPLICATION NUMBER: US 08/708,661
, PRIOR FILING DATE: 1996-09-05
, NUMBER OF SEQ ID NOS: 13
, SOFTWARE: fastseq for Windows Version 4.0
, SEQ ID NO 3
, LENGTH: 1812
, TYPE: DNA
, ORGANISM: Homo sapiens
US-09-750-240-3

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Query Match 100.0%; Score 1812; DB 29; Length 1812;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1812; Conservative 0; Mismatches 0; Indels 0;

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Qy	61	CCGCGCAGCCCTCTCTGGGGCCCTCTGGTGGCCCTGTCTTCTTATACATCCGATACACG	120
Db	61	CCGCGCAGCCCTCTCTGGGGCCCTCTGGTGGCCCTGTCTTCTTATACATCCGATACACG	120
Qy	121	CTCTTCCCCATCCGCATCGCGGGTGGCGTCTCAGCGGCCCTGGGCCCTCTCCACCTTTGCAT	180
Db	121	CTCTTCCCCATCCGCATCGCGGGTGGCGTCTCAGCGGCCCTGGGCCCTCTCCACCTTTGCAT	180
Qy	181	TTGATCTTGGCTGGCGAACCTTAACCGTGTGATGCTTCTCTGGGAAGCAGCTCGGTGCC	240
Db	181	TTGATCTTGGCTGGCGAACCTTAACCGTGTGATGCTTCTCTGGGAAGCAGCTCGGTGCC	240
Qy	241	AATGTGCTGCTGTCTCTGCAACAAGTCAATTAGCATCTGCACACATATCCAGCAGAG	300
Db	241	AATGTGCTGCTGTCTCTGCAACAAGTCAATTAGCATCTGCACACATATCCAGCAGAG	300
Qy	301	GTGTCTCAGCGCCAGGCCCTTTTCAGGAGACCCGAGTTTACATCCAGGCCCGGGCTCCACCTG	360
Db	301	GTGTCTCAGCGCCAGGCCCTTTTCAGGAGACCCGAGTTTACATCCAGGCCCGGGCTCCACCTG	360
Qy	361	CAGCATCAGAAATCGGCGACGAGGCGCTGCTGTCTGGTATTGCCCGACGAGTTGGC	420
Db	361	CAGCATCAGAAATCGGCGACGAGGCGCTGCTGTCTGGTATTGCCCGACGAGTTGGC	420
Qy	421	ATGGAGATGAAGAAGACATCAACACAAAAAAGAGACATGTTCCACAAGATCTACATA	480
Db	421	ATGGAGATGAAGAAGACATCAACACAAAAAAGAGACATGTTCCACAAGATCTACATA	480
Qy	481	CAGAAGCATGACAAATGTTCAGCATCTCTTTTCGACAGCATTTGAGGGCTTCACGACCTGGCA	540
Db	481	CAGAAGCATGACAAATGTTCAGCATCTCTTTTCGACAGCATTTGAGGGCTTCACGACCTGGCA	540
Qy	541	TCCAGTGTGCACTGGCGAGGAGCTGGTCATGACCCCTGAATGAGCTCTTTGCCCGGGTTGAC	600
Db	541	TCCAGTGTGCACTGGCGAGGAGCTGGTCATGACCCCTGAATGAGCTCTTTGCCCGGGTTGAC	600
Qy	601	AAGCTGGCTCGGAGAAATCACTGCTCAGGATCAAGATCTTGGGGACTGTTACTACTGT	660
Db	601	AAGCTGGCTCGGAGAAATCACTGCTCAGGATCAAGATCTTGGGGACTGTTACTACTGT	660
Qy	661	GTTCAGGGCTTGGCGGAGGCCCGGCGACCATGCCACCTGCTGTGTGGAGATGGGGGTA	720
Db	661	GTTCAGGGCTTGGCGGAGGCCCGGCGACCATGCCACCTGCTGTGTGGAGATGGGGGTA	720
Qy	721	GACATGATTTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATCGCG	780
Db	721	GACATGATTTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATCGCG	780
Qy	781	GTGGGCATCCACAGCGGCGCTGCACTGCGGGCTCTTGGCTTGGGAAATGGCAGTTTC	840
Db	781	GTGGGCATCCACAGCGGCGCTGCACTGCGGGCTCTTGGCTTGGGAAATGGCAGTTTC	840

Db 781 GTGGGATCCACAGCGGGCGGTGCACACTGCGGCGTCTTGGCTTGGGAAATGCGAGTTC 840  
QY 841 GATGTGTGGTCCCAATGATGTGACCCCTGGCCAAACCATGGAAGCAGGAAGCCGGGTGGC 900  
Db 841 GATGTGTGGTCCCAATGATGTGACCCCTGGCCAAACCATGGAAGCAGGAAGCCGGGTGGC 900  
QY 901 CGCATCCACATCACTCGGGCAACACTGCAGTACCTGAAACGGGACTACGAAGTGGAGCCA 960  
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QY 1021 CTGGGCGCCAGCAGAAACGGAAGAGGAGGAAAGGATGCTGCGCAAGCTGCGAGCGGACT 1080  
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QY 1081 CGGGCCAACCTCCATGAAAGGGCTGATGCCCGGATGGTTCTCTGATGCTGCTTCTCCCGG 1140  
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QY 1141 ACCAAGGACTCCAGGCTTCCCGCAGATGGGCAATTTGATGATTTCCAGCAAGACACCGG 1200  
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QY 1261 GATGCCCGCAGCATTTGATCAGCTGCGGAAGACCATGTGCGCGGGTTTTTGTCTCACTTC 1320  
Db 1261 GATGCCCGCAGCATTTGATCAGCTGCGGAAGACCATGTGCGCGGGTTTTTGTCTCACTTC 1320  
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QY 1381 GTTGCTGTGCCCTGTGTGCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTCCCA 1440  
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QY 1501 CTGATCTGTGCTGTACTCTGCTGCTTCTGCTTCCCTTAAGCCCTGCAACGCTCTGTCC 1560  
Db 1501 CTGATCTGTGCTGTACTCTGCTGCTTCTGCTTCCCTTAAGCCCTGCAACGCTCTGTCC 1560  
QY 1561 CGCAGATTGTCCGCTCAGGGCAGCATAGCAGCGAGTTGGCATCTTTTCCGTCCTGCTT 1620  
Db 1561 CGCAGATTGTCCGCTCAGGGCAGCATAGCAGCGAGTTGGCATCTTTTCCGTCCTGCTT 1620  
QY 1621 GTGTTTACTTCTGCCATTTGCCAATGTTTCACTGTAAACACACACCCCATACGGAGCTGT 1680  
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QY 1681 GCAGCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCGCAGCTGCGAGAGCTC 1740  
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QY 1741 AATTACTTCTGTGGCCTGGATGCTCCCTGTGTGAGGGGACCAATGCCCCACCTGCAGCTTT 1800  
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RESULT 3  
US-09-472-667-5

; Sequence 5, Application US/09472667  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. Kirk  
; APPLICANT: Insel, Paul A.  
; APPLICANT: Ping, Peipei  
; APPLICANT: Post, Steven R.  
; APPLICANT: Gao, Meihua  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
; TITLE OF INVENTION: FAILURE  
; FILE REFERENCE: 220002056722  
; CURRENT APPLICATION NUMBER: US/09/472,667  
; CURRENT FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: PCT/US99/02702  
; PRIOR FILING DATE: 1999-02-09  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 09/021,773  
; PRIOR FILING DATE: 1998-02-11  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: PCT/US97/15610  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/058,209  
; PRIOR FILING DATE: 1996-09-05  
; PRIOR APPLICATION NUMBER: PCT/US96/02631  
; PRIOR FILING DATE: 1996-02-27  
; PRIOR APPLICATION NUMBER: US 08/396,207  
; PRIOR FILING DATE: 1995-02-28  
; PRIOR APPLICATION NUMBER: US 08/485,472  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 3549  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-472-667-5

Query Match 99.8%; Score 1808.4; DB 18; Length 3549;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 636 TAACGTGGTCTGGGCATCTGGCGCAGTGCAGGTGCGGGCGCTTTCGCACGACAGCC 695  
QY 63 GCGCAGCCCTCTGCGGGCTCTGCGTCCCTGTTTGTATACATCGCATACAGCT 122  
Db 696 GCGCAGCCCTCTGCGGGCTCTGCGTCCCTGTTTGTATACATCGCATACAGCT 755  
QY 123 CTTCCCATCCGATCGGGCTCCCTGCTCAGCGGCTGGGCTCTTCCACCTTGCAATTT 182  
Db 756 CTTCCCATCCGATCGGGCTCCCTGCTCAGCGGCTGGGCTCTTCCACCTTGCAATTT 815  
QY 183 GATCTTTGGCTGCACTTAACCGTGGTATGCTTCTCTCGAAGCAGCTCGGTGCCAA 242  
Db 816 GATCTTTGGCTGCACTTAACCGTGGTATGCTTCTCTCGAAGCAGCTCGGTGCCAA 875  
QY 243 TGTGCTGCTGTTCTCTGCAACCAACGTCATTAGCATCTGCACACACTATCCAGCAGAGT 302  
Db 876 TGTGCTGCTGTTCTCTGCAACCAACGTCATTAGCATCTGCACACACTATCCAGCAGAGT 935  
QY 303 GTCTCAGCCAGCGCTTTTCAGGAGACCGCAGTTTACATCCAGGCCGGCTCCACCTGCA 362  
Db 936 GTCTCAGCCAGCGCTTTTCAGGAGACCGCAGTTTACATCCAGGCCGGCTCCACCTGCA 995  
QY 363 GCATGAGATCGCAGCAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422  
Db 996 GCATGAGATCGCAGCAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1055

Qy 423 GGAGATGAAGAAGACATCAACAAAAAAGAGACATGTTCCACAAGATCTACATACA 482  
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Qy 483 GAAGATGACAAATGTACGATCCTGTGTTTGAGACATTTGAGGGCTTCACCAAGCTGGCATC 542  
Db 1116 GAAGATGACAAATGTACGATCCTGTGTTTGAGACATTTGAGGGCTTCACCAAGCTGGCATC 1175  
Qy 543 CCAGTGCCTCGGAGAGCTGGTCATGACCTGAATGAGCTCTTTGCCCGGTTTGACAA 602  
Db 1176 CCAGTGCCTCGGAGAGCTGGTCATGACCTGAATGAGCTCTTTGCCCGGTTTGACAA 1235  
Qy 603 GCTGGCTCGGAGAAATCACTGCTGAGGATCAAGATCTTTGGGGACTGTTACTACTGTGT 662  
Db 1236 GCTGGCTCGGAGAAATCACTGCTGAGGATCAAGATCTTTGGGGACTGTTACTACTGTGT 1295  
Qy 663 GTCAGGGCTCGGAGAGCCCGGGCGGACCATGCCACHTGCTGTGGAGATGGGGGTAGA 722  
Db 1296 GTCAGGGCTCGGAGAGCCCGGGCGGACCATGCCACHTGCTGTGGAGATGGGGGTAGA 1355  
Qy 723 CATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTAATGTGAACATGCGCGT 782  
Db 1356 CATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTAATGTGAACATGCGCGT 1415  
Qy 783 GGGCATCCACAGCGGGCGGTGCATCGCGGTCTCTTGGCTTGGGAAATGGCAGTTTCCA 842  
Db 1416 GGGCATCCACAGCGGGCGGTGCATCGCGGTCTCTTGGCTTGGGAAATGGCAGTTTCCA 1475  
Qy 843 TGTGTGTCCAAATGATGTACCTGTGGCCCAACACATGAAGACAGAACCGGGGTGGCG 902  
Db 1476 TGTGTGTCCAAATGATGTACCTGTGGCCCAACACATGAAGACAGAACCGGGGTGGCG 1535  
Qy 903 CATCCATCACTCGGCAACACACTGCAGTACCTGACGGGACTACGAAGTGGAGCCAGG 962  
Db 1536 CATCCATCACTCGGCAACACACTGCAGTACCTGACGGGACTACGAAGTGGAGCCAGG 1595  
Qy 963 CCGTGGTGGCAAGCGCAACCGGTACCTCAAGSAGCAGCACATTTCCCTCATCCT 1022  
Db 1596 CCGTGGTGGCAAGCGCAACCGGTACCTCAAGSAGCAGCACATTTCCCTCATCCT 1655  
Qy 1023 GGGGCCAGCAGAAACGGAAGAGGAAAGGATGCTGSCCAAGCTGCAGCGGACTCG 1082  
Db 1656 GGGGCCAGCAGAAACGGAAGAGGAAAGGATGCTGSCCAAGCTGCAGCGGACTCG 1715  
Qy 1083 GGCCAACCTCCATGGAAGGGCTGATGCCCGATGGGTTCCCTGATGCTGCTTCTCCCGAC 1142  
Db 1716 GGCCAACCTCCATGGAAGGGCTGATGCCCGATGGGTTCCCTGATGCTGCTTCTCCCGAC 1775  
Qy 1143 CAAGGACTCCAAAGGCTTCCGCCAGATGGGATTTGATGATTCAGCAAGACAAACCGGG 1202  
Db 1776 CAAGGACTCCAAAGGCTTCCGCCAGATGGGATTTGATGATTCAGCAAGACAAACCGGG 1835  
Qy 1203 CACCAAGATGCCCTGAACCTGAGGATGAGGTGATGATGCTGAGCCGTGCCATCGA 1262  
Db 1836 CACCAAGATGCCCTGAACCTGAGGATGAGGTGATGATGCTGAGCCGTGCCATCGA 1895  
Qy 1263 TGCCCGCAGCATTTGATAGCTGCGGAAGGACCATGTCGCCCGGTTTTTGGCTCACCTTCCA 1322  
Db 1896 TGCCCGCAGCATTTGATAGCTGCGGAAGGACCATGTCGCCCGGTTTTTGGCTCACCTTCCA 1955  
Qy 1323 GAGAGAGGATTTGAGAAGAAGTACTCCCGAAGGTGGATCCCGCTTTCGGAGGCTTAGT 1382  
Db 1956 GAGAGAGGATTTGAGAAGAAGTACTCCCGAAGGTGGATCCCGCTTTCGGAGGCTTAGT 2015  
Qy 1383 TGCGTGTGCCCTGTGGTCTTCTGCTTCATGCTGCTCATTCAGCTTCAATTTTCCACACA 1442  
Db 2016 TGCGTGTGCCCTGTGGTCTTCTGCTTCATGCTGCTTCATCCAGCTTCAATTTTCCACACA 2075  
Qy 1443 CTCACCCCTGATGCTGGGATTTATGCCAGCATCTTCTGCTGCTTCAATCAGCGTCT 1502  
Db 2076 CTCACCCCTGATGCTGGGATTTATGCCAGCATCTTCTGCTGCTTCAATCAGCGTCT 2135

Qy 1503 GATCTGTCTGTGTACTCTCTGTGGTTCTCTGTTCCTAAGGCCCTGCAACGCTCTGTCCCG 1562  
Db 2136 GATCTGTCTGTGTACTCTCTGTGGTTCTCTGTTCCTAAGGCCCTGCAACGCTGTCCCG 2195  
Qy 1563 CAGCAATTCCTCGCTCACGGGCACATAGACCGCAGTTGGCATCTTTTCCGTCCTGCTTGT 1622  
Db 2196 CAGCAATTCCTCGCTCACGGGCACATAGACCGCAGTTGGCATCTTTTCCGTCCTGCTTGT 2255  
Qy 1623 GTTACTTCTGCATTGCTCAACATGTTCCACCTGTAAACACACCCCCATACGGAGCTGTGC 1682  
Db 2256 GTTACTTCTGCATTGCTCAACATGTTCCACCTGTAAACACACCCCCATACGGAGCTGTGC 2315  
Qy 1683 AGCCCGGATGCTGAATTTAAACACCTGCTGACATCACTGCTGCCACCTGCAGCAGTCAA 1742  
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Qy 1743 TTACTCTCTGGCCTGGATGCTCCCTGTGTGAGGGCACCACCTGCAGCTTTC 1802  
Db 2376 TTACTCTCTGGCCTGGATGCTCCCTGTGTGAGGGCACCACCTGCAGCTTTC 2435  
Qy 1803 TGAGGTGTTCC 1812  
Db 2436 TGAGGTGTTCC 2445

RESULT 4  
US-09-750-240-5  
; Sequence 5, Application US/09750240  
; GENERAL INFORMATION:  
; APPLICANT: Hammon, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
; FILE OF INVENTION: FAILURE  
; FILE REFERENCE: 220002056723  
; CURRENT APPLICATION NUMBER: US/09/750.240  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/472,667  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 3549  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-750-240-5

Query Match 99.8%; Score 1808.4; DB 29; Length 3549;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TAACGTGGTGTCTGGGCATCTCTGGCGCAGTGCAGGTTCGGGGCGCTTTTCGCAGCAGACCC 62  
Db 636 TAACGTGGTGTCTGGGCATCTCTGGCGCAGTGCAGGTTCGGGGCGCTTTTCGCAGCAGACCC 695  
Qy 63 GGGCAGCCCCCTCGCGGGCTCTGTGGCCCTGTGTCTTTGTATACATGCATACACGCT 122  
Db 696 GGGCAGCCCCCTCGCGGGCTCTGTGGCCCTGTGTCTTTGTATACATGCATACACGCT 755  
Qy 123 CCTCCCCATCCGCATCGCGGGCTGCTCTCAGCGGCCCTGGGCCCTTCCACCTTGCATTT 182  
Db 756 CCTCCCCATCCGCATCGCGGGCTGCTCTCAGCGGCCCTGGGCCCTTCCACCTTGCATTT 815

QY 183 GATCTTGGCGCTGCAACTTAAACCGTGGTGATGCTTCTCTGGAAGCAGCTCGTGCCAA 242  
DB 816 GATCTTGGCGCTGCAACTTAAACCGTGGTGATGCTTCTCTGGAAGCAGCTCGTGCCAA 875  
QY 243 TGTGCTGCTGCTCTCTGCAACAGCTCATAGCATCTGCACACACTATCCAGCAGAGT 302  
DB 876 TGTGCTGCTGCTCTCTGCAACAGCTCATAGCATCTGCACACACTATCCAGCAGAGT 935  
QY 303 GTCTCAGCGCCAGCGCTTTCAGGAGAGCCCGCAGTTACATCCAGCCCGGCTCCACCTGCA 362  
DB 936 GTCTCAGCGCCAGCGCTTTCAGGAGAGCCCGCAGTTACATCCAGCCCGGCTCCACCTGCA 995  
QY 363 GCATGAGAATCGCAGCAGAGCGGCTGCTGCTGCTGGTATTCGCCAGCAGCTTGCCAT 422  
DB 996 GCATGAGAATCGCAGCAGAGCGGCTGCTGCTGCTGGTATTCGCCAGCAGCTTGCCAT 1055  
QY 423 GGAGATGAAGAAGACATCAACACAAAAAAGAGACATCTCCACAAGATCTACATACA 482  
DB 1056 GGAGATGAAGAAGACATCAACACAAAAAAGAGACATCTCCACAAGATCTACATACA 1115  
QY 483 GAAGCATGACAATGTCAGCATCTCTGTTGTCAGACATTTAGGGGCTTCACCAAGCCTGGCATC 542  
DB 1116 GAAGCATGACAATGTCAGCATCTCTGTTGTCAGACATTTAGGGGCTTCACCAAGCCTGGCATC 1175  
QY 543 CCAGTGACTGCGCAGAGAGCTGTGATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAA 602  
DB 1176 CCAGTGACTGCGCAGAGAGCTGTGATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAA 1235  
QY 603 GCTGGCTGCGGAGAACTACCTGCTGAGGATCAAGATCTTGGGGGACTGTACTACTGTGT 662  
DB 1236 GCTGGCTGCGGAGAACTACCTGCTGAGGATCAAGATCTTGGGGGACTGTACTACTGTGT 1295  
QY 663 GTCAGGGCTGCCGAGGCGCGGCGCACCATGCCCCACTGCTGTGTGAGATGGGGTAGA 722  
DB 1296 GTCAGGGCTGCCGAGGCGCGGCGCACCATGCCCCACTGCTGTGTGAGATGGGGTAGA 1355  
QY 723 CATGATTGAGGCCATCTCGCTGTGTAGTGTGAGGTGACAGGTGTGAATGTGAACATGCGCGT 782  
DB 1356 CATGATTGAGGCCATCTCGCTGTGTAGTGTGAGGTGACAGGTGTGAATGTGAACATGCGCGT 1415  
QY 783 GGGCATCCACAGCGGCGCTGCTGCTGCGGCTCTTGGCTTGGGAATGGCAGTTGCA 842  
DB 1416 GGGCATCCACAGCGGCGCTGCTGCTGCGGCTCTTGGCTTGGGAATGGCAGTTGCA 1475  
QY 843 TGTGTGCTCAATGATGTACCTTGGCCAAACCATGGAAGCAGGAGCGGCTGGCGG 902  
DB 1476 TGTGTGCTCAATGATGTACCTTGGCCAAACCATGGAAGCAGGAGCGGCTGGCGG 1535  
QY 903 CATCCACATCCTCGGCGACACTGCACTGACCTGACGGGGACTACGAAGTGAGCGAGG 962  
DB 1536 CATCCACATCCTCGGCGACACTGCACTGACCTGACGGGGACTACGAAGTGAGCGAGG 1595  
QY 963 CCGTGTGGCAAGCGCAACGCTACCTAAGGAGCAGCAGCATTTGCTCTCATCCT 1022  
DB 1596 CCGTGTGGCAAGCGCAACGCTACCTAAGGAGCAGCAGCATTTGCTCTCATCCT 1655  
QY 1023 GGGCGCCAGCCAGAAACGGAAAGAGGAGAAAGCATGCTGGCCAAAGCTGCAGCGGACTCG 1082  
DB 1656 GGGCGCCAGCCAGAAACGGAAAGAGGAGAAAGCATGCTGGCCAAAGCTGCAGCGGACTCG 1715  
QY 1083 GGGCAACTCATGAGAGGCTGATGCGCGCATGGTTCCTGATGCTGCTCCCGGAC 1142  
DB 1716 GGGCAACTCATGAGAGGCTGATGCGCGCATGGTTCCTGATGCTGCTCCCGGAC 1775  
QY 1143 CAAGGACTCCAAGCGCTTCGCCAGATGGCATTGATTCAGCAAGAACACCGGG 1202  
DB 1776 CAAGGACTCCAAGCGCTTCGCCAGATGGCATTGATTCAGCAAGAACACCGGG 1835  
QY 1203 CACCCAGATGCCCTGAACCCCTGAGGATGAGGTGAGTTCCTGAGCGGTGCCATCGA 1262  
DB 1836 CACCCAGATGCCCTGAACCCCTGAGGATGAGGTGAGTTCCTGAGCGGTGCCATCGA 1895  
QY 1263 TGCCCGCAGCATTGATCAGCTGCGGAGGACCATGTGCGCGCGGTTTTTGTCTACCTTCCA 1322

DB 1896 TGCCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCGCGGTTTTTGTCTACCTTTCCA 1955  
QY 1323 GAGAGAGGATTTTCAGAAGAAGTACTCCCGGAAGGTGGATCCCGGCTTCGGAGCCTACGT 1382  
DB 1956 GAGAGAGGATTTTCAGAAGAAGTACTCCCGGAAGGTGGATCCCGGCTTCGGAGCCTACGT 2015  
QY 1383 TGCTGTGCCCTGTGTGCTTCTCTCTCATCTGCTTCATCAGCTTCTAATTTTCCACACA 1442  
DB 2016 TGCTGTGCCCTGTGTGCTTCTCTCTCTCATCTGCTTCATCAGCTTCTAATTTTCCACACA 2075  
QY 1443 CTCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCTCTGCTGCTGCTAATCAGCTGCT 1502  
DB 2076 CTCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCTCTGCTGCTGCTAATCAGCTGCT 2135  
QY 1503 GATCTGTGCTGTACT 1562  
DB 2136 GATCTGTGCTGTACT 2195  
QY 1563 CAGCATTTGCTCGCTCAGGGCAGACATAGCAGCTTGGCATCTTTTCCGCTCTGCTTGT 1622  
DB 2196 CAGCATTTGCTCGCTCAGGGCAGACATAGCAGCTTGGCATCTTTTCCGCTCTGCTTGT 2255  
QY 1623 GTTACTTCTGCAATTTTAAACCTGCTGACATCTGCTGACCTGTAAACCAACCCCATAGGAGCTGTGC 1682  
DB 2256 GTTACTTCTGCAATTTTAAACCTGCTGACATCTGCTGACCTGTAAACCAACCCCATAGGAGCTGTGC 2315  
QY 1683 AGCCCGGATGCTCAATTTTAAACCTGCTGACATCTGCTGACCTGTAAACCAACCCCATAGGAGCTGTGC 1742  
DB 2316 AGCCCGGATGCTCAATTTTAAACCTGCTGACATCTGCTGACCTGTAAACCAACCCCATAGGAGCTGTGC 2375  
QY 1743 TTACTCTCTGGGCTGGATGCTCTCTCTGCTGAGGGCAGCATGCCACCTGCGAGCTTTTC 1802  
DB 2376 TTACTCTCTGGGCTGGATGCTCTCTCTGCTGAGGGCAGCATGCCACCTGCGAGCTTTTC 2435  
QY 1803 TGAGGTGTTTC 1812  
DB 2436 TGAGGTGTTTC 2445

## RESULT 5

US-09-472-667-10  
; Sequence 10, Application US/09472667  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. Kirk  
; APPLICANT: Insel, Paul A.  
; APPLICANT: Ping, Peipei  
; APPLICANT: Post, Steven R.  
; APPLICANT: Gao, Melhua  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
; FILE REFERENCE: 22002056722  
; CURRENT APPLICATION NUMBER: US/09/472, 667  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: PCT/US99/02702  
; PRIOR FILING DATE: 1999-02-09  
; PRIOR APPLICATION NUMBER: US 09/008, 097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 09/021, 773  
; PRIOR FILING DATE: 1998-02-11  
; PRIOR APPLICATION NUMBER: US 08/924, 757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: PCT/US97/15610  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 08/708, 661  
; PRIOR FILING DATE: 1996-09-05  
; PRIOR APPLICATION NUMBER: US 60/048, 933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/058, 209  
; PRIOR FILING DATE: 1996-09-05  
; PRIOR APPLICATION NUMBER: PCT/US96/02631  
; PRIOR FILING DATE: 1996-02-27  
; PRIOR APPLICATION NUMBER: US 08/396, 207



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; PRIOR FILING DATE: 1995-02-28
; PRIOR APPLICATION NUMBER: US 08/485,472
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 3552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-472-667-10

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Query Match 97.3%; Score 1763.4; DB 18; Length 3552;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 1789; Conservative 0; Mismatches 21; Indels 3; Gaps 1;

QY	3	TACGCTGGTCTGGGGATCCTTGGCGGCAGTGCAGGTGGGGGCGCTTTGCGAGCAGACCC	62
Db	636	TTACGTGTGTCTGGGCATCCTTGGCGGCAGTGCAGGTGGGGGCGCTCTCGACGACAGACCC	695
QY	63	GCSCAGCCCTCTGGGGGCTCTGTGTGCCCTGTGTCTTTGTATATACATCGCATACACGCT	122
Db	696	GGCAGCCCTCTGGGGGCTCTGTGTGCCCTGTGTCTTTGTCTACATCGCTTACAGCT	755
QY	123	CTTCCCATCCGCATCGGGGCTGCGCTCTCAGGGGCTGGGCGCTCTCCACCTTGCATTT	182
Db	756	CTTCCCATCCGCATCGGGGCTGCGCTCTCAGGGGCTGGGCGCTCTCCACCTTGCATTT	815
QY	183	GATCTTGGGCTGGCAACTTAACCGTGTGTATGCCCTTCTCTGGAAGCAGCTCGGTGCCAA	242
Db	816	GATCTTGGGCTGGCAACTTAACCGTGTGTATGCCCTTCTCTGGAAGCAGCTCGGTGCCAA	875
QY	243	TGTGCTGTGTCTCTGCAACAGCTCATTAGCATCTGCACACACTATCCAGCAGAGGT	302
Db	876	TGTGCTGTGTCTCTGCAACAGCTCATTAGGCATCTGCACACACTATCCAGCAGAGGT	935
QY	303	GTCTCAGCGCCAGGCGCTTTCAGGAGACCCGCGAGTTACATCCAGGCCGCGCTCCACCTGCA	362
Db	936	GTCTCAGCGCCAGGCGCTTTCAGGAGACCCGCGGTTACATCCAGGCCGCGCTCCACCTGCA	995
QY	363	GCATGAGAAATCGGCAGCAGCGGCTGCTGCTGCGTATTGCCCGACACGTTGGCAT	422
Db	996	GCATGAGAAATCGGCAGCAGCGGCTGCTGCTGCGTATTGCCCGACACGTTGGCAT	1055
QY	423	GGAGATGAAGAGAGACATCAACACAAAAAGAAC --- ATGTTCCACAGATCTACAT	479
Db	1056	GGAGATGAAGAGAGACATCAACACAAAAAGAGACATGATGTTCCACAGATCTACAT	1115
QY	480	ACAGAGCATGACAATGTCAAGATCCTGTTTTCAGACATTTAGGGCTTCCAGCGCTGGC	539
Db	1116	ACAGAGCATGACAATGTCAAGATCCTGTTTTCAGACATTTAGGGCTTCCAGCGCTGGC	1175
QY	540	ATCCCAAGTGCATTCGCGAGGAGCTGGTCATGACCTGAATGAGCTCTTTGCCGCGTTTGA	599
Db	1176	ATCCCAAGTGCATTCGCGAGGAGCTGGTCATGACCTGAATGAGCTCTTTGCCGCGTTTGA	1235
QY	600	CAAGCTGGCTCGGAGAATCACTGCTGAGGATCAAGATCTTGGGGAGCTTTACTACTG	659
Db	1236	CAAGCTGGCTCGGAGAATCACTGCTGAGGATCAAGATCTTGGGGAGCTTTACTACTG	1295
QY	660	TGTGTAGGGCTCCGGAGCGCGGCGACCATCCCACTGCTGTGTGTGGAGATGGGGT	719
Db	1296	TGTGTAGGGCTCCGGAGCGCGGCGACCATCCCACTGCTGTGTGTGGAGATGGGGT	1355
QY	720	AGACATGATTGAGGCCATCTCGCTGGTACGTGAGTGCAGGTGTAATGTGAACATCG	779
Db	1356	AGACATGATTGAGGCCATCTCGCTGGTACGTGAGTGCAGGTGTAATGTGAACATCG	1415
QY	780	CGTGGGCATCCAGCGGGCGGTGCATTCGGCGCTCTTGGCTTGCAGAAATGGCAGTT	839
Db	1416	CGTGGGCATCCAGCGGGCGGTGCATTCGGCGCTCTTGGCTTGCAGAAATGGCAGTT	1475
QY	840	CGATGTGTGTCAAATGATGTACGCTTGCCCAACCAATTTGGAAGCAGGAACCGGCGCTGG	899

Db	1476	CGATGTGTGGTCCATATGATGTGACCCCTGGCCCAACACATATGAGGAGGAGGAGCCGGCGGTGG	1533
Qy	900	CCGCATCCACATCACCCTCGGGCAACACTGCAGTACCTGAACGGGAGACTACGAAGTGGAGCC	959
Db	1536	CCGCATCCACATCACCCTCGGGCAACACTGCAGTACCTGAACGGGAGACTACGAAGTGGAGCC	1595
Qy	960	AGGCGTGTGGCAAGCGCAACGGGTACCTCAAGGAGCAGCACATTTGAGACTTTCCTCAT	1019
Db	1596	AGGCGTGTGGCGAGCGCAACGGGTACCTCAAGGAGCAGCACATTTGAGACTTTCCTCAT	1655
Qy	1020	CTTGGGCGCCAGCCACAAACGGAAAGAGAGAAAGGCGATGCTGCCAAGCTGCACGCGAC	1079
Db	1656	CTTGGGCGCCAGCCACAAACGGAAAGAGAGAAAGGCGCATGCTGCCAAGCTGCACGCGAC	1715
Qy	1080	TCGGGGCAACTCCATGAAAGGGCTGATGCCGCGATGGGTTCCTGATCGTGCCTTCTCCCG	1139
Db	1716	TCGGGGCAACTCCATGAAAGGGCTGATGCCGCGCTGGGTTCCTGATCGTGCCTTCTCCCG	1775
Qy	1140	GACCAAGGACTCCAAGGCCCTTCGGCCAGATGGCAATGATATTCACGCAAGACAACCG	1199
Db	1776	GACCAAGGACTCCAAGGCCCTTCGGCCAGATGGCAATGATATTCACGCAAGACAACCG	1835
Qy	1200	GGGCACCACAGATGCCCTGAACCCCTGAGATCAGGTGGATGAGTTCCTGAGCCCGTGCAT	1259
Db	1836	GGGCACCACAGATGCCCTGAACCCCTGAGATCAGGTGGATGAGTTCCTGAGCCCGTGCAT	1895
Qy	1260	CGATGCCCGCAGATTTGATCAGCTCGGGAAGACCATTGCGCCGGTTTTTGGTCAACCTT	1319
Db	1896	CGATGCCCGCAGCATTTGATCAGCTCGGGAAGACCATTGCGCCGGTTTTTGGTCAACCTT	1955
Qy	1320	CCAGAGAGAGGATTTTGAGAAAGTACTTCCCGGAAGGTGGATCCCCCGCTTCGGAGCGTA	1379
Db	1956	CCAGAGAGAGGATTTTGAGAAAGTACTTCCCGGAAGGTGGATCCCCCGCTTCGGAGCGTA	2015
Qy	1380	CGTTGCTGTGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTCAATTTCCC	1439
Db	2016	CGTTGCTGTGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTCAATTTCCC	2075
Qy	1440	ACACTCCACCCGTGATGCTGGGATTTATGCCAGCATCTTCTGTGTGTGCTAAATACCGT	1499
Db	2076	ACACTCCACCCGTGATGCTGGGATTTATGCCAGCATCTTCTGTGTGTGCTAAATACCGT	2135
Qy	1500	GCTGATCTGTGTGCTGACTCCTGTGGTTCTCTGTTCCTTAGGCCCTGCACACCTGTGC	1559
Db	2136	GCTGATCTGTGTGCTGACTCCTGTGGTTCTCTGTTCCTTAGGCCCTGCACACCTGTGC	2195
Qy	1560	CCGCGAGATTTGCCGCTCACGGGCAATAGCACCCGAGTTGGCATCTTTCCGCTCCTGCT	1619
Db	2196	CCGCGAGATTTGCCGCTCACGGGCAATAGCACCCGAGTTGGCATCTTTCCGCTCCTGCT	2255
Qy	1620	TGTGTTTTACTTCTGGCATTTGCCAACATGTTACCTGTAAACACACCCCATACGAGGTG	1679
Db	2256	TGTGTTTTACTTCTGGCATTTGCCAACATGTTACCTGTAAACACACCCCATACGAGGTG	2315
Qy	1680	TGCAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCCACCTGCACGAGCT	1739
Db	2316	TGCAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCCACCTGCACGAGCT	2375
Qy	1740	CAATTACTCTCTGGGCTTGGATGCTCCCTGTGTGAGGGCAGCATGCCACCTGCAGGTT	1799
Db	2376	CAATTACTCTCTGGGCTTGGATGCTCCCTGTGTGAGGGCAGCATGCCACCTGCAGGTT	2435
Qy	1800	TCCGTGAGGTTTC 1812	
Db	2436	TCCTGAGTACTTC 2448	

RESULT 6  
US-09-750-240-10  
; Sequence 10. Application US/09750240  
; GENERAL INFORMATION:  
; APPLICANT: Hammon, H. K.  
; APPLICANT: Insel, P. A.



QY 1740 CAATTACTCTGGGCTGGATGCTCCCTGTGTGGGCGACCATGCCCACCTGCGAGCTT 1799  
|||||  
Db 2376 CAATTACTCTGGGCTGGATGCTCCCTGTGTGGGCGACCATGCCCACCTGCGAGCTT 2435  
|||||  
QY 1800 TCCTGAGTGTTTC 1812  
|||||  
Db 2436 TCCTGAGTACTTC 2448  
|||||  
RESULT 7  
US-60-245-228-549  
; Sequence 549, Application US/60245228  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL000878  
; CURRENT APPLICATION NUMBER: US/60/245,228  
; CURRENT FILING DATE: 2000-11-03  
; NUMBER OF SEQ ID NOS: 630  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 549  
; LENGTH: 3356  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-60-245-228-549  
Query Match 97.3%; Score 1763; DB 68; Length 3356;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 1788; Conservative 0; Mismatches 20; Indels 3; Gaps 1;  
QY 5 AGCTGGTGTCTGGGCTCTGGGCGGAGTGCAGGTGGGGGGCTTTTCGAGCAGACCCGC 64  
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Db 421 AGCTGGTGTGGGCTCTGGGCGGAGTGCAGGTGGGGGGCTCTCGCAGCAGACCCGC 480  
|||||  
QY 65 GCAGCCCTCTGGGGGCTCTGGTGGCTGTCTTTGTATATCATCATACAGCTCC 124  
|||||  
Db 481 GCAGCCCTCTGGGGGCTCTGGTGGCTGTCTTTGTATATCATCATACAGCTCC 540  
|||||  
QY 125 TCCCATCCGATGGGCTGGGCTCCAGGCTGGGCTGGGCTCTCCACCTTGCATTGA 184  
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Db 541 TCCCATCCGATGGGCTGGGCTCCAGGCTGGGCTGGGCTCTCCACCTTGCATTGA 600  
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QY 185 TCTGGCTTGGCACTTAACCGTGTGTATGCTTCTCTGGAAGCAGCTCGGTGCAATG 244  
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Db 601 TCTGGCTTGGCACTTAACCGTGTGTATGCTTCTCTGGAAGCAGCTCGGTGCAATG 660  
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QY 245 TGTGCTGTCTCTGACCAACGCTATAGCATCTGCACACATATCCAGCAGAGGTGT 304  
|||||  
Db 661 TGTGCTGTCTCTGACCAACGCTATAGCATCTGCACACATATCCAGCAGAGGTGT 720  
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QY 305 CTCAGGCGCAGGCTTTCAGGAGACCCGAGTTACATCCAGCCCGGCTCCACCTGCAGC 364  
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Db 721 CTCAGGCGCAGGCTTTCAGGAGACCCGAGTTACATCCAGCCCGGCTCCACCTGCAGC 780  
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QY 365 ATGAGAATCGGAGCAGGAGCGGCTGCTGCTCGGTATGTCGCCAGCAGCTTGCATGG 424  
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Db 781 ATGAGAATCGGAGCAGGAGCGGCTGCTGCTCGGTATGTCGCCAGCAGCTTGCATGG 840  
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QY 425 AGATGAAAGAAGACATCAACACAAAAAAGAGAC- - - ATGTTCCACAGATCTACATAC 481  
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Db 841 AGATGAAAGAAGACATCAACACAAAAAAGAGACATGATGTTCCACAGATCTACATAC 900  
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QY 482 AGAAGCATGACAAATGTCAGCATCTCTGTTTGCAGACATTTAGGGCTTCCAGCCTGGCAT 541  
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Db 901 AGAAGCATGACAAATGTCAGCATCTCTGTTTGCAGACATTTAGGGCTTCCAGCCTGGCAT 960  
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QY 542 CCCAGTGCACTCGCAGGAGCTGGTCAATGACCTTCAATGAGCTCTTTCGCCGCTTTGACA 601  
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Db 961 CCCAGTGCACTCGCAGGAGCTGGTCAATGACCTTCAATGAGCTCTTTCGCCGCTTTGACA 1020  
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QY 602 AGCTGGCTCGGAGAAATCACTGCCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTG 661  
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Db 1021 AGCTGGCTCGGAGAAATCACTGCCTGAGATCAAGATCTTGGGACATGTTACTACTGTG 1080  
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QY 662 TGTGAGGCTGCCGAGGCGCGGCGGACCATGCCACATGCTGTGTGAGATGGGGGTAG 721  
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Db 1081 TGTGAGGCTGCCGAGGCGCGGCGGACCATGCCACATGCTGTGTGAGATGGGGGTAG 1140  
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QY 722 ACATGATTGAGGCCATCTCGTGTGTACGTGAGGTGACAGGTGAATGTGAACATGCGCG 781  
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Db 1141 ACATGATTGAGGCCATCTCGTGTGTACGTGAGGTGACAGGTGAATGTGAACATGCGCG 1200  
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QY 782 TGGGCATCCACAGCGGCGGTGCACTGCGGGCTCTTGGGTGCGGAAATGGCAGTTGG 841  
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Db 1201 TGGGCATCCACAGCGGCGGTGCACTGCGGGCTCTTGGGTGCGGAAATGGCAGTTGG 1260  
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QY 842 ATGTGTGTCCTCAATGATGACCCCTGGCCCAACCATGGAAGCAGGAGCGGCTGGCC 901  
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Db 1261 ATGTGTGTCCTCAATGATGACCCCTGGCCCAACCATGGAAGCAGGAGCGGCTGGCC 1320  
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QY 902 GCATCCACATCACTCGGCGCACACTGCAGTACCTGAACGGGAGCTACGAAGTGGAGCCAG 961  
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Db 1321 GCATCCACATCACTCGGCGCACACTGCAGTACCTGAACGGGAGCTACGAAGTGGAGCCAG 1380  
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QY 962 GCCGTGTGGCAAGCGCAACCGTACCTCAAGGAGCAGACATTTCTCTCATCC 1021  
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Db 1381 GCCGTGTGGCAAGCGCAACCGTACCTCAAGGAGCAGACATTTCTCTCATCC 1440  
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QY 1022 TGGGCGCCAGCCAGAAAGAGAGAGAGAGGATGCTGCCAAGCTGCAGCGGACTC 1081  
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Db 1441 TGGGCGCCAGCCAGAAAGAGAGAGAGGATGCTGCCAAGCTGCAGCGGACTC 1500  
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QY 1082 GGGCAACTCCATGGAAGGGCTGATGCGCGGATGGGTTCCTGATGCTGCTCTCCCGGA 1141  
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Db 1501 GGGCAACTCCATGGAAGGGCTGATGCGCGGATGGGTTCCTGATGCTGCTCTCCCGGA 1560  
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QY 1142 CCAAGGACTCCAAGGCTTCCGCCAGATGGGCAATTTGATGATTTCCAGCAAGAACACCGGG 1201  
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Db 1561 CCAAGGACTCCAAGGCTTCCGCCAGATGGGCAATTTGATGATTTCCAGCAAGAACACCGGG 1620  
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QY 1202 GCACCAAGATCCCTGAACCTGAGGATGAGTGGATGAGTTCCTGAGCCGTGCCATCG 1261  
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Db 1621 GCACCAAGATCCCTGAACCTGAGGATGAGTGGATGAGTTCCTGAGCCGTGCCATCG 1680  
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QY 1262 ATGCCCGCAGCATTTGATGAGTGGGAGGACCATGTGCGCGGTTTTTGTCTCACCTTCC 1321  
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Db 1681 ATGCCCGCAGCATTTGATGAGTGGGAGGACCATGTGCGCGGTTTTTGTCTCACCTTCC 1740  
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QY 1322 AGAGAGAGATTTTGAAGAAGTACTCCCGGAAGTGGATCCCGCTTCGGAGCGCTAGC 1381  
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Db 1741 AGAGAGAGATTTTGAAGAAGTACTCCCGGAAGTGGATCCCGCTTCGGAGCGCTAGC 1800  
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QY 1382 TTGCTGTGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCAC 1441  
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Db 1801 TTGCTGTGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCAC 1860  
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Db 1861 ACTCCACCTGTGCTTGGGATTTATGCCAGCATCTTCTGCTGTGCTGCTAATCACCGTGC 1920  
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QY 1502 TGATCTGTGCTGTACTCTCTGTGTCTTCCCTAAGGCCCTGCAACGCTGTGTGCC 1561  
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Db 1921 TGATCTGTGCTGTACTCTCTGTGTCTTCCCTAAGGCCCTGCAACGCTGTGTGCC 1980  
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QY 1562 GCAGCATTTGCCCTCACGGGCACATAGCACCGGAGTGGCATCTTTCGCTGCTGCTG 1621  
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Db 1981 GCAGCATTTGCCCTCACGGGCACATAGCACCGGAGTGGCATCTTTCGCTGCTGCTG 2040  
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QY 1622 TGTACTTCTGCCATTTGCCAATGTTTCACTCTGAACACACACCCCATACGAGGTGTG 1681  
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Db 2041 TGTACTTCTGCCATTTGCCAATGTTTCACTCTGAACACACACCCCATACGAGGTGTG 2100  
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QY 1682 CAGCCCGGATGCTGAATTTAACAACCTGTGATCATCTGCTGCCCTGCCACCTTCGAGCAGCTCA 1741  
|||||



Qy 1682 CAGCCCGGATGCTGAATTAACACCTGCTGACATCACTGCTGCCACCTGCGACGAGCTCA 1741  
Db 2451 CAGCCCGGATGCTGAATTAACACCTGCTGACATCACTGCTGCCACCTGCGACGAGCTCA 2510  
Qy 1742 ATTACTCTCTGGGCTGGATGCTCCCTGCTGTGTGAGGCGCACCACCTGCCAGCTTTC 1801  
Db 2511 ATTACTCTCTGGGCTGGATGCTCCCTGCTGTGTGAGGCGCACCACCTGCCAGCTTTC 2570  
Qy 1802 CTGAGGTGTTTC 1812  
Db 2571 CTGAGTACTTC 2581

RESULT 9  
US-10-201-000-1  
; Sequence 1, Application US/10201000  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, James E.  
; APPLICANT: COR Therapeutics, Inc.  
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL  
; TITLE OF INVENTION: CYCLASE  
; FILE REFERENCE: 44481-5028-01-US  
; CURRENT APPLICATION NUMBER: US/10/201,000  
; CURRENT FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: US/09/474,076  
; PRIOR FILING DATE: 1999-12-12  
; PRIOR APPLICATION NUMBER: PCT/US98/13694  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/070,904  
; PRIOR FILING DATE: 1997-07-01  
; PRIOR APPLICATION NUMBER: 08/886,550  
; PRIOR FILING DATE: 1997-07-01  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4942  
; TYPE: DNA  
; ORGANISM: human type VI adenylyl cyclase  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (145)..(3648)  
US-10-201-000-1

Query Match 97.3%; Score 1763; DB 42; Length 4942;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 1788; Conservative 0; Mismatches 20; Indels 3; Gaps 1;  
Qy 5 ACGTGGTCTGGGATCTCTGGGCGCAGTGCAGGTGCGGGGGCGCTTCGCAGCAGACCCGC 64  
Db 782 ACGTGGTCTGGGATCTCTGGGCGCAGTGCAGGTGCGGGGGCGCTTCGCAGCAGACCCGC 841  
Qy 65 GCAGCCCTCTGCGGGCTCTGGTGGCCCTGTGTTCTTTATACATCGCATACAGCTCC 124  
Db 842 GCAGCCCTCTGCGGGCTCTGGTGGCCCTGTGTTCTTTATACATCGCATACAGCTCC 901  
Qy 125 TCCCATCCGATCGGGCTCCGCTCCCTCAGCGGCTGGGCTCTCCACCTTGCATTGA 184  
Db 902 TCCCATCCGATCGGGCTCCGCTCCCTCAGCGGCTGGGCTCTCCACCTTGCATTGA 961  
Qy 185 TCTTGGCTGGCACTTAACCGTGGTGTGCTTCCCTTGAAGCAGCTCGGTGCCAATG 244  
Db 962 TCTTGGCTGGCACTTAACCGTGGTGTGCTTCCCTTGAAGCAGCTCGGTGCCAATG 1021  
Qy 245 TGCTGCTCTCTCTGCACCAACGTCATTAGCATCTGCACACACTATCCAGCAGAGTGT 304  
Db 1022 TGCTGCTCTCTCTGCACCAACGTCATTAGCATCTGCACACACTATCCAGCAGAGTGT 1081  
Qy 305 CTCAGCGCAGGCTTTTCAGGAGACCCGCGAGTTACATCCAGCGCGGCTCCACCTGCAGC 364  
Db 1082 CTCAGCGCAGGCTTTTCAGGAGACCCGCGGTTACATCCAGCGCGGCTCCACCTGCAGC 1141  
Qy 365 ATGAGATCGGACGAGGCGGTGCTGCTGCGGTATGCCCCAGCAGCTTGCATGG 424

Db 1142 ATGAGAATCGCAGCAGGAGCGGCTGCTGCTGTCGGTATTGCCCGCAGCACGTTGCCATGG 1201  
Qy 425 AGATGAAGAAGACATCAACACAAAAAAGAGAC-- --ATGTTCCACAAAGATCTACATAC 481  
Db 1202 AGATGAAGAAGACATCAACACAAAAAAGAGACATGATGTTCCACAAAGATCTACATAC 1261  
Qy 482 AGAAGCATGACAATGTGAGCATCTCTGTTTGCAGACATTTGAGGGCTTCCACGAGCTGGCAT 541  
Db 1262 AGAAGCATGACAATGTGAGCATCTCTGTTTGCAGACATTTGAGGGCTTCCACGAGCTGGCAT 1321  
Qy 542 CCCAGTGCAGCTGCCGAGGAGCTGCTGATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACA 601  
Db 1322 CCCAGTGCAGCTGCCGAGGAGCTGCTGATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACA 1381  
Qy 602 AGCTGGCTGCCGAGGAATCACTGCTGAGGATCAAGATCTTGGGGACTGTTTACTACTGTG 661  
Db 1382 AGCTGGCTGCCGAGGAATCACTGCTGAGGATCAAGATCTTGGGGACTGTTTACTACTGTG 1441  
Qy 662 TGTGAGGCTGCCGAGGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 721  
Db 1442 TGTGAGGCTGCCGAGGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1501  
Qy 722 ACATGATTGAGGCGCATCTCGCTGCTGAGGTGACAGGTGATGATGTAACATGACGCGG 781  
Db 1502 ACATGATTGAGGCGCATCTCGCTGCTGAGGTGACAGGTGATGATGTAACATGACGCGG 1561  
Qy 782 TGGCATCCACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 841  
Db 1562 TGGCATCCACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1621  
Qy 842 ATGTGTGCTCCAATGATGTGACCCCTGGCCCAACCATATGGAAGCAGGAGCCGGCGTGC 901  
Db 1622 ATGTGTGCTCCAATGATGTGACCCCTGGCCCAACCATATGGAAGCAGGAGCCGGCGTGC 1681  
Qy 902 GCATCCACATCACTCGGCGCACACTGCACTACCTGAAAGCGGAGCTACCAAGTGGAGCCAG 961  
Db 1682 GCATCCACATCACTCGGCGCACACTGCACTACCTGAAAGCGGAGCTACCAAGTGGAGCCAG 1741  
Qy 962 GCGGTGGTGGCAAGCGCAACCGTACCTCAAGGAGCAGCAGATTCAGAGCTTTCCTCATCC 1021  
Db 1742 GCGGTGGTGGCAAGCGCAACCGTACCTCAAGGAGCAGCAGATTCAGAGCTTTCCTCATCC 1801  
Qy 1022 TGGGCGGCGAGCAAGCGCAAG 1081  
Db 1802 TGGGCGGCGAGCAAGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1861  
Qy 1082 GGGCCAACTCCATGGAAGGCGTGTGCGCGCTGATGCGCGCTGCGGTTCCTGCTCCCGGA 1141  
Db 1862 GGGCCAACTCCATGGAAGGCGTGTGCGCGCTGATGCGCGCTGCGGTTCCTGCTCCCGGA 1921  
Qy 1142 CCAAGGACTCCAAAGGCGCTTCGCGCCAGATGGGCATTGATGATTCCAGCAAGAGCAACCGGG 1201  
Db 1922 CCAAGGACTCCAAAGGCGCTTCGCGCCAGATGGGCATTGATGATTCCAGCAAGAGCAACCGGG 1981  
Qy 1202 GCACCAAGATGCCCCGTAACCCCTGAGGATGAGGTGAGTTCCTGAGCCGCTGCCATCG 1261  
Db 1982 GCACCAAGATGCCCCGTAACCCCTGAGGATGAGGTGAGTTCCTGAGCCGCTGCCATCG 2041  
Qy 1262 ATGCCCGCAGCATTTGATCAGCTGCGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1321  
Db 2042 ATGCCCGCAGCATTTGATCAGCTGCGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2101  
Qy 1322 AGAGAGAGGATTTTTCAGAGAGAGTACTCCCGGAAGGTGGATCCCGGCTTCGGAGCTACG 1381  
Db 2102 AGAGAGAGGATTTTTCAGAGAGAGTACTCCCGGAAGGTGGATCCCGGCTTCGGAGCTACG 2161  
Qy 1382 TTGCCCTGCCCCCTGTTGCTTCTGCTTCATCTGCTTCATCCAGCTTCTTAATTTCCAC 1441  
Db 2162 TTGCCCTGCCCCCTGTTGCTTCTGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCAC 2221  
Qy 1442 ACTCCACCTGATGCTGGGATTTATGCCAGCATCTTCCGCTGCTGCTAATACCCGTCG 1501  
Db 2222 ACTCCACCTGATGCTGGGATTTATGCCAGCATCTTCCGCTGCTGCTAATACCCGTCG 2281

Qy	1502	TGATCTGCTGTGTACTCCTGTGGTTCTCTGTTCCCTTAAGGCCCTGCAAGCTGTGCC	1561
Db	2382	TGATCTGTGCTGTGTACTCCTGTGGTTCTCTGTTCCCTTAAGGCCCTGCAAGCTGTGCC	2341
Qy	1562	GCAGCATTGTCGCCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTTG	1621
Db	2342	GCAGCATTGTCGCCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTTG	2401
Qy	1522	TGTTTACTTCTGCCATTGCCAATGTTTCACCTGTAAACCACACCCCCCATACGGAGCTGTG	1681
Db	2402	TGTTTACTTCTGCCATTGCCAATGTTTCACCTGTAAACCACACCCCCCATACGGAGCTGTG	2461
Qy	1682	CAGCCCGGATGCTGAATTTAAACACCTGCTGACATCACTGCGCTGCCACCTGCAGCAGCTCA	1741
Db	2462	CAGCCCGGATGCTGAATTTAAACACCTGCTGACATCACTGCGCTGCCACCTGCAGCAGCTCA	2521
Qy	1742	ATTACTCTCTGGGCCCTGGATGCTCCCTGTGTGAGGGCACCATGCCACCTGCAAGCTTTC	1801
Db	2522	ATTACTCTCTGGGCCCTGGATGCTCCCTGTGTGAGGGCACCATGCCACCTGCAAGCTTTC	2581
Qy	1802	CTGAGGTGTTTC	1812
Db	2582	CTGAGTACTTC	2592

## RESULT 10

US-09-750-240-12

03 03 750 240 12  
; Sequence 12, Application US/09750240

; GENERAL INFORMATION:

APPLICANT: Hammon, H. K.

APPLICANT: Insel, P. A.

; APPLICANT: Ping, P.

; APPLICANT: POST, S. R.

; APPLICANT: Gao, M.

; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART

; TITLE OF INVENTION: FAILURE

FILE REFERENCE: 220002056723

; CURRENT APPLICATION NUMBER: US/09/750,240  
 ; CURRENT FILING DATE: 2001-10-12

; CURRENT FILING DATE: 2001-10-12  
 : PRIOR APPLICATION NUMBER: US 09/

; PRIOR APPLICATION NUMBER: US 09/412,661  
 : PRIOR FILING DATE: 1999-12-27

PRIOR FILING DATE: 1999-12-27  
PRIOR APPLICATION NUMBER: IIS 09/008 097

: PRIOR FILING DATE: 1998-01-16

: PRIORITY APPLICATION NUMBER: US 08/924,757

PRIOR FILING DATE: 1997-09-05

; PRIOR APPLICATION NUMBER: US 60/048,933

PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: US 08/708,661

: PRIOR FILING DATE: 1996-09-05

; NUMBER OF SEQ ID NOS: 13

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; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 12

; LENGTH: 3582

; TYPE: DNA

; ORGANISM:

; FEATURE:

; OTHER IN 24

US-09-750-240-12

Quinn Votak

Query Match	91.5%	Score 1657.8;	DB 29;	Length 3582;
Best Local Similarity	95.48;	Pred. No. 0;		
Matches 1730; Conservative	0;	Mismatches	77;	Indels 6; Gaps

QY	3	TAACGTGGTGC	TGGGCATC	CTGCGGGAGTGC	AGTGCAGGCGGCGCTTT	CGCAGCAGACCC	62
Db	657	TTACGTGGTGC	TGGGCATC	CTGCGGGAGTGC	AGTGCAGGCGGCGCTCT	CGCAGCAGACCC	716
QY	63	GCAGAGCCCTC	TGCGGGCCT	CTGGTGCCT	TGTTGTATACATACGCATACACGT		122
Db	717	GCAGAGCCCTC	TGCGGGCCT	CTGGTGCCT	TGTTGTATACATACGCCTACACGT		776
QY	123	CCCTCCCATCCG	CATGCGGGCT	GCCGCTCCT	CACGGCGCTCTCCACACCTTGCAATT		182



Db	1854	GGGTGCCCAAGATGCTCTGAACCCCTGAAGATGAGGTGGATGAGTTCTCTGGCCGAGCCAT	1913
QY	1260	CGATGCCCGCAGCATTTGATCAGCTGCGGAAGACCATGTGCGCGGTTTTTTTGCTCACCTT	1319
Db	1914	CGATGCCCGCAGCATTTGATCAGCTGCGGAAGACCATGTGCGCGGTTTTCTGTFCACCTT	1973
QY	1320	CCAGAGAGAGATTTTGAGAAGAAGTACTCCCGGAAGGTGGATCCCGCTTCCGAGGCCTA	1379
Db	1974	CCAGAGAGAGATTTTGAGAAGAAGTACTCCCGGAAGGTGGATCCCGCTTCCGAGGCCTA	2033
QY	1380	CGTTGCTCTGCGCCTGTTTGGTCTTTCGCTTCATCTGCTTCATCCAGCTTCTAAATTTTCCC	1439
Db	2034	CGTTGCCCTGCGCCTGTTTGGTCTTTCGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCC	2093
QY	1440	ACACTCCACCCCTGATGCTTTGGGATTTATGCCAGCATCTTCGTGCTGTGCTTAATCACCGT	1499
Db	2094	ACACTCCACCCCTGATGCTTTGGGATCTATGCCAGCATCTTCGTGCTGTGCTTAATCACCGT	2153
QY	1500	GCTGATCTCTGCTGTGTAATCCTCTGTGGTCTCTTCCTCAAGCCCTGAAACGTCTGTC	1559
Db	2154	GCTGATCTCTGCTGTGTAATCCTCTGTGGTCTCTTCCTCAAGCCCTGAAACGTCTGTC	2213
QY	1560	CCGACGATTTGCCGCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCT	1619
Db	2214	CCGACGATTTGCCGCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCT	2273
QY	1620	TGTGTTTTACTTCTGCATTTGCCAATGTTCACTGTAAACACACCCCCCATACGGAGCTG	1679
Db	2274	TGTGTTTTACTTCTGCATTTGCCAATGTTCACTGTAAACACACCCCCCATACGGAGCTG	2333
QY	1680	TGCAGCCCGGATGCTGAATTTAACACCTGCTGCATCACTGCCTGCCACCTGCAGAGCT	1739
Db	2334	TGCAGCCCGGATGCTGAATTTAACACCTGCTGCATCACTGCCTGCCACCTGCAGAGCT	2393
QY	1740	CAATTACTCTCTGGGCCTGGATGCTCCGCTGTGTGAGGGCACCATGCCACCTGCAGCTT	1799
Db	2394	CAATTACTCTCTGGGCCTGGATGCTCCGCTGTGTGAGGGCACCATGCCACCTGCAGCTT	2453
QY	1800	TCCTGAGGTGTTCT	1812
Db	2454	TCCTGAGTACTTC	2466

RESULT 11	
US-09-491-404-837	
Sequence 837, Application US/09491404	
GENERAL INFORMATION:	
APPLICANT: Tang, Yuanhua T.	
APPLICANT: Tillinghast, John	
APPLICANT: Sinku, Ankura	
APPLICANT: Liu, Chenghua	
APPLICANT: Drmanac, Radoje T.	
TITLE OF INVENTION: Novel Contigs Obtained	
TITLE OF INVENTION: From Various Libraries	
FILE REFERENCE: 785	
CURRENT APPLICATION NUMBER: US/09/491.404	
CURRENT FILING DATE: 2000-01-27	
NUMBER OF SEQ ID NOS: 3796	
SOFTWARE: PL_SP_genes Version 1.0	
SEQ ID NO 837	
LENGTH: 5353	
TYPE: DNA	
ORGANISM: Homo sapiens	
FEATURE:	
NAME/KEY: sig_peptide	
LOCATION: (1669)...(1804)	
OTHER INFORMATION: this location contains the signal peptide sequence,	
OTHER INFORMATION: MLGIVASIFLLLLITVLICAVVSGSLFPKALQRLSRIVSRRAH, Run with SignalP	
FEATURE:	
NAME/KEY: misc_feature	
LOCATION: (3)...(2946)	
OTHER INFORMATION: similar to gi2887419 in the genepept database release 114,	
OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters	
OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters	









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Qy 1082 GGGCAACTCCATCGAAGGGCTGATGCGCGATGGGTTCCTGATCGTGCCTTCCTCCGGA 1141
Db 1807 GGGCAACTCCATCGAAGGACTGATGCGCGCTGGTTCCTGACCGTGCCTTCCTCCGGA 1866
Qy 1142 CCAAGGACTCAAGGCTTCGCGCAGATGGGCATGATGATTCAGCAAGAACACACCGG 1201
Db 1867 CCAAGGACTCAAGGCTTCGCGCAGATGGGCATGATGATTCAGCAAGAACACACCGG 1926
Qy 1202 GCACCAAGATGCTTGAACCTCAGGATGAGTGGGATGATGCTGAGCGGTGCCATCG 1261
Db 1927 GTGCCCAAGATGCTTGAACCTCAGGATGAGTGGGATGATGCTGAGCGGTGCCATCG 1986
Qy 1262 ATGCCCGAGCATGATGATGATGCGGAGGACCATGATGCGCGGTGTTTGTCTACCTTCC 1321
Db 1987 ATGCCCGAGCATGATGATGATGCGGAGGACCATGATGCGCGGTGTTTGTCTACCTTCC 2046
Qy 1322 AGAGAGGATTTGAGAGAGTACTCCCGAAGTGGATCCCGCTTCGGAGCCTACG 1381
Db 2047 AGAGAGGATTTGAGAGAGTACTCCCGAAGTGGATCCCGCTTCGGAGCCTACG 2106
Qy 1382 TTGCTGTGCCCTGTTGCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCAC 1441
Db 2107 TCGCTGTGCCCTGTTGCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCAC 2166
Qy 1442 ACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTAATCACTGCC 1501
Db 2167 ACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTAATCACTGCC 2226
Qy 1502 TGATCTGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1561
Db 2227 TGATCTGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2286
Qy 1562 GCAGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1621
Db 2287 GCATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2346
Qy 1622 TGTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1681
Db 2347 TGTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2406
Qy 1682 CAGCGGATGCTGAATTAACCTGCTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1741
Db 2407 CAGCGGATGCTGAATTAACCTGCTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2466
Qy 1742 ATTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1801
Db 2467 ATTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2526
Qy 1802 CTGAGGTGTT 1812
Db 2527 CTGAGTACTTC 2537
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RESULT 15

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US-08-538-815-11
; Sequence 11, Application US/08538815
; GENERAL INFORMATION:
; APPLICANT: Tang, Wei-Jen
; APPLICANT: Gilman, Alfred G.
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL
; TITLE OF INVENTION: CYCLASE AND USES THEREFOR
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/538.815
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSD:450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4131 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; US-08-538-815-11

Query Match 79.3%; Score 1437.2; DB 9; Length 4131;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 1584; Conservative 0; Mismatches 223; Indels 3; Gaps 1;

Qy 5 ACGTGGTCTCGGGCATCTCGCGGCGAGTCGAGGTGCGGGGGCGCTTCCAGCAGACCCGC 64
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Qy 65 GCAGCCCTCTCGCGGCGCTCTGGTGCCTGTGTTCTTTGTATACATCCATACACAGCTCC 124
Db 747 GCAGCCCTCTCGAGCGCTTTGGTGCCTGTGTTCTGCTCTACATACCTACACACTTC 806
Qy 125 TCCCATCCGATCGGGGCTCGCTCTCAGCGGCTGGGCTCTCCACCTTCGATTTGA 184
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Qy 185 TCTTGGCTGCACTTAACGCTGGTGATGCTCTCTCGAAGCAGCTCGTGCAATG 244
Db 867 TTTGGCTGCACTCAACATGCTGACCCCTCTCTTTGGAAGCAGCTCGTGTAAG 926
Qy 245 TCGTGTCTCTCTGCAACCACTGATTTAGCATCTGCACACATATCCAGCAGAGGTGT 304
Db 927 TGGTGTCTCTCTGCAACCAATGCCATCGGTGCTGCACGCACTACCCGCTGAAGTGT 986
Qy 305 CTCAGCGCCAGGCTTTTCAGGAGACCCGATTTACATCCAGCGCGGCTCCACCTGCAAG 364
Db 987 CTCAGCGCCAAAGCTTTTCAGGAGACCCGATTTACATCCAGCGCGGCTGCACTTGCAG 1046
Qy 365 ATGAGATCGCAGCAGGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 424
Db 1047 ATGAGATCGCAGCAGGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1106
Qy 425 AGATGAAAGAGACATCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 481
Db 1107 AAATGAAAGAGATCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1166
Qy 482 AGAGATGACAATGTCAGATTCCTGTTTTCAGACATTTAGGGGCTTCCAGCGCTGGCAT 541
Db 1167 AGAAGCATGACAATGTCAGATTCCTGTTTTCAGACATTTAGGGGCTTCCAGCGCTGGCAT 1226
Qy 542 CCCAGTGCAGTGCAGGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
Db 1227 CCCAGTGCAGTGCAGGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1286
Qy 602 AGCTGGTGCAGGAGATCACCTGCTGAGGATCAAGATCTTGGGGAGCTGTTACTACTGTG 661
Db 1287 AGCTGGTGCAGGAGATCACCTGCTGAGGATCAAGATCTTGGGGAGCTGTTACTACTGTG 1346
Qy 662 TGTAGGCTGCCGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 721
Db 1346 TGTAGGCTGCCGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 721
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Db	1347	TGTCGGGGCTGCCGGAGGCCCGGACAGACCATGCCCACTGCTGTGTGGAGATGGGGTAG	1406
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Db	1407	ACATGATCGAGGGCATCTCGCTGTGGTGTGAGGTAACTGTAACATGGCGC	1466
QY	782	TGGGCATCCACAGCGGCGGTGCACATGCGCGCTCTTGGCTTCCGGAATGSCAGTTGC	841
Db	1467	TGGGCATCCACAGCGGCGGTGCACATGCGCGTGTCTGTGCTGCGGAATGSCAGTTG	1526
QY	842	ATGTGTGGTCCAATGATGTGACCTGTGCCAACCACTGGAAGCAGGAAAGCCGGGCTGCC	901
Db	1527	ATGTGTGGTCCAAGGATGTGACCTGTGCCAACCACTGGAAGCAGGAAAGCCGGGCTGCC	1586
QY	902	GCATCCACATCACTCGGGCAACACTGAGTACCTGAACGGGGACTACGAAGTGGAGCCAG	961
Db	1587	GCATCCACATCACTCGGGCCACACTGCAGTACCTGAACGGGGACTATGAGTGGAGCCAG	1646
QY	962	GCGTGTGTGGCAAGCGCAAGCGTACCTCAAGGAGCAGCATTGAGACTTTCTCTATCC	1021
Db	1647	GCGTGTGTGGCAAGCGCAAGCGTACCTCAAGGAGCAGTGCATTGAGACCTTCTCTATAC	1706
QY	1022	TGGGGCCACGCAAGAAAGGAGAGAAAGGCATGCTGGCCAAAGCTGCAGCGGACTC	1081
Db	1707	TAGGAGCCACGCAAGAAAGGAGAGAAAGGCATGCTGGTCAAGCTGCAGGGGAGCC	1766
QY	1082	GGGCCAACTCCATGGAAGGCTGATGCCGCGATGGGTTCTGTATCGTGTGCTTCTCCGGA	1141
Db	1767	GGGCCAACTCCATGGAAGGCTGATGCCGCGTGGGTTCTGTATCGTGTGCTTCTCCGGA	1826
QY	1142	CCAAGGACTCCAAGGCTTCCGCGACATGGGCATTGATGATTCAGCAAGAGCAACCGGG	1201
Db	1827	CCAAGGACTCCAAGGCTTCCGCGACATGGGCATTGATGATTCAGCAAGAGCAACCGGG	1886
QY	1202	GCACCAAGATGCCCTGAACCCCTGAGGATGAGGTGATGATTCCTGAGCCGTGCCATCG	1261
Db	1887	GTGCCCAAGATGCTGAAACCCCTGAGGATGAGGTGAGGATTCCTGGGCGGAGCCATCG	1946
QY	1262	ATGCCCGCAGCATTGATCAGCTCGGGAAGACCATGTGCCCGGTTTTGCTCACCTTCC	1321
Db	1947	ATGCCCGCAGCATTGATCAGCTCGGGAAGACCATGTGCCCGGTTTTGCTCACCTTCC	2006
QY	1322	AGAGAGAGGATTTTGAGAAAGTACTCCCGGAAGTGGATCCCGCTCGGAGCCCTACG	1381
Db	2007	AGAGAGAGGATTCGAGAAAGTATTACGGGAAGTAGACCTCGTTTCGGAGCCCTACG	2066
QY	1382	TTGCCCTGTGCCCTGTGGTCTTCTGTCTCATCTGCTTCACTCCAGCTTCTAATTTTCCCAC	1441
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QY	1442	ACTCCACCTGATGCTTGGGATTTATGCCAGCATCTCCTGTGCTGCTAATCACCGTGC	1501
Db	2127	ACTCCACCTGATGCTTGGGATTTATGCCAGCATCTCCTGTGCTGCTAATCACCGTGC	2186
QY	1502	TGATCTGTGCTGTACTCTGTGGTCTCTGTTCCTTAAGGCCCTGCAACGCTGTGCC	1561
Db	2187	TCATCTGTGCTGTGCTCTGTGGTCTTCTTCCCAAGCCCTGCACCGCTGTGCC	2246
QY	1562	GCAGCATGTGCCCTCACGGGCACATAGCACCGCAGTGGCATCTTTTCCGTCCTGCTTG	1621
Db	2247	GCAGTATGCTGCCCTCACGGGTGCACAGCACGGCTGTGGAGTCTTCTCGGTTCTGCTTG	2306
QY	1622	TGTTTACTTCTGCCATTGCCAATGTTTACCTGTAAACACACCCCGCATACGAGCTGTG	1681
Db	2307	TGTTTACTTCTGCCATTGCCAATGTTTACCTGTAAACACACCCCGCATACGAGCTGTG	2366
QY	1682	CAGCCGGATGCTGAATTTAAACACCTGCTGACATCACTGCCACCTGCAGCAGCTCA	1741
Db	2367	CGCCCGGATGCTGAATTTAAACACCTGCTGACATCACTGCCACCTGCAGCAGCTCA	2426
QY	1742	ATTACTCTTGGGCCCTGGATGCTCCCTGTGTGAGGGCACCATGCCACCTGCAGCTTTC	1801
Db	2427	ATTACTCTTGGGACTGGAAGCTCCCTGTGTGAGGGCACCGCACCTGCAGCTTTC	2486

Search completed: February 23, 2003, 07:31:52  
Job time : 3608.79 secs

QY 1802 CTGAGGTGTT 1811  
Db 2487 CTGAGTACTT 2496

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1454.2	80.3	5826	6	US-10-144-771-5921	Sequence 5921, Ap
2	829.8	45.8	4349	6	US-10-144-771-18529	Sequence 8529, A
3	432.8	23.9	1386	1	PCR-US02-36759-83	Sequence 83, Appl
4	346	19.1	2253	6	US-10-144-771-16113	Sequence 16113, A
5	339	18.7	2949	5	US-09-724-676-11593	Sequence 11593, A
6	339	18.7	2949	5	US-09-724-676A-11593	Sequence 11593, A
7	339	18.7	3756	5	US-09-724-676A-11592	Sequence 11592, A
8	339	18.7	3756	5	US-09-724-676A-11592	Sequence 11592, A
9	338.2	18.7	4079	6	US-10-305-720-1412	Sequence 1412, Ap
10	338.2	18.7	5370	5	US-09-724-676-11576	Sequence 11576, A
11	338.2	18.7	5370	5	US-09-724-676A-11576	Sequence 11576, A
12	338.2	18.7	5680	5	US-09-724-676-11577	Sequence 11577, A
13	338.2	18.7	5680	5	US-09-724-676A-11577	Sequence 11577, A
14	333.2	18.4	4633	6	US-10-144-771-16338	Sequence 16338, A
15	320.6	17.7	3358	6	US-10-144-771-14946	Sequence 14946, A
16	316.6	17.5	6196	1	PCR-US02-34621-1	Sequence 1, Appl
17	316.6	17.5	6196	6	US-10-282-942-1	Sequence 1, Appl
18	314.4	17.4	5124	6	US-10-144-771-18424	Sequence 18424, A
19	311.4	17.2	2731	6	US-10-305-720-1344	Sequence 1344, Ap
20	286	15.8	4008	7	US-60-436-643-3039	Sequence 3039, Ap
21	284.8	15.7	3820	6	US-10-144-771-855	Sequence 855, App
22	284	15.7	3518	6	US-10-121-911A-2	Sequence 2, Appl
23	273.6	15.1	320	6	US-10-264-237-588	Sequence 588, App
24	264.2	14.6	3458	6	US-10-144-771-3825	Sequence 3825, Ap
25	256.2	14.1	3357	6	US-10-338-044-2053	Sequence 2053, Ap
26	216.8	12.0	4457	6	US-10-144-771-18978	Sequence 18978, A

Db 1147 AGATGAAGAGACATCAACACAAAAAGAGACATGATGTTCCATAAGATCTACATCC 1206  
QY 482 AGAAGCATGACATGTCAGCATCTGTTGCAGACATTTAGAGGCTTACACAGCCTGSCAT 541  
Db 1207 AGAAGCATGATGTCAGCATCTGTTTGGGACATTTAGAGGCTTACACAGCCTGGCCT 1266  
QY 542 CCCAGTGCATGGCGAGAGCTGTCTATGACCTGAATGAGCTTTTGGCCGGTTTGACA 601  
Db 1267 CCCAGTGCATGGCACAGAACTGGTCATGACCTTGAATGAGCTTTTGGCCGGTTTGACA 1326  
QY 602 AGCTGGCTGGGAGAACTACCTGCTGAGGATCAAGATCTTTGGGGGAGCTGTACTACTGTG 661  
Db 1327 AGCTGGCTGGGAGAACTACCTGCTGAGGATCAAGATCTTTAGGAGAGCTGTACTACTGCG 1386  
QY 662 TGTGAGGGCTGGCGAGGCGCGGCCACCATGCCACTGCTGTGTGGAGATGGGGTAG 721  
Db 1387 TGTGAGGGCTGGCGAGGCGCGGCCAGATCACGCCCACTGCTGTGTGGAGATGGGGTAG 1446  
QY 722 ACATGATTGAGGCCATCTCGCTGCTGCTGAGGTGACAGGTGTAATGTGAACATGGCGG 781  
Db 1447 ACATGATCGAAGCACTCTCGCTGCTGCTGAGGTGAACAGGTGTAACAGTGAACATGGGTG 1506  
QY 782 TGGGCATCCACAGCGCGGTGCACTGCGCGCTGCTTGGCTTGGCGGAAATGGCAGTTTCG 841  
Db 1507 TGGGCATCCACAGCGGAGCTGTGCATTTGGCGCTTCTTGGCCTACGGAAATGGCAGTTTCG 1566  
QY 842 ATGTGTGTCCTCAATGATGTACCTGSCCAACACATGGAAGCAGGAAGCGGCTGGCC 901  
Db 1567 ATGTGTGTCCTCAACGATGTGACCTGCTTAACACATGGAAGCGGCGGCGGCGGCC 1626  
QY 902 GCATCCACATCACTCGGGCAACACTGCTGCTGAGGTGACAGGTGTAATGTGAACATGGCGG 961  
Db 1627 GCATCCACATCACTCGGGCTACACTGCTGCTGAGGTGTAATGTGAACATGGCGG 1686  
QY 962 GCGTGGTGCAGAGCGGCTGCTGCTGAGGTGTAATGTGAACATGGCGGCTGCTGCTGCTGCT 1021  
Db 1687 GCGTGGTGGTGAACGCAATGCTGCTGCTGAGGTGTAATGTGAACATGGCGGCTGCTGCTGCT 1746  
QY 1022 TGGCGCGCAGCCAGAAAG 1081  
Db 1747 TGGCGCGCAGCCAGAAAG 1806  
QY 1082 GGCCCAACTCCATGGAGGCTGATGCGCGGATGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1141  
Db 1807 GGCCCAACTCCATGGAGGAGCTGATGCGCGGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTG 1866  
QY 1142 CCAAGGACTCCAGGCGCTTCCGCGAGATGGCATTTGATGATTTCCAGCAAGAACACCGGG 1201  
Db 1867 CCAAGGACTCCAGGCAATCCGCGAGATGGCATTTGATGATTTAGCAAGAACACCGGG 1926  
QY 1202 GCACCAAGATGCCCTGAACCCCTGAGGATGAGGTGATGATTTCCAGGCGGTGCCATCG 1261  
Db 1927 GTGCCCAAGATGCTGGAACCCCTGAAGATGAGGTGATGATTTCCAGGCGGTGCCATCG 1986  
QY 1262 ATGCCCGCAGCATGATGATGCTGCGGAAGACCATGTGCGCGGTTTGTGCTCACCTTCC 1321  
Db 1987 ATGCCCGCAGCATGATGATGCTGCGGAAGACCATGTGCGCGGTTTGTGCTCACCTTCC 2046  
QY 1322 AGAGAGGAGTTTGAAGAAGTACTCCCGGAAGTGGATTCGCCGTTCCGAGGCTTCCGAGCCTACG 1381  
Db 2047 AGAGAGGAGTCTTGAGAAGAAGTATTCACGGAAGTAGATTCCTCGCTTCCGAGGCTTCCGAG 2106  
QY 1382 TTGCTGTGCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1441  
Db 2107 TCGCTGTGCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2166  
QY 1442 ACTCCACCTGATGCTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1501  
Db 2167 ACTCCACCTGATGCTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2226  
QY 1502 TGATCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1561

Db 2227 TGATCTGTGCGCTGTGCTGCTGCGGTTCTTTTCTTCCCAAGGCCCTGCAAGCCTGTGCC 2286  
QY 1562 GCAGCATTTGCGCTCAGCGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTGCTG 1621  
Db 2287 GCATATTTGCGCTCAGCGGTGCACAGCACCGCGGTGGAACTTCTTCTGCTGCTGCTG 2346  
QY 1622 TGTTTACTTCTGCGCATTTGCCAATGTTACCTGTAAACACACACCCCATACGGAGCTGTG 1681  
Db 2347 TGTTTACTTCTGCGCATTTGCCAATGTTTACCTGTAAACACACCCCAATAAGGACCTGCG 2406  
QY 1682 CAGCCCGGATGCTGAATTTAACACCTGCTGACATGCTGCTGCCACCTGCAGCAGCTCA 1741  
Db 2407 CGGCCCGGATGCTGAATTTAACACCGGATGTTACCGCTGTAATCACACCCCAATAAGGACCTCA 2466  
QY 1742 ATTACTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1801  
Db 2467 ATTACTTCTGCGACTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2526  
QY 1802 CTGAGTGTTC 1812  
Db 2527 CTGAGTGTTC 2537

RESULT 2  
US-10-144-771-19529  
; Sequence 19529, Application US/10144771  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF  
; FILE REFERENCE: CL001321  
; CURRENT APPLICATION NUMBER: US/10/144,771  
; CURRENT FILING DATE: 2002-05-15  
; NUMBER OF SEQ ID NOS: 47235  
; SEQ ID NO 19529  
; LENGTH: 4349  
; TYPE: DNA  
; ORGANISM: HUMAN  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(4349)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-144-771-19529

Query Match 45.8%; Score 829.8; DB 6; Length 4349;  
Best Local Similarity 67.8%; Pred. No. 1.1e-198;  
Matches 1240; Conservative 0; Mismatches 547; Indels; 42; Gaps 4;

QY 5 ACGTGGTGTGCGCATCTCGCGCGCAGTCGAGGTGCGGGGCGCTTTCGCGAGCAGACCCGC 64  
Db 416 ATGCGCTCATTTGAGTGGTGTGCTGCGCGTCCAGGTAGTGGGCGCTTGTGCTGCCACAGCCAC 475  
QY 65 GCAGCCCTCTGCGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 124  
Db 476 GCAGCGCTCCGAGGCGATCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 535  
QY 125 TCCCATTCGCGCATCGGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 184  
Db 536 TGCCTGTGCGCATGAGGCTGCGGTGCTGCTGCGGGGTGCTTCTGCTGCGGTCTCCACTTGG 595  
QY 185 TCTTGGCTGGCAACTTAACCGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244  
Db 596 CCATCTCTGCGACCACTCCAGGACCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 655  
QY 245 TGTGCTGTTTCTCTGCGCAAGTCTATAGCATCTGCGACACATCTGCGACACATCTCCAGCAGAGAGTGT 304  
Db 656 TCTCATCTCTCTGCGCAAGTCTATAGCATCTGCGACACATCTGCGACACATCTCCAGCAGAGAGTGT 715  
QY 305 CTCAGCGCCAGGCTTTTCAGGAGACCGCGAGTTTACATCCAGGCGCGGCTCCACCTGCAGC 364  
Db 716 CCCAGAGACAGGCTTTCAGGAGACCGCGAGTGTATCCAGGCTCGGCTCCACTTCCAGC 775  
QY 365 ATGAGAAATCGGACAGGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 424

Db 776 GGGAAACCAAGCAAGAGAGGCTCTCCCTGCTGTCTCTCCCGTCTATGTCCTCAGG 835  
Qy 425 AGATGAAAGAACATCAACACAAAAGAGAG- -CATGTTCCACAGATCTACATAC 481  
Db 836 AGATGAAAGAACATCAACGCCAAGCAGGAGATATGATGTTCCACAGATCTACATCC 895  
Qy 482 AGAAGCATGACAATGTCAGCATCTCTGTTTGGAGACATTTAGGGCTTCCACAGCCTGGCAT 541  
Db 896 AGAAGCATGACAATGTCAGCATCTCTGTTTGGAGACATTTAGGGCTTCCACAGCCTGGCTT 955  
Qy 542 CCCAGTGCATGCGGAGAGAGTGGTATGACACCTGAAATGAGCTCTTTCGCCGGTTTGACA 601  
Db 956 CCCAGTGTACTGCCCCAAGAACTGTGTCATGACCCCTCAATGAGCTCTTCCGCCGCTTTGACA 1015  
Qy 602 AGCTGGCTGCGGAGAACTCACTGCCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTG 661  
Db 1016 AGTTGGCTGCGGAGAACTCACTGTTTACGGATTAAAGATCCTCGGGGATTGTTACTACTCGG 1075  
Qy 662 TGTCAAGGCTGCCGAGGCGCGGCCGACCATGCCCCACTGCTGTGTGGAGATGGGGTAG 721  
Db 1076 TCTCGGGCTGCCCTGAAGCCAGAGCCGACCATGCCACTGCTGCTGGATGGGAATGG 1135  
Qy 722 ACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATGCCCG 781  
Db 1136 ACATGATCGAGGCCATCTCGTTGGTCCGGGAGGTGACAGGGGTGAACGTGAACATGCCCG 1195  
Qy 782 TGGGCATCCAGCGGGCGCTGCACTCGCGCTCTTGGCTTGGGAAATGGCAGTTTCG 841  
Db 1196 TGGGAATTCACAGCGGAGAGTACACTCGGTGTCCTTGGTCTCAGAAGTGGCAATTCG 1255  
Qy 842 ATGTGTGTCCAATGATGTACCTTGCCCAACCAATGGAAGCAGGAAGCGGGCTGCCC 901  
Db 1256 ACGTGTGTCTAAAGATGTCACTCTGCGCAACCAATGGAAGCTGGTGGCAAGCGGGCC 1315  
Qy 902 GCATCCACATCACTCGGCGACATGTCAGTACCTGAAAGCGGACTACGAAGTGGAGCCAG 961  
Db 1316 GCATCCACATCAACCAAGCCCACTCAACTACCTGAATGGGAGCTATGAGTGGGAACCCAG 1375  
Qy 962 GCGTGTGTGGCAAGCGCAACCGTACCTCAAGGAGCAGCAGATTTGAGACTTTCCTCATCC 1021  
Db 1376 GCTGTGTGGCATGCGCAATGCCATACCTCAAGGAGCAGCATTTGAGACCTTCTCATCC 1435  
Qy 1022 TGGGCGCAGCAGAAACGGAAGAGAGAAAGGATGCTGCCAAGTGGAGCGGAGTC 1081  
Db 1436 TGAGCTGTACCCAGAGCGGAAGAGAGAGAGGCGCATGATGCCAAGATGAACGCCCAGA 1495  
Qy 1082 GGGCAACTCCATGGAAGGGCTGATGCGCGCATGGTTCTTCTGATCGTCCCTTCT- - - - - 1135  
Db 1496 GAACCAACTCCATCGGACACAATCCGCTCACTGGGGAGCGGAGCGCCCTTCTACAAACC 1555  
Qy 1136 - - - - -CCCGGACCAAGGACTCCAAGGCGTTCCGCGCAGATGGGCATTGATTCACAGCA 1189  
Db 1556 ACTTGGGCGGCAACCAAGTGTCAAGAGAGATGAAGAGATGCTTCCCTATCTCTGCCCTG 1615  
Qy 1190 AAGCAACCGGGGCAACCAAGATGCCCTGAAACCCGTGAGGATGAGTGTGATGATTCCTGA 1249  
Db 1616 GTTTTTCAGGAATGCCCAGGAAAGTGGCAACCCAGAGAGTGAAGTGGCAGATTTCTGG 1675  
Qy 1250 GCGTGGCATCGATGCCCGCAGCATTTGATCAGCTCGCGAAGGACCATGTGGCCCGTTT 1309  
Db 1676 GTGCGGCCATCGATGCCAGGAGATCGGACACTCGCATCTGAACACCTCGCAGAGTTCC 1735  
Qy 1310 TGCTCACCTCCAGAGAGGATTTTGAGAGAAGTACTCCCGGAAGGTGGATCCCGCT 1369  
Db 1736 TCCTGACCTTCAGGAGGCCCATTTAGAGAGAAGTACTCCAAGCAGGTGATGACCAT 1795  
Qy 1370 TCGGAGCCATGCTGCGCTGCGCTGTTGGTCTTCTGCTCATCTGCTTCACTCCAGCTTC 1429  
Db 1796 TTGTGCGCTATGTGCGCTGCGCTGCTGTTTCTCTCTCATCTGCTTTGTGCCAGATCA 1855  
Qy 1430 TAATTTTCCACACTCCACCCCTGATGCTGGATTTATGCCAGCATCTTCTGCTGCTGCG 1489  
Db 1856 CCAATTTGCCCCACCTCCCTGTTTCATGCTGAGTTTCTACCTGTGCTGCTGCTGCTG 1915

Qy 1490 TAATCACCGTGTGATCTGTGCTGTACTCTCTGTGTTTCTCTGTTCCTTAAGGCCCTGC 1549  
Db 1916 CTTGGTGGTGTGTTGTGTGTGTGATCTATGCTGTG- - - - -TGA 1954  
Qy 1550 AACGTCTGTCCGCGAGCATTTGCCCTCACGGGCACATAGCACCCGAGTTGGCATCTTTT 1609  
Db 1955 AGACACTCTCCAGGAAGATAGTGGCATCCAAGAAGAACAGCACCTCTGTCGGGGTATTCA 2014  
Qy 1610 CCGTCTCTGTGTGTTTACTTCTGCCATTGCCAATGTTCACTGTGAACACACCCCA 1669  
Db 2015 CCATCACCTGTGTGTTCTCTCGGCTTTGTCAACATGTTGTCGAACCTCTAAGAACC 2074  
Qy 1670 TACGAGCTGTGCAGCCCGGATGCTGAATTTAAACACCTGCTGACATCACTGCTGCCACC 1729  
Db 2075 TGGTGGGTGCTGGCAGAGGAGCACACATCACGGTGAACGAGTCAACGATGTATG 2134  
Qy 1730 TGCAGCAG- - - - -CTCAATTACTCTCTGGGCGCTGGATGCTCCCTGTGTAGGAGCACCA 1783  
Db 2135 TGATGGAGTCGGCTTCAACTACAGCTTGGCGCAGCAGGAGGCTTCTGTGCGAGCCCC 2194  
Qy 1784 TGCCCACTGCGAGCTTTCTCTGAGGTGTTTC 1812  
Db 2195 AGCCCAACTGCAACTTCCAGAGTACTTC 2223  
RESULT 3  
PCT-US02-36759-83  
; Sequence 83, Application PC/TUS0236759  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: DUGGAN, Brendan M.  
; APPLICANT: YANG, Junming  
; APPLICANT: GIETZEN, Kimberly J.  
; APPLICANT: LEE, Soo Yeun  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: AZIMZAI, Yalda  
; APPLICANT: WALIA, Narinder K.  
; APPLICANT: WARREN, Bridget A.  
; APPLICANT: BARROSO, Ines  
; APPLICANT: BECHA, Shanya D.  
; APPLICANT: YUE, Henry  
; APPLICANT: LEHR-MASON, Patricia M.  
; APPLICANT: THANGAVELU, Kavitha  
; APPLICANT: LEE, Sally  
; APPLICANT: EMERLING, Brooke M.  
; APPLICANT: KABLE, Amy E.  
; APPLICANT: KHARE, Reena  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: GANDHI, Aneena R.  
; APPLICANT: TRAN, Uyen K.  
; APPLICANT: RICHARDSON, Thomas W.  
; APPLICANT: MARQUIS, Joseph P.  
; APPLICANT: LAL, Preeti G.  
; APPLICANT: FORSYTHE, Ian J.  
; APPLICANT: LEE, Ernestine A.  
; APPLICANT: SWARNAKAR, Anita.  
; APPLICANT: KALLICK, Deborah A.  
; APPLICANT: GRIFFIN, Jennifer A.  
; APPLICANT: ELLIOTT, Vicki S.  
; APPLICANT: GORVAD, Ann E.  
; APPLICANT: HAFALIA, April J.A.  
; APPLICANT: ISON, Craig H.  
; APPLICANT: JIN, Pei  
; APPLICANT: JIANG, Xin  
; APPLICANT: JACKSON, Alan  
; APPLICANT: BHATIA, Umesh  
; APPLICANT: BURRILL, John D.  
; APPLICANT: BLAKE, Julie J.  
; APPLICANT: HO, Ann  
; APPLICANT: ZHENG, Wenjin  
; APPLICANT: GAO, Jing  
; TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS



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; FILE REFERENCE: PF-1279 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/36759
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 60/333,097
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,274
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/340,542
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/342,166
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/347,580
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/348,687
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PERL Program
; SEQ ID NO 83
; LENGTH: 1386
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7506194CBI
PCT-US02-36759-83

Query Match      23.9%; Score 432.8; DB 1; Length 1386;
Best Local Similarity 95.3%; Pred. No. 6.2e-99;
Matches 446; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 5 ACCTGGTGTGGGATCCTGGCGGAGTCAGTGGGGGCGTTTGGCAGCAGACCCCGC 64
DB 662 ACCTGGTGTGGGATCCTGGCGGAGTCAGTGGGGGCGTTTGGCAGCAGACCCCGC 721

QY 65 GCAGCCCTCTGGGCGCTCTGCTGCGCTTCTTGTATACATCGCATACACGCTCC 124
DB 722 GCAGCCCTCTGGGCGCTCTGCTGCGCTTCTTGTATACATCGCATACACGCTCC 781

QY 125 TCCCATCCGCATCGGGGCTCGCGTCTCTCAGCGGCTGGGCGCTCTCACCTTGCATTGTA 184
DB 782 TCCCATCCGCATCGGGGCTCGCGTCTCTCAGCGGCTGGGCGCTCTCACCTTGCATTGTA 841

QY 185 TCTTGGCTGGCAACTTAACCGTGGTATGCCCTTCTCTGGAAGCAGCTCGGTGCCAATG 244
DB 842 TCTTGGCTGGCAACTTAACCGTGGTATGCCCTTCTCTGGAAGCAGCTCGGTGCCAATG 901

QY 245 TGCTGCTGTTCTCTGCACCAAGTCATTAGCATCTGCACACACTATCCAGCAGAGGTGT 304
DB 902 TGCTGCTGTTCTCTGCACCAAGTCATTAGCATCTGCACACACTATCCAGCAGAGGTGT 961

QY 305 CTCAGCGCCAGGCTTTTCAGGAGACCCGCGAGTTACATCCAGGCGCGCTCCACCTGCAGC 364
DB 962 CTCAGCGCCAGGCTTTTCAGGAGACCCGCGAGTTACATCCAGGCGCGCTCCACCTGCAGC 1021

QY 365 ATGAGAAATCGGACGAGGCGGCTGCTGCTGCGTATTTGCCCGCAGCGTTGCCATGG 424
DB 1022 ATGAGAAATCGGACGAGGCGGCTGCTGCTGCGTATTTGCCCGCAGCGTTGCCATGG 1081

QY 425 AGATGAAGAAGACATCAACACAAAAAAGACAGCATGTTCCACAAGA 472
DB 1082 AGATGAAGAAGACATCAATGAGCACTCTCTTCAACAAATTTCCAGATGA 1129

RESULT 4
US-10-144-771-16113
; Sequence 16113, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
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; SEQ ID NO 16113
; LENGTH: 2253
; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-16113

Query Match      19.1%; Score 346; DB 6; Length 2253;
Best Local Similarity 70.4%; Pred. No. 5.4e-77;
Matches 463; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

QY 379 CAGGAGGGGCTGCTGCTGATTTGCCCGCAGCACCTTCCCATGGAGATGAAGAAGAC 438
DB 2 CAGGAGGGGCTGCTGCTGATTTGCCCGCAGCACCTTCCCATGGAGATGAAGAAGAC 61

QY 439 ATCAACACAAAAAAGACAGCATGTTCCACAAGATCTACATACAGAGACGATGACAATGTC 498
DB 62 TTCTTGAAGCCCTTGAGAGGATTTTCAACAAGATTTACATCCAGAGGATGACAATGTC 121

QY 499 AGCATCCTGTTTGCAGACATTTGAGGGCTTCCACGAGCCTGGCATCCCATGTCACCTGCCGAG 558
DB 122 AGCATCCTGTTTGCAGACATCTGTTGGGTTTTCACAGGTTCTGGCGTCCCATGTCACAGCCGAG 181

QY 559 GAGCTGCTCATGACCCCTGAATGAGCTCTTTGGCCCGGTTTTCACAAGCTGGCTGGGAGAAT 618
DB 182 GAGCTGCTGAAGCTGCTCAATGAAGTCTTTGGCAAGTTTCAGATGAGTTAGCCAGGAAAC 241

QY 619 CACTGGCTGAGGATCAAGATCTTTGGGGGACTGTTACTACTGCTGTCAGGCTGCCGAG 678
DB 242 CACTGGCTGAGGATCAAGATCTTTGGGGGACTGTTACTACTGCTGTCAGGCTGCCGAG 301

QY 679 GCCCGGCGCCACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGATTTGAGGCCATC 738
DB 302 CCTAAGACGGATCACGCCCACTGCTGTGTGGAGATGGGACTTGCATGATCGATACCATC 361

QY 739 TCCTGTGCTAGCTGAGTGACAGGTGTAATGTAACATGCGCGTGGGCTCCACAGCGGG 798
DB 362 ACATCCGTGGCTGAGGCTACTGAAGTAGACCTGAACATGCGGTGGGCTTACACCGGC 421

QY 799 CGGCTGCATCGCGGCTGCTTGGCTTGGGAAATGGCAGTTTCGATGTTGTTGCTCAATGAT 858
DB 422 AGGCTCTCTGCTGCTGCTGGGCTACGAAAGTGGCAGTATGATGTTGTTGCTCAATGAT 481

QY 859 GTGACCTGCGCCAAACACATGGAAGCAGGAAAGCGGGCTGGCGGCTATCCACATCACTCGG 918
DB 482 GTGACCTGCGCCAAATGTCATGAGGCTGCTGGCTTACCAGGAAAGTTCACATCACAAAG 541

QY 919 GCACACTCGAGTACCTGACGCGGGACTAGAAAGTGGAGCCAGCCGCTGTTGCCAGCGC 978
DB 542 ACAGCCTCGCGTGTGTAACGGGGACTAGAGGTGGAGCCAGGTGATGGCCATGAGAGG 601

QY 979 AACGCGTACTCTAAGGAGGAGCAGCATTTGAGACTTTTCTCTATCTTGGGCGCCAGCCAGA 1036
DB 602 AACACCTTCTGAGAACTCACACATTTGAGACCTTCTTTATTGTCATCCCATCGGA 659

RESULT 5
US-09-724-676-11593
; Sequence 11593, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11593
; LENGTH: 2949
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-11593

Query Match      18.7%; Score 339; DB 5; Length 2949;
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Best Local Similarity 63.8%; Pred. No. 3.5e-75;  
Matches 552; Conservative 0; Mismatches 300; Indels 13; Gaps 2;

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Qy 228 GCAGCTCGTCCCAATGTGCTGCTTCTCTGCACCAACGCTATTAGCATCTGCACACA 287
Db 819 GGAGATCCTGGCCAACTCTTCTCTACCTGTGCGCCATCTGTGGGCATCATGTCTCTA 878
Qy 288 CTATCCAGCAGAGGTGTCTACGCGCCAGGCTTTCCAGGAGACCCGCACTTACATCCAGGC 347
Db 879 CTACATGCTGACCGCAGCAGCCGAGGCTTCTTGAGGCGCCGCACTGCTGGAGGT 938
Qy 348 CCGGCTCCACCTGACAGCATGAGATCGGCACGAGAGGCGGTGCTGCTGCTGGTATTGCC 407
Db 939 GAAGATCAACTGGAAGACGAGCCAGCAGCAGGAGAACCTCATGCTTTCCATCCTGCC 998
Qy 408 CCAGCAGTTGCCATGGAGATGAAGAGACATCAACACA-----AAAAAGA 455
Db 999 CAAGCAGCTGGCTGACGAGATGCTGAAGACATGAAGAAAGACGAGAGCCAGAGGACCA 1058
Qy 456 AGACATGTTCCACAAGATCTATACAGAAAGCATGACAATGTACGATCCTGTTTGACAGA 515
Db 1059 GCAGCAGTTCAACACCATGTACATGTACCGTACGAGAACTGACGATCCTCTTTGCCGA 1118
Qy 516 CATTGAGGCTTACAGCCTGGCATCCCATGTCAGCTGCGCAGGAGCTGTCATGACCT 575
Db 1119 CATCTGGGCTTTACCCAGCTGCTTCTGCTGCGAGTGCACGAGGAGCTTGTGAAGCTGT 1178
Qy 576 GAATGAGCTCTTCCCGTTTGACAAGCTGGCTGCGGAGAGTCACTCCCTGAGGATCAA 635
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US-09-724-676A-11593  
; Sequence 11593, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: CompuGen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 CompuGen  
; CURRENT APPLICATION NUMBER: US/09/724.676A  
; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 11593  
; LENGTH: 2949  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-11593

Query Match 18.7%; Score 339; DB 5; Length 2949;

Best Local Similarity 63.8%; Pred. No. 3.5e-75;  
Matches 552; Conservative 0; Mismatches 300; Indels 13; Gaps 2;

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Db 1659 CCAGAAATGGCCTCAATGGCTCGGCC 1683
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Qy 667 GGGCTGCCGGAGGCCCGGGCGACCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATG 726  
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Qy 727 ATTGAGGCCATCTCGCTGGGTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGC 786  
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Search completed: February 23, 2003, 07:48:52  
Job time : 376.092 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 22:03:04 ; Search time 2279.13 Seconds  
(without alignments)  
12876.070 Million cell updates/sec

Title: US-09-750-240-3

Perfect score: 1812

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estnu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	593.4	32.7	676	12	BE840188
2	540.2	29.8	581	13	BG993320
3	463.4	25.6	565	12	BG872335
4	442.4	24.4	525	13	BM090325
5	418.6	23.1	682	14	BQ180663
6	393.2	21.7	442	9	AI905602

C	7	393.2	21.7	466	9	AI905641
C	8	392.8	21.7	453	12	BE838164
C	9	387.8	21.4	417	12	BE840138
	10	377	20.8	939	13	BI873142
	11	372	20.5	1016	14	BQ881496
	12	361.8	20.0	625	12	BF369868
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C	15	342.4	18.9	367	10	BE001572
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	18	311	17.2	567	13	BI739363
	19	296.8	16.4	1076	13	BM548851
	20	293.6	16.2	515	14	BQ370137
	21	289.4	16.0	944	9	AL558455
	22	285.4	15.8	770	13	BI562576
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	31	232.4	12.8	1075	12	BF982389
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	33	223	12.3	243	12	BF817426
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ALIGNMENTS

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DEFINITION	BE840188			
ACCESSION	BE840188			
VERSION	BE840188.1	GI:10272566		
KEYWORDS	EST			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 676) Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.			
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)			
MEDLINE	20202663			
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-01q, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001			



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Db 256 CCCTGGCCAAAGCACATGGAGCGAGAGCGGGCTGGCGCATCCACATCACTCGGCAA 315
QY 923 CACTGCAGTAGTACCTGAACCGGGAGCTACCAAGTGGAGCGCAGCCGNGTGGCAAGCGCAACG 982
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QY 1043 AAGAGGAGAAAGGCATCTGGCCAAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGCG 1102
Db 436 AAGAGGAGAAAGGCATCTGGCCAAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGCG 495
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DEFINITION 602792616F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4923890 5',
mRNA sequence.
ACCESSION BG872335
VERSION BG872335.1 GI:14222875
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rcgaps@remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI0845 row: p column: 03
High quality sequence start: 11
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Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 133 a 141 c 174 g 117 t
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Best Local Similarity 91.2%; Pred. No. 2.1e-100;
Matches 515; Conservative 0; Mismatches 46; Indels 4; Gaps 2;

QY 434 AAGACATCACACAAAAAAGAAGAC---ATGTTCCACAGATCTACATACAGAGCATG 490
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Db 1 AAGACATCAACACAAAAAAGAGGACATGATGTTCCATAAGATCTACATCCAGAAGCATG 60
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QY 731 AGGCCATCTCGCTGGTACGTGAGGTGACAGGTGAATGTGAACATGCGCGTGGGCATCC 790
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RESULT 4
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DEFINITION 505523 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
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VERSION BM090325.1 GI:17000953
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 525)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.,
Portea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
JOURNAL 21180013
MEDLINE
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTTCCAGTCACGACG

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## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue procurement: Dr. James Lin, University of Iowa  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)

## FEATURES

Seq primer: pYX-5.  
Location/Qualifiers

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Bonaldi, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured mRNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded  
cDNA was size selected according to mRNA size fraction,  
ligated with EcoR I adaptor, digested with Not I, and then  
cloned directionally into pYX-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is GTGCGTGAA. This library was created for the  
University of Iowa Mouse Brain Molecular Anatomy Project  
(BMAP): 'Gene Discovery in the Developing Mouse Nervous  
System', supported by National Institutes of Mental Health  
(NIMH), Hemlin chin, Ph.D., program coordinator."  
BASE COUNT 142 a 195 c 187 g 156 t  
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Db 61 CTTTACAGCGGCTGGGCTCTCCACCTTGCATTTGATCTTGGCTGGCAACTTAACCGTGG 120  
QY 210 TGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTCTCTGTCGACCAAGCT 269  
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QY 507 GTTTGACAGACATTTGAGGGCTTACAGCGCTGCGATCCAGTGTGCTGCGCAGGAGCTGGT 566  
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Db 481 CATGACCTGAACGAGCTCTTTCCCGGTTTGACAGCTGGCTGC 525

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LOCUS B0180663  
DEFINITION UI-M-EX0-bxb-p-18-0-UI.r1 NIH\_BMAP\_EX0 Mus musculus cDNA clone  
IMAGE:5706065 5', mRNA sequence.

ACCESSION B0180663  
VERSION B0180663.1  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 682)  
TITLE NIH-MGC <http://mhc.nci.nih.gov/>  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

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LOCUS AI905602 442 bp mRNA linear EST 30-MAR-2000
DEFINITION CM-BT094-050299-173 BT094 Homo sapiens cdna, mRNA sequence.
ACCESSION AI905602
VERSION AI905602.1 GI:6495989
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
DIAS Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=CM&t2=CM-BT094-173.html
&t3=050299&t4=1)
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/clone_lib="BT094"
/sex="female"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site:1; SmaI; Site:2;
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 102 a 116 c 136 g 88 t
ORIGIN

Query Match 21.7%; Score 393.2; DB 9; Length 442;
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Best Local Similarity 96.7%; Pred. No. 1.4e-83;
Matches 412; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

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Db 372 TGCCTTCTCCCGGACCAAGGACTCCAGGCTTCCGCCAGATGGGCATTGATATCCAG 313
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QY 1488 GCTAAT 1493
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LOCUS AI905641 466 bp mRNA linear EST 30-MAR-2000
DEFINITION CM-BT094-110299-173 BT094 Homo sapiens cdna, mRNA sequence.
ACCESSION AI905641
VERSION AI905641.1 GI:6496028
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
DIAS Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=CM&t2=CM-BT094-173.html
&t3=110299&t4=1)
Seq primer: puc 18 forward.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="BT094"
/sex="female"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 107 a 125 c 143 g 91 t
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Query Match 21.7%; Score 393.2; DB 9; Length 466;
Best Local Similarity 96.7%; Pred. No. 1.4e-83;
Matches 412; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
QY 1069 CTCACGCGACTCGGCGCAACTCCATCGAAGGCG-TGATGCCGCGATGGTTCTCTGATCG 1127
Db 456 CAGCAGCGACTCGGCGCAACTCCATCGAAGGCGTTGATGCCGCGCTGGTTCTCTGATCG 397
QY 1128 TGCCTTCTCCGCGACCAAGACTCCAAGGCTTCCGCCAGATGGGCAATTGATGATCCAG 1187
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QY 1188 CAAAGACAACCGGGGACCCCAAGATGCCCTGAACCTGAGGATGAGTGGATGAGTTCCT 1247
Db 336 CAAAGACAACCGGGGACCCCAAGATGCCCTGAACCTGAGGATGAGTGGATGAGTTCCT 277
QY 1248 GAGCGGTGCATCGATGCCGCGACGATTCATCAGCTGCCGAGGACCATGTGCCCGGTT 1307
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Db 96 TCTCATCTTCCACACTCCACCTCGATGCTTGGGATCTATGCCAGCATCTTCCCGCTGCT 37
QY 1488 GCTAAT 1493
Db 36 GGAAAT 31
RESULT 8
BE838164/c
LOCUS
DEFINITION
CM1-FN0105-200600-280-f02 FN0105 Homo sapiens linear EST 22-SEP-2000
ACCESSION
BE838164
VERSION
BE838164.1 GI:10270542
KEYWORDS
EST.
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 453)
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
```

```
20202663
MEDLINE
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM1-FN0105-200
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/note="Organ: prostate_normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT 75 a 141 c 134 g 103 t
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Query Match 21.7%; Score 392.8; DB 12; Length 453;
Best Local Similarity 96.7%; Pred. No. 1.7e-83;
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QY 941 GGGACTACGAGTGGAGCGCGGCTGGTGGCAAGCGCAACGCTACCTCAAGGAGCAGC 1000
Db 393 GGGACTACGAGTGGAGCGCGGCTGGTGGCAAGCGCAACGCTACCTCAAGGAGCAGC 334
QY 1001 ACATTGAGACTTTTCTTCATCTCTGGCGCCAGCCAGAAAGAGAGAAAGGCGATGC 1060
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RESULT 9
BE840138/c
LOCUS
DEFINITION
QV0-FN0181-280700-321-d07 FN0181 Homo sapiens cDNA, mRNA sequence.
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BE840138.1 GI:10272516  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 417)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=st2-QV0-FN0181-280  
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High quality sequence start: 10  
High quality sequence stop: 415.

# TITLE JOURNAL MEDLINE COMMENT

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Application No. 196,716 - Ludwig Institute for Cancer  
Research) profiles into the puc 18 vector. Reverse  
transcription of tissue mRNA and cDNA amplification were  
performed under low stringency conditions."  
88 a 119 c 124 g 86 t  
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Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 3.3 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."  
208 a 271 c 256 g 204 t  
BASE COUNT  
ORIGIN

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RESULT 10  
BI873142  
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DEFINITION  
BI873142  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
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house mouse.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 939)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: The Cepko Laboratory  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
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Average insert size 3.3 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."  
208 a 271 c 256 g 204 t  
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ORIGIN

# Query Match Best Local Similarity Matches 521; Conservative 0; Mismatches 160; Indels 8; Gaps 4;

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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
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Seq primer: puc 18 forward  
High quality sequence stop: 625.  
Location/Qualifiers

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application No. 196,716 - Ludwig Institute for Cancer  
Research) profiles into the puc 18 vector. Reverse  
transcription of tissue mRNA and cDNA amplification were  
performed under low stringency conditions."  
128 a 198 c 163 g 136 t

Query Match 20.0%; Score 361.8; DB 12; Length 625;  
Best Local Similarity 77.4%; Pred. No. 4.7e-76;  
Matches 465; Conservative 0; Mismatches 132; Indels 4; Gaps 2;

QY 115 TACAGCTCTCCCTCCGATCCGCGCTGCGCTGCTCCTCAGCGCGCTGCGCTCTCCA-C 173  
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LOCUS  
DEFINITION  
QV4-GN0122-201100-555-h12 GN0122 Homo sapiens cDNA, mRNA sequence.  
ACCESSION  
BG004182  
VERSION  
BG004182.1 GI:12445098  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens

## REFERENCE

AUTHORS  
1 (bases 1 to 611)  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,  
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,  
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.

## TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

## JOURNAL

sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

## MEDLINE

20202663

## COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1-QV4&t2-QV4-GN0122-  
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Location/Qualifiers

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products derived from ORESTES PCR (U.S. Letters Patent  
application No. 196,716 - Ludwig Institute for Cancer  
Research) profiles into the puc 18 vector. Reverse  
transcription of tissue mRNA and cDNA amplification were  
performed under low stringency conditions."  
133 a 162 c 187 g 129 t

## BASE COUNT

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Best Local Similarity 77.5%; Pred. No. 1.5e-72;  
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VERSION
BQ370134.1 GI:21045648
KEYWORDS
EST.
SOURCE
human.
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 673)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
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application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
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Query Match 19.1%; Score 345.8; DB 14; Length 673;
Best Local Similarity 76.4%; Pred. No. 3.3e-72;
Matches 438; Conservative 0; Mismatches 132; Indels 3; Gaps 1;
performed under low stringency conditions."
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ACCESSION
BQ001572.1 GI:8261805
VERSION
BQ001572.1
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SOURCE
human.
ORGANISM
Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 367)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
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GenCore version 5.1.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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5	3379.2	95.2	3582	6	AX189768	Sequence AX189768
6	3156.8	88.9	5877	9	AB007882	Homo sapi AB007882
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13	2743.2	77.3	6036	10	RATADC	L01115 Rattus norv
14	2734	77.0	3465	10	MUSADNLCYC	M96653 Mus musculu
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ALIGNMENTS

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ACCESSION AR174473  
VERSION AR174473.1 GI:17914793  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 3549)  
AUTHORS Hammond H.Kirk., Insel, P.A., Ping, P., Post, S.R. and Gao, M.  
TITLE Gene therapy for congestive heart failure  
JOURNAL Patent: US 6306830-A 5 23-OCT-2001;  
FEATURES Location/Qualifiers

linear PAT 17-DEC-2001

source		1. .3549																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		</	
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Db	3121	GGGCTGAAGCCAGCACCTAGGATCAGGTGGCGCGCTCCACATCACTGCCTGGCTGAC	3180			
Qy	3181	TACCCATGCGGCTCATCGAGCAGATGAAGACACATCAATGAGCACTCCTTTCAACAATTTT	3240			
Db	3181	TACCCATGCGGCTCATCGAGCAGATGAAGACACATCAATGAGCACTCCTTTCAACAATTTT	3240			
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Db	3241	CAGATGAAGATTGGGCTGAACATGCGGCCAGTCGTGCGCAGGTGTCATCGGGGCTCGGAAG	3300			
Qy	3301	CCACAGTATCACATCTCTGGGGAAACACAGTGAATGCTCTTAGTCTGATGGACAGCAGCGGG	3360			
Db	3301	CCACAGTATCACATCTCTGGGGAAACACAGTGAATGCTCTTAGTCTGATGGACAGCAGCGGG	3360			
Qy	3361	GTCCCCAGCCGAATCCAGGTGACCCAGCGACTGTACACAGGTTCTAGCTGCGCAAGGGCTAC	3420			
Db	3361	GTCCCCAGCCGAATCCAGGTGACCCAGCGACTGTACACAGGTTCTAGCTGCGCAAGGGCTAC	3420			
Qy	3421	CAGTGTGAGTGTGAGGGGTGGTCAAGGTGAAGGGCAAGGGGGAGATGACCACTACTTC	3480			
Db	3421	CAGTGTGAGTGTGAGGGGTGGTCAAGGTGAAGGGCAAGGGGGAGATGACCACTACTTC	3480			
Qy	3481	CTCAATGGGGCCCCACAGCTTAACAGGGCCCCAGCCACAATTCAGCTGAAGGACCAAG	3540			
Db	3481	CTCAATGGGGCCCCACAGCTTAACAGGGCCCCAGCCACAATTCAGCTGAAGGACCAAG	3540			
Qy	3541	GTGGGCACCT 3549				
Db	3541	GTGGGCACCT 3549				
RESULT 2						
LOCUS	AX189761	3549 bp	DNA linear PAT 08-AUG-2001			
DEFINITION	Sequence 5 from Patent WO0148164.					
ACCESSION	AX189761					
VERSION	AX189761.1	GI:15143135				
KEYWORDS	human.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
TITLE	1 (bases 1 to 3549)					
JOURNAL	Hammond.H.K. and Gao.M.					
FEATURES	Gene therapy for congestive heart failure					
	Patent: WO 0148164-A 5 05-JUL-2001;					
	THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)					
source	Location/Qualifiers					
	1..3549					
BASE COUNT	/organism="Homo sapiens"					
ORIGIN	/db_xref="taxon:9606"					
Query Match 100.0%; Score 3549; DB 6; Length 3549;						
Best Local Similarity 100.0%; Pred. No. 0;						
Matches 3549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	1	ATGTCATGGTTTACTGGCTCTCTGGTCCCTAAAGTGGATGACCGAAAAACAGCCTGGGGT	60			
Db	1	ATGTCATGGTTTACTGGCTCTCTGGTCCCTAAAGTGGATGACCGAAAAACAGCCTGGGGT	60			
Qy	61	GAACGCAATGGCGAAGAGCGTTTCGCGCGCGCTGGCACTCGGGCAGGTGCTTCGACG	120			
Db	61	GAACGCAATGGCGAAGAGCGTTTCGCGCGCGCTGGCACTCGGGCAGGTGCTTCGACG	120			
Qy	121	CCCGCTATATGAGCTGCCTCCGGGATGCGAGCCACCCAGCCCCACCTTCGGGGCCCC	180			
Db	121	CCCGCTATATGAGCTGCCTCCGGGATGCGAGCCACCCAGCCCCACCTTCGGGGCCCC	180			
Qy	181	CCTCGGTGCCCTTGGCAGGATGAGCCCTTCATCCGGAGGGCGGCCAGGCAAGGGCAAG	240			
Db	181	CCTCGGTGCCCTTGGCAGGATGAGCCCTTCATCCGGAGGGCGGCCAGGCAAGGGCAAG	240			

QY 241 GAGCTGGGCTGGGCACTGGCCCTCGGGCTTCGAGATACCGAGTGACAAACGACGG 300  
|||||  
Db 241 GAGCTGGGCTGGGCACTGGCCCTCGGGCTTCGAGATACCGAGTGACAAACGACGG 300  
QY 301 GGGGGACGGCTGAGTGGGCGCCCGACGGCGTGCCAGAGTGGGATCCTGCTGGCG 360  
|||||  
Db 301 GGGGGACGGCTGAGTGGGCGCCCGACGGCGTGCCAGAGTGGGATCCTGCTGGCG 360  
QY 361 CPTTGGTCAGGTGTCAGTGAAGCAGTCCGTTGCGGCCAAGCTGAGCGCCCTGTAC 420  
|||||  
Db 361 CGTTGGTCAGGTGTCAGTGAAGCAGTCCGTTGCGGCCAAGCTGAGCGCCCTGTAC 420  
QY 421 CAGCGTACTTTTCCAGATGAACCAAGACAGCCTGACGCTGCTGGCGGTGCTGGTG 480  
|||||  
Db 421 CAGCGTACTTTTCCAGATGAACCAAGACAGCCTGACGCTGCTGGCGGTGCTGGTG 480  
QY 481 CTGCTCACAGCGTGTCTGGCTTTTCCAAGCGCACCGCGCCCTCAGCCTGCTCTAT 540  
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Db 481 CTGCTCACAGCGTGTCTGGCTTTTCCAAGCGCACCGCGCCCTCAGCCTGCTCTAT 540  
QY 541 GTGGCACTGTGGCCCTGTGCGCGCCCTGTTCTGTTGGGCTCATGTTGTTGTAACCG 600  
|||||  
Db 541 GTGGCACTGTGGCCCTGTGCGCGCCCTGTTCTGTTGGGCTCATGTTGTTGTAACCG 600  
QY 601 CATAGTTCGGCGAGACTCCATGTTGGGTGGTGAAGTAACTGTTGTTGGGCAATTAACCG 660  
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Db 601 CATAGTTCGGCGAGACTCCATGTTGGGTGGTGAAGTAACTGTTGTTGGGCAATTAACCG 660  
QY 661 GCAGTCAGTGGGGCGCTTTCGACGACAGACCGCGCGCCCTCTCGGGCCCTCTGG 720  
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Db 661 GCAGTCAGTGGGGCGCTTTCGACGACAGACCGCGCGCCCTCTCGGGCCCTCTGG 720  
QY 721 TGCCCTGTGTTCTTATACATCGCATACAGCTCCTCCCATCGCATCGGGCTGCC 780  
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Db 721 TGCCCTGTGTTCTTATACATCGCATACAGCTCCTCCCATCGCATCGGGCTGCC 780  
QY 781 GTCCCTCAGCGGCTGGGCTCTCCACCTTGCAATTTGATCTTGGCCTGGCAACTTAACCG 840  
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Db 781 GTCCCTCAGCGGCTGGGCTCTCCACCTTGCAATTTGATCTTGGCCTGGCAACTTAACCG 840  
QY 841 GGTGATGCCCTCTCTGGAAGCAGCTCGGTGCCAATGTCGTCTCTGTCGACCAAC 900  
|||||  
Db 841 GGTGATGCCCTCTCTGGAAGCAGCTCGGTGCCAATGTCGTCTCTGTCGACCAAC 900  
QY 901 GTCAATTAGCATCTGCACACACTATCCAGCAGAGTGTCTCAGCGCCAGGCTTTCAAGAG 960  
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Db 901 GTCAATTAGCATCTGCACACACTATCCAGCAGAGTGTCTCAGCGCCAGGCTTTCAAGAG 960  
QY 961 ACCCGAGTTACATCCAGGCGCGGCTCCACCTGCAGCATGAGAATCGGACGAGGCGG 1020  
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Db 961 ACCCGAGTTACATCCAGGCGCGGCTCCACCTGCAGCATGAGAATCGGACGAGGCGG 1020  
QY 1021 CTGCTCTCTCGTATTGCCCGAGCAGTTGCCATGGAGTGAAGAAGACATCAACACA 1080  
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Db 1021 CTGCTCTCTCGTATTGCCCGAGCAGTTGCCATGGAGTGAAGAAGACATCAACACA 1080  
QY 1081 AAAAAAGAGACATGTTCCACAAGATCTACATACAGAAGCATGACAAATGTCAGCATCTG 1140  
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Db 1081 AAAAAAGAGACATGTTCCACAAGATCTACATACAGAAGCATGACAAATGTCAGCATCTG 1140  
QY 1141 TTTGACAGATTGAGGGCTTACACAGCCTGGCATCCAGTGCAGTGGCAGGAGCTGGTC 1200  
|||||  
Db 1141 TTTGACAGATTGAGGGCTTACACAGCCTGGCATCCAGTGCAGTGGCAGGAGCTGGTC 1200  
QY 1201 ATGACCTCAATGAGCTCTTGCCTGGTTGACAAGCTGGCTCGGAGAACTCACTGCCCTG 1260  
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Db 1201 ATGACCTCAATGAGCTCTTGCCTGGTTGACAAGCTGGCTCGGAGAACTCACTGCCCTG 1260  
QY 1261 AGGATCAAGATCTTGGGGACTGTTACTACTGTGTGTGTCAGGGCTGCGGAGGCCGGGCC 1320  
|||||  
Db 1261 AGGATCAAGATCTTGGGGACTGTTACTACTGTGTGTGTCAGGGCTGCGGAGGCCGGGCC 1320

QY 1321 GACCATTGCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTGGTA 1380  
|||||  
Db 1321 GACCATTGCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTGGTA 1380  
QY 1381 CGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGATCCACAGCGGGCGCTGCAC 1440  
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Db 1381 CGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGATCCACAGCGGGCGCTGCAC 1440  
QY 1441 TCGGGCTCTCTTGGCTTGGGAATGCGAGTTCGATGTGTGGTCCCAATGATGTGACCCCTG 1500  
|||||  
Db 1441 TCGGGCTCTCTTGGCTTGGGAATGCGAGTTCGATGTGTGGTCCCAATGATGTGACCCCTG 1500  
QY 1501 GCCAACACATGGAAGCAGGAAGCGGGCTGGCCGATCCACATCATCTCGGGCAACACTG 1560  
|||||  
Db 1501 GCCAACACATGGAAGCAGGAAGCGGGCTGGCCGATCCACATCATCTCGGGCAACACTG 1560  
QY 1561 CAGTACCTGAACGGGACTACGAAGTGGAGCCAGGCGGTGGTGGCAAGCCACGCGGTAC 1620  
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QY 1621 CTCAAGGAGCAGCACATTGAGACTTTCTCTATCTCTGGCGCCAGCCAGCAAAACGAAAGAG 1680  
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Db 1621 CTCAAGGAGCAGCACATTGAGACTTTCTCTATCTCTGGCGCCAGCCAGCAAAACGAAAGAG 1680  
QY 1681 GAGAAAGGATGTCGCCAAGCTGACGAGACTTCGGGGCAACTTCCATGGAAGGGCTGATG 1740  
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Db 1681 GAGAAAGGATGTCGCCAAGCTGACGAGACTTCGGGGCAACTTCCATGGAAGGGCTGATG 1740  
QY 1741 CGCGATGGTTCCTGATCGTCCGACCAAGGACTTCCAAAGGCTTCCGCCAG 1800  
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Db 1741 CGCGATGGTTCCTGATCGTCCGACCAAGGACTTCCAAAGGCTTCCGCCAG 1800  
QY 1801 ATGGGCTTATGATTTCCAGCAAAAGCAACCGGGGCAACCAAGATCCCTGAAACCTTGAG 1860  
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Db 1801 ATGGGCTTATGATTTCCAGCAAAAGCAACCGGGGCAACCAAGATCCCTGAAACCTTGAG 1860  
QY 1861 GATGAGGTGGATGAGTTCCTGAGCCGTGCATGATGTCGCCGAGCATGATGAGTGGCG 1920  
|||||  
Db 1861 GATGAGGTGGATGAGTTCCTGAGCCGTGCATGATGTCGCCGAGCATGATGAGTGGCG 1920  
QY 1921 AAGGACCATGTGCGCGGTTTGTGCTACCTTCCAGAGAGAGATTTTCCAGAAAGTAC 1980  
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Db 1921 AAGGACCATGTGCGCGGTTTGTGCTACCTTCCAGAGAGAGATTTTCCAGAAAGTAC 1980  
QY 1981 TCCCGAAGGTGGATCCCGCTTCGGAGCTAGTTCCTGTCCTGTCCTGTTGTTCTCTGC 2040  
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QY 2041 TTCATCTGCTTATCCAGCTTCTAATTTTCCACACTCCACCTGATGCTTGGGATTTAT 2100  
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QY 2101 GCAGCATCTCTGCTGCTGCTAATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160  
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QY 2221 AGCAGCGAGTGGGATCTTTCCCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280  
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QY 2281 TTCACCTGTAACACACACCCCAATACCGAGCTGTGAGCCCGGATGCTGAATTTAACACCT 2340  
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QY 2341 GGTGACATCACTGCTGCGCACCTGACAGCTCAATTAATCTCTGCGGCTTGGATGCTCCC 2400  
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QY 2401 CTGTGTGAGGGACCAATGCCACCTGCTGAGGTGCTCCATCGGGAAACATGCTG 2460



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Db 2581 TTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAAATGAGACCTTT 2640  
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Db 2641 GATGGGCTGACCTGCTCAGCTGAGGGAGGCTGCCCTCAATATATGACCCCTGTGATT 2700  
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QY 2701 CTGCTGTGTCTTGGCTGGCGCTGTATCTCATCTGCTCAGCAGGTGGAATCGACTGCCCGC 2760  
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QY 2821 GCATACACCGGAGGCTGCTGCATACATCTGCCAAGGACGTGGCGGCCACTTCCCTG 2880  
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Db 2881 GCCCGGAGCGCGCAATGATGAACCTACTATCAGTCGTGTGAGTGTGGTGTATTG 2940  
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|||  
QY 3061 GAGCGGTTCCGGAGCTGGAAGATCAAGACGATTTGGTAGCACTACATGGCTGCTCA 3120  
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|||  
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QY 3241 CAGATGAAGATTGGGCTGAACATGGGCCAGTCTGTCAGGAGTGTATCGGGGCTCGGAAG 3300  
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Db 3541 GTGGGCACT 3549  
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RESULT 3  
AX189766 AX189766 3552 bp DNA linear PAT 08-AUG-2001  
LOCUS Sequence 10 from Patent WO0148164.  
DEFINITION AX189766  
ACCESSION AX189766  
VERSION AX189766.1 GI:15143139  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 3552)  
AUTHORS Hammond,H.K. and Gao,M.  
TITLE Gene therapy for congestive heart failure  
PATENT: WO 0148164-A 10 05-JUL-2001;  
JOURNAL THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
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AUTHORS	Wicker R., Gascon Catalan A., Cailieux A.-F., Starenki D., Stengel D., Sarasin A. and Suarez H.G.		
TITLE	Direct Submission		
JOURNAL	Submitted (28-MAR-2000) Lab Etude des Relations - Instabilite genetique et Cancer UPR 2169, Institut de Recherches sur le Cancer CNRS IFR 1221, 7 rue Guy Moquet, Villejuif 94801, France		
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VERSION AX189768.1 GI:15143140  
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REFERENCE 1 (bases 1 to 3582)  
AUTHORS Hammond, H. K. and Gao, M.  
TITLE Gene therapy for congestive heart failure  
JOURNAL Patent: WO 0148164-A 12 05-JUL-2001;  
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REFERENCE 1  
AUTHORS Ishikawa,K., Nagase,T., Nakajima,D., Seki,N., Ohira,M., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.  
TITLE Prediction of the coding sequences of unidentified human genes. VIII. 78 new cDNA clones from brain which code for large proteins in vitro  
JOURNAL DNA Res. 4 (5), 307-313 (1997)  
MEDLINE 98116655

9455477  
2 (bases 1 to 5877)  
Ohara,O.  
Direct Submission  
Submitted (06-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology, Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel: +81-438-52-3913, Fax: +81-438-52-3914)  
On May 9, 2002 this sequence version replaced gi:2887418.  
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1 (bases 1 to 4046)  
Katsushika, S., Chen, L., Kawabe, J., Nilakantan, R., Halnon, N.J.,  
Homcy, C.J. and Ishikawa, Y.  
Cloning and characterization of a sixth adenylyl cyclase isoform:  
types V and VI constitute a subgroup within the mammalian adenylyl  
cyclase family  
Proc. Natl. Acad. Sci. U.S.A. 89 (18), 8774-8778 (1992)  
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ACCESSION 129958
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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4046)
AUTHORS Ishikawa,Y.
TITLE Cloning and characterization of a cardiac adenylyl cyclase
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JOURNAL Patent: US 5578481-A 1 26-NOV-1996;
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ORGANISM Mus musculus  
REFERENCE 1  
AUTHORS Ishikawa,K., Asai,S., Takahashi,Y., Nagata,T. and Ishii,Y.  
TITLE Method for examining ischemic conditions  
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School Juridical Person Nihon University (JP)  
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Db 2967 CTGGCCCGGAGCGCGCAACGATGAGCTGTACTACAGTCTGTGAATGTGTGGCTGTC 3026  
QY 2938 ATGTTTTCCTTCCATTTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAACAATGAG 2997  
Db 3027 ATGTTTTCCTTCCATGCCAAATTTCTCGGAGTTCTACGTGGAGCTCGAGGCAACAACGAG 3086  
QY 2998 GGTGCGAGTGTCTCGGCTGTCAACGAGATCATCGTGTACTTGTATGAGATTTACAG 3057  
Db 3087 GGTGCGAGTGTCTCGGCTGTCAATGAGATCATCGCAGACTTTGACGAGCATCATCAGT 3146  
QY 3058 GAGGAGCGTTCCGGCAGCTTGGAAAAAGATCAACACATTTGGTAGCACCTACATGGCTGCC 3117  
Db 3147 GAGGAGAGATTCGGCAGTTGGAGAAAGATCAAGACCATCGGTAGCACCTACATGGCCGCC 3206  
QY 3118 TCAGGCTGAAGCCACGACCTACGATCAGGTGGGCGCTCCACACATCACTGCGCTGGCT 3177  
Db 3207 TCTGGCTTAAATGCCAGCACCTATATACAGGTGCGGCCCTCACACATCACGGCGCTGGCT 3266  
QY 3178 GACTACGCCATGGGCTCATGAGCAGATGAAGCAGCATCAATGAGCAGCTTCTTCAACAAT 3237  
Db 3267 GACTACGCCATGGGCTCATGAGCAGATGAACACATCAATGAACACTCTTTTCAACAAT 3326  
QY 3238 TTTCCAGATGAAGATTCGGCTGAACATGGGCCAGTGTGGCAGGTGTCTACGCGGCTCGG 3297  
Db 3327 TTTCCAGATGAAGATTCGGCTGAACATGGGTGCGGTGTGAGCAGCGCTCATTTGGGGCCGA 3386  
QY 3298 AAGCCACAGTATGACATCTGGGGAAACACAGTGAATGTCTCTAGTCTGTATGGACAGCAG 3357  
Db 3387 AAGCCACAGTATGACATCTGGGGAATACCGTGAATGTTTCCAGTCTGTGGACAGCACT 3446  
QY 3358 GGGGTCCCCACCGAATCAGGTGACCGAGCTCTACAGGTTCTAGTGTCCAGAGGC 3417  
Db 3447 GGAGTTCTCAGCGAATACAGGTGACTACGGACTATACCGGTTCTAGTGTCCAAAGGC 3506  
QY 3418 TACCAGCTGAGTGTGAGGGGTGTCAGGTGAAGGCAAGGGGAGATGACCACTAC 3477  
Db 3507 TACCAGCTGAGTGTGAGGGGTGTCAGGTGAAGGAAAGGGGAGATGACCACTAC 3566



Qy	3478	TTCTCTCAATGGGGGGCCCCCAGCAGTATTACAGAGGCCCCAGCCAC	-AAATTACAGCTGAGGGAC	3536
Db	3567	TTCTCTCAAGGGGGGGCCCCCAGCAGTATTAGCAGAGTGCGAGCGCTGAGATT	CAACCCGAAGGAC	3626
Qy	3537	CAAGGTGGGCCT	3549	
Db	3627	CAAGGTGGGCATT	3639	

RESULT 10	
MUSADCYC	
LOCUS	MUSADCYC 5841 bp mRNA linear ROD 27-APR-1993
DEFINITION	Mouse adenylyl cyclase type VI mRNA, complete cds.
ACCESSION	M93422
VERSION	M93422.1 GI:191690
KEYWORDS	adenylyl cyclase; adenylyl cyclase type VI.
SOURCE	Mus musculus cDNA to mRNA.
ORGANISM	Mus musculus
REFERENCE	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE	1 (bases 1 to 5841)
	Yoshimura, M. and Cooper, D.M.
	Cloning and expression of a Ca(2+)-inhibitable adenylyl cyclase
	from NCB-20 cells
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 89 (15), 6716-6720 (1992)
MEDLINE	92357702
PUBMED	1379717

BASE COUNT	1214 a	1558 c	1673 g	1396 t
ORIGIN	KVAAGRGEMILIFLNGRGSS			
Query Match	77.9%; Score 2765; DB 10; Length 5941;			
Best Local Similarity	87.1%; Pred. No. 0;			
Matches 3095; Conservative	0; Mismatches 445; Indels 13; Gaps 5;			

Qy	121	CCCCGGTATATAGAGCTCGCTCCGGGATGACAGAGCACCCAGCCACCCCTGCGGGCCCC	180
Db	213	CCTCGCTACATGAGCTCGCTCAAGAATCGGGAGCCACCCAGCCCACTCTTCGAGCTCAC	272
Qy	181	CTCTGGTGGCCCTGGCAGATGACGCCTTCATCCGGAGGGCGGCCAGGCAAGGCAG	240
Db	273	ACTCGGTGCCCTTGGCAGATGAAGCCTTCATCAGAGGGCGGGCCGGCAGGGGTGTG	332
Qy	241	GAGCTGGGGCTGCGGCAGTGGCCCTGGCTTCGAGGATACCGAGGTGACACAGACAGC	300
Db	333	GAGCTGGGGCTGCGGTCAGTGGCCTTGGGGTGTGACGACACTGAGTGAACCAACCGATG	392
Qy	301	GGCGGACGCTGAGCTGGCGCCGACGCGGTGCCAGAGTGGGGATCCTGCTGGCGC	360
Db	393	GGC---ACAGCTGAAGTGACCGGATACATCGCTCGGAGGGTCCGTCTCTCTGGCAC	449
Qy	361	CGTTTGGTGCAGGTGTTCCAGTCAAGCAGTTCGGTTCGGCCAAAGCTGAGCGCTGTAC	420
Db	450	CGCTTGTGACGTGTTCCAGTCAAGCAGTTCGGCTCTGCCAAGCTGAGCGGCTGTAC	500
Qy	421	CAGCGGTACTTTTCCAGATGAACAGACAGCTGACGCTGCTGGTGGCGGTGCTGGT	480
Db	510	CAGCGGTACTTCTTCCAGATGAACAGACAGCCTCACGCTCATGCGGTGCTGGT	569
Qy	481	CTGCTCACACGCGTGTCTGGCTTTCAAAGCGCACCGCCGCGCTCAGCTTCCCTAT	540
Db	570	CTGCTCATGCTACTATGTGTGACTTCCAGCTGCGCTGCCAGCCTCAGCCTGCTTAC	629
Qy	541	GTGGCACTGTGGCCTGTGCGCGGCCCTGTCTGTGGGGCTCATGTTGGTGTAAACGG	600
Db	630	GTGGCCCTGTGACCTGTGCTCTGTCCTTTTGTGGTACTCATGGTGTGTGAACGA	689
Qy	601	CATGAGTTCGCGCAGACACTCAATGTGGGTGTGACTTAAGCTGGTCTGGGCATCTGGG	660
Db	690	CACAGCTTCGCGCAGACTCCATGTGGGTGTGAGCTATGTGGTCTGGGCATCTGACA	749
Qy	661	GCAGTTCGCGCAGGTCGGGGCGCTTTCGCAGACAGCCGCGACGCCCTCTGCGGGCCTCG	720
Db	750	GCCTGCAAGTCGGGGTGGCTTGGCAGCAATCCACACAGCCCCCTGCGCGGCCTTTGG	809
Qy	721	TGCCCTGTGTTCTTTGTATACATCGATACACGCTCCTCCCATCGCATGGGGCTGCC	780
Db	810	TGCCCGGTGTTCTTCTGTACATCACCTACACTCTCTTCCCATTCGATGGAGCCGCA	869
Qy	781	GTCTCAGCGCCTGGGCCTCTCCACTTGCATTTGATCTGGCCTGGCAACTTAACGT	840
Db	870	GTACTCAGCGCCTGGGCCTCTCTACTCTGCATTTGATTTTGGCCTGGCAGCTCAACGC	929
Qy	841	GGTGATGCCCTTCTCTGGAAAGCAGCTCGGTGCCAATGTGCTGTCTCTGCAACCAAC	900
Db	930	AGCGACCCCTTCTTTTGGAAAGCAGCTCGGTGTGAAGTGTGCTCTCTCTGCAACCAAT	989
Qy	901	GTCAATTAGCATCTGCACACTATCCAGACAGGTGCTCTCAGCGCAGGSCCTTTCCAGAG	960
Db	990	GCCATCGGTGTCTGCACACACTACCTGCTGAAGTGTCTACGGCCAGAGCTTTTCAGAG	1049
Qy	961	ACCGCAGTTTACATCCAGGCGCCGGCTCCACCTGCAAGTGAAGTGGCAGCAGGAGCGG	1020
Db	1050	ACCGAGGTTTACATCCAGGCGCGGCTGCACCTGCAGCATGAGAACCGTCAGCAGAACGG	1109
Qy	1021	CTGCTGCTGTGCGTATTGCCCGCAGCAGTTGCCATGGAGATGAAGAGACATCAACACA	1080
Db	1110	CTGCTGCTATTCGTTGTGCCCGCAGCAGTTGCCATGGAGATGAAGAGACATCAACACA	1169
Qy	1081	AAAAAAGAAC--ATGTTTCCACAAGATCTACATACAGAAGCATGACAAATGTCAGCATC	1133
Db	1170	AAAAAGAGCAGCATGATGTTTCCATAGATCTACATCCAGACATGATAATGTCAGCATC	1229
Qy	1138	CTGTTTGCAGACATTCAGGGCTTCCACGCTGGCATTCACAGTGCAGTGCAGGAGGTG	1199
Db	1230	CTGTTTGCAGACATTCAGGGCTTCCAGCAGCTGGCTCCGCTCCAGTGCAGTGCAGGAGCT	1289

QY 1198 GTCATGACCCGTGAATGAGCTCTTTGGCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGC 1257  
DB 1290 GTCATGACCTTTGAATGAGCTCTTTGGCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGT 1349  
QY 1258 CTGAGGATCAAGATCTTTGGGGACTGTTACTACTGTGTGTCAGGGCTGCGGGAGGCCCGG 1317  
DB 1350 CTGAGGATCAAGATCTTAGGAGACTGTTACTACTGGGTGTGACGGCTGCGCGAGGCCCGG 1409  
QY 1318 GCGGACCATGCCACATGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG 1377  
DB 1410 GCAGATACGCCACATGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG 1469  
QY 1378 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGGTGGGCATCCACAGCGGGCGGTG 1437  
DB 1470 GTCCGTGAGGTAAACAGGTGTGAACGTGAACATGCGGTGGGCATCCACAGCGACGTGTG 1529  
QY 1438 CACTGCGGGCTCCTTGGCTTGGCGAATGGCAGTTTCGATGTGTGGTCCAAATGATGACC 1497  
DB 1530 CATTTGGGGCTCCTTGGCCCTACGGAAATGGCAGTTTTCGATGTGTGGTCAACAGCATGTGACC 1589  
QY 1498 CTGGCCAAACCACATGGAAGCAGCAAGCCGGCTGGCGCATCCACATCACTCGSGCAACA 1557  
DB 1590 CTGGCTAAACACATGAGGCGGGGGG- --GGCCGGGCATCCACATCACTCGGGCTACA 1646  
QY 1558 CTGCACTACTGAACGGGGACTACGAAGTGGAGCCAGGCGGTGGTGGCAAGCCCAACGGC 1617  
DB 1647 CTCGACTACTTGAACGGGACTATGAGGTGGAGCCAGGCGGTGGTGAACCAATGCG 1706  
QY 1618 TACCTCAAGAGCAGACATTTGAGACTTTCCTCATCTCTGGGCCACAGCCCAAGCAAGAA 1577  
DB 1707 TACCTCAAGAGCAGTGCATTTGAGACTTTCCTCATCTTGGCCCAAGCCCAAAACAGGAA 1766  
QY 1678 GAGGAGAAAGGCATGCTGGCCAAAGTGCAGCGACTTCGGGCCAACTCCATGGAAGGCGTG 1737  
DB 1767 GAGGAGAAAGCCATGCTGGCCAAAGTGCAGCGACTTCAGCGACACAGGGCCAACTCCATGGAAGACTG 1826  
QY 1738 ATGCCCGATGGTTCCTGATCTGTGCTTCTCCCGGACCAAGGACTCCAAGGCTTTCGCG 1797  
DB 1827 ATGCCCGCTGGGTTCTTGACCGTGTCTTCCCGGACCAAGGACTCTAAGGCAATTCGCG 1886  
QY 1798 CAGATGGCATTCATATCCACGAAGACCAACCGGGGACCCCAAGATGCCCTGAAACCT 1857  
DB 1887 CAGATGGCATTCATATTCAGCAAGACCAACCGGGGTGCCCAAGATGCTCTGAACCT 1946  
QY 1858 GAGGATGAGGTGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTTGATCAGCTG 1917  
DB 1947 GAAGATGAGGTGATGATTCCTTGGCCGAGCCATCGATGCCCGGAGCATCGACCAACTG 2006  
QY 1918 CGGAAGACCATGTGCGCGGTTTTTGTCTACCTTCCAGAGAGGATTTTGAGAAGAAG 1977  
DB 2007 CGTAAGGACCATGTGCGCGGTTCTGCTCACCTTCCAGAGAGGATCTTGAGAAGAAG 2066  
QY 1978 TACTCCCGAAGTGTGATCCCGCTTCGAGCCATAGTTGCTGCTGCCCTGTGGTCTTC 2037  
DB 2067 TATTCAGGAAGTAGATCCTCGCTTCGAGCCATAGCTCGCTGCTGCCCTGTGGTGT 2126  
QY 2038 TGTCTCATCTGCTTCATCGAGCTTCATTTTCCACACTCCACCTCGATGCTTGGGAT 2097  
DB 2127 TGTCTCATCTGTTTTATCAGCTCCTGTGTGTTCCCATACTCCACCTGATCTACGCGGAT 2186  
QY 2098 TATGCCAGCATCTCCTGTGCTGTGCTAATCACCGTCTGATCTGTGCTGTACTCCTGT 2157  
DB 2187 TATGCCGCTATCTCTCTGCTGTGGTGGTCACTGTGCTGATCTGTGCGGTGTGCTCCTG 2246  
QY 2158 GGTTCCTGTTCCCTAAGGCCCTGCAAGCTCTGTCCCGCAGGATTTGCTCGCTCACGGCA 2217  
DB 2247 GGTTCCTTCTCCCAAGGCCCTGCAAGCGCTGTCCGCAATATTCTCGCTCACGGGTG 2306  
QY 2218 CATAGCACCGCATTTGGCATCTTTTCCGCTCCTGCTTGTGTTTACTTCTGCAATTCGAAC 2277  
DB 2307 CACAGCACCGGTTGGATCTTCTCGGTCTGCTGTGTTCTATCTCTGCCATCGCCAAC 2366  
QY 2278 ATGTTCACTGTAAACCACACCCCATACGAGACTGTGCAAGCCGGATGTGAATTTAACA 2337

DB 2367 ATCTTTACCTGTAAATCACACCCCAATAAGGACCTGGCGGCCGATGCTGAATTTAACA 2426  
QY 2338 CCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAATTTACTCTCTGGGCCCTGGATGCT 2397  
DB 2427 CCAGCGGATGTCAACCGCTGCCACCTACAACAGCTCAATTTACTCTCTGGGACTGGATGCT 2486  
QY 2398 CCCCTGTGTGAGGGCACCATGCCACCTGCAGCTTTCTCGAGGTGTCATCGGGAACATG 2457  
DB 2487 CCCCTGTGTGAGGGCACCGCACCCACCTGCAGCTTCCCTGAGTACTTCTCGGGAAGCTG 2546  
QY 2458 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCTGACATCAAGCAGCATCGGGAAGTTGGCC 2517  
DB 2547 CTGCTGAGTCTTCTAGCAGCTCTGTCTTCTACACATCAAGCAGCATCGGGAAGCTGGCC 2606  
QY 2518 ATGATCTTGTCTTGGGGCTCATCTATTTGGTGTCTCTGCTGGGTCCCCCAGCGGCC 2577  
DB 2607 ATGACCTTCACTCTTGGGGTTTCACTTCTTGGTGTCTCTTGTGGGTCCCCCGCGGCC 2666  
QY 2578 ATCTTTGACAACATGACCTTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC 2637  
DB 2667 ATCTTTGACAACATGATCTACTGCTTGGCTCCATGGCTTGGCTTCTTCCAATGAGACC 2726  
QY 2638 TTTGATGGGTGACTGTCCAGCTGCAGGAGGTGGCCCTCAAAATATATATGACCCCTGTG 2697  
DB 2727 TTTGATGGGTGACTGCCAGCTGTGGGAGGTAGCGCTCAAAATATATATGACCCCGTG 2786  
QY 2698 ATTCTGCTGGTGTGGGTGGCGCTGTATCTGCATGCTCAGCAGGTGGGAATGCACTGCC 2757  
DB 2787 ATTCTGCTGGTGTGGGTGGCGCTGTATCTGCATGCAACAGAGTGGGAATCGACTGCC 2846  
QY 2758 CGCTTAACTTCTCTGGAACCTACAGGCAACAGGGGAAAAAGAGAGATGGAGGAGCTA 2817  
DB 2847 CGCTGGACTTCTGTGGAGATTACAGGCAACAGGGGAGAGAGAGATGGAGGAGCTA 2906  
QY 2818 CAGGCATACAACCGAGGTGCTGCATAACATTTCTGCCCAAGAGCTGGGGGCCCACTTC 2877  
DB 2907 CAGGCATACAACCGAGGTGCTGCATAACATTTCTCCCAAGGACGTGGCGGCCCACTTC 2966  
QY 2878 CTGGCCCGGAGCGCGCAATGATGAACCTACTATCAGTCGCTGAGTGTGGTGGCTGTT 2937  
DB 2967 CTGGCCCGGAGCGCGCAACGATGAGCTGTACTACAGTCTGTGAATGTGGTGTGTC 3026  
QY 2938 ATGTTTGCCTCCATTTGCCAATTTCTCTGATTTCTATGTGGAGCTGGAGGCAACAATGAG 2997  
DB 3027 ATGTTTGCCTCCATTTGCCAATTTCTCGGAGTTCTACGTGGAGCTCGAGGCAACAACGAG 3086  
QY 2998 GGTGCCAGTGTGCTGCGGTGCTCAAGAGATCATCGTGCAGCTTTGATGAGATTTACAGC 3057  
DB 3087 GGCCTGGAGTGTGCGGTGCTCAATGAGATCATCGCAGACTTTGACGAGATCATCAGT 3146  
QY 3058 GAGGAGCGTTCCGGCAGCTGGAAAAAGATCAACAGATTTGGTAGCACCTACATGGCTGCC 3117  
DB 3147 GAGGAGATTTCCGGCAGTTGGAGAGATCAAGACCATCGGTAGCACCTACATGGCGGCC 3206  
QY 3118 TCAGGCTCAACGCCAGCACCTACGATCAGTGGGGCGCTCCCAACATCACTGCGCTGGCT 3177  
DB 3207 TCTGGCTAAATGCCAGCACCTATGACCAGTTCGGCGCTCACACATCAGCGCGCTGGCT 3266  
QY 3178 GACTAGCCATCGGCTCATGAGCAGATGAAGCAGCATCAATGAGCAGCTCTTTCAACAAT 3237  
DB 3267 GACTATGCCATCGGCTCATGAGCAGATGAACACATCAATGAACACTCTTTCAACAAT 3326  
QY 3238 TTCCAGATGAAGATTTGGCTGAACATGGGCCAGTGGCAGGTGCTCATCGGGGTCCG 3297  
DB 3327 TTCAGATGAAGATTTGGGTGAACATGGGTTCGGTTCGATGAGCAGCGTCAATGGGGCCGA 3386  
QY 3298 AAGCCAGATGACATCTGGGGAAACAGTGAATGTCTCTAGTGTGATGGAGCAGCAG 3357  
DB 3387 AAGCCAGATGACATCTGGGGAAATACCGTGAATGTTTCCAGTCTGTATGAGACAGCT 3446  
QY 3358 GGGGTCCCGACCGAATCAGGTGACGACGACCTGTACCAGGTTCCTAGTGTCCAGGGC 3417



Db 3447 GGAGTTCTTCCAGCCGAATACAGGTGACTACGAGCACTATACAGGTCTTAGCTGCAAGGCG 3506

Qy 3418 TACCAGCTGGAGTCTCAGGGGTGCTCAAGGTGAAGGCAAGGGAGAGATCAACACCTAC 3477

Db 3507 TACCAGCTGGAGTCTCAGGGGTGCTCAAGGTGAAGGCAAGGGAGAGATCAACACCTAC 3566

Qy 3478 TTCTTCAATGGGGGCCCCAGCAGGTAAACAGGGCCAGCCAC-AAATTCAGCTGAAGGAC 3536

Db 3567 TTCTTCAACGGGGGCCCCAGCAGTTAGCAGAGTGCAGCAGCTGAGATTCAACCCAGGAC 3626

Qy 3537 CAAGGTGGGCACT 3549

Db 3627 CAAGGTGGGCATT 3639

RESULT 11

LOCUS AR106659 4131 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 11 from patent US 6107076.

ACCESSION AR106659

VERSION AR106659.1 GI:12821189

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 4131)

AUTHORS Tang, W.-J. and Gilman, A.G.

TITLE Soluble mammalian adenyl cyclase and uses therefor

JOURNAL Patent: US 6107076-A 11 22-AUG-2000;

FEATURES

Location/Qualifiers

source 1..4131

BASE COUNT 835 a 1190 c 1182 g 924 t

ORIGIN

Query Match 77.5%; Score 2751.2; DB 6; Length 4131;

Best Local Similarity 86.7%; Pred. No. 0;

Matches 3080; Conservative 0; Mismatches 463; Indels 11; Gaps 4;

Qy 1 ATGTCATGGTTAGTGCCCTCCTGGTCCCTAAAGTGATGAACGGAAGCAAGCGCTGGGT 60

Db 56 ATGTCATGGTTAGTGCCCTCCTGGTCCCTAAAGTGATGAACGGAAGCAAGCGCTGGGC 115

Qy 61 GAACGCAATGGGCAAGACGCTTCGCGCGCGCTGGGCACTCGGGAGGTGGCTTCGACG 120

Db 116 GAACGCAATGGGCAAGACG--CCACGCGACGCGACCGCGCTGGCTTCGCGG 172

Qy 121 CCCGCTATATAGCTGCTCCGGGATGCAGAGCCACCCAGCCGCCCTTCGGGGCCC 180

Db 173 CCCGCTATATAGCTGCTCCGGGATGCAGAGCCACCCAGCCGCCCTTCGCGAGCTCG 232

Qy 181 CCTCGGTGCCCTGGCAGGATGAGCCCTTCATCCGAGGGCGGCCCGCAAGGCAAG 240

Db 233 ACTCGGTGCCCTGGCAGGATGAGCCCTTCATCAGAGGGCTGGCCGGAGGGGTGTG 292

Qy 241 GAGCTGGGGTGGGGCAGTGGCCCTGGGCTTCGAGGATACCCAGGTGCACAAACACAGCG 300

Db 293 GAGCTGGGGTGGCGTCACTGGGCTGGGTTTTCATGACACTGAGGTG---ACCACACCG 349

Qy 301 GCGGGAGCGCTAGGTGGGCGCCGCGAGCGGTCGCCAGGAGTGGCGCATCTGCTGGGCG 360

Db 350 ATGGGAGACGCTGAAGTGGCCACCGACACATCGCCTCGAAGCGGTCCGCTCGTGGCAC 409

Qy 361 CGTTTGTGAGGTGTTCCAGTCCAAAGCAGTTCCGTTTCGGGCAAGCTGGAGCGCTGTAC 420

Db 410 CGGCTACGCGAGGTGTTCCAGTCTAAGCAGTTCCGCTCCGCGCAAGCTGGAGCGTCTGAC 469

Qy 421 CAGCGGTACTTTTCCAGATGAACAGAGCAGCTGACGCTGCTGGTGGCGGTGCTGGTG 480

Db 470 CAGCGGTACTTTTCCAGATGAACAGAGCAGCTGACGCTGCTCATGGCGGTGCTGGTG 529

Qy 481 CTGCTCAGCGGTGCTGCTGGCTTTTCCAGCGCGACCCCGCCCTCAGCTGCGCTAT 540

Db 530 CTCTCTATGGCTGACTGTTGACCTTCACAGCCGCGCTGCGCTCAGCCTGCTTAT 589

Qy 541 GTGCACTGTTGGCTCTGTCGCGCGCCCTGTTCTGGGGGCTCATGGTGGTGAACCGG 600

Db 590 GTGCGCTGCTGACTGTGCGCTCGCTCTTTTGTGGTACTCATGGTGTAGTGTGAACCGA 649

Qy 601 CATAGCTTCCGCCAGGACTCCATGTGGTGTGAGTAACTGAGTGGTCTGGGATCCTGGCG 660

Db 650 CATAGCTTCCGCCAGGACTCCATGTGGTGTGAGTAACTGAGTGGTCTGGGATCCTTAGCA 709

Qy 661 GCAGTGCAGGTGCGGGGGCTTTTCGACGACAGCCGCGCAGCCCTCTGCGGGGCTCTGG 720

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Qy 721 TGCCCTGTGTTCTTTGTATACATCGCATACAGCTCCTCCCATCCGATCGGCGCTGCC 780

Db 770 TGCCCGGTGTTCTTCGCTACATCACCTACACACTTCTTCCCATTCGTATCGGAGCGCC 829

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Db 830 GTGCTCAGTGGCTGGGTCTTTCCACCTGCATTTGATTTGGCTGGCATCTCAACAAT 889

Qy 841 GGTGATGCTTCTCTGGAAGCAGCTCGTGCCCAATGTGCTGTGTTCTCTGCAACAAC 900

Db 890 GGTGACCCCTTCTTTTGAAGCAGCTCGGTGCTAACGTGGTCTCTCTCTGCAACAAT 949

Qy 901 GTCAATTAGCATCTGCACACACTATCCAGCAGGTGCTCAGCGGCTGCGGCTTTTCAGGAG 960

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Db 1010 ACCCGGTTCATCCAGGCGCGCTGCATTTGCAGCATGAGAAATCGACAGCAGGAACG 1069

Qy 1021 CTGCTGCTGCTGGTATGTCGCCAGCAGCTTGCCTATGGAGATGAAGAAGACATCAACA 1080

Db 1070 CTGCTGCTGCTGGTATGTCGCCAGCAGCTTGCCTATGGAATGAAGAAGATATCAACA 1129

Qy 1081 AAAAAGAAGAC---ATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATC 1137

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Qy 1138 CTGTTTGCAGACATAGGGGCTTCACCAAGCTTGGCATCCCAAGTGCACCTGCGCAGAGCTG 1197

Db 1190 CTGTTTGCAGACATCGAGGGCTTCACCAAGCTTGGCATCCCAAGTGCACCTGCGCAGGA 1249

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Db 1310 CTGAGGATCAAGATCTTAGGAGACTGTTACTTACTGTGTGTCGGGCTGCCGAGGCGCG 1369

Qy 1318 GCCAGCATGCCACTGCTGTGTGAGATGGGGGTAGACATGATTTAGGCGCATCTCGGTG 1377

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Qy 1378 GTAGCTGAGGTGACAGGTGTGAATGTGAACATGCGCTGGGCATCCACAGCGGGCGCGTG 1437

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Db 1550 CTGGCCCAACCATGGAAGCAGGGCGGGCGGGCGGCGCCATCCACATCACTCGGGCCACA 1609

Qy 1558 CTGCACTACCTGACGGGACTACGAAGTGCAGGCGGCGGTGGTGGCAAGCGCAACGCG 1617

Db 1610 CTGCACTACCTGACGGGACTATGAGTGGAGCGGCGGCGGTGGCGGTGAGCGCAACGCG 1669

Qy	1618	TAC	TCTCAAGGACGACACATGTGAGACTTTCTCATCTCTGGGCGCCAGCAGAAACCGGAAA	16177
Db	1670	TAC	TCTCAAGGACGAGTGCATTTGAGACTTCTCTCATACTAGGACCCAGCAGAAACCGGAAA	1729
Qy	1678	GAG	GAGAAAGGCATGCTGGCCCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGCGTG	1737
Db	1730	GAG	GAGAAAGGCCATGCTGGTTCAGCTGCAGCGGACGCGGGCCAACTCCATGGAAGAGACTG	1789
Qy	1738	ATG	CCCGCATGGGTTCCTGATCGTGCTTCTCCCGGACCAAGGACTCCAAAGCCCTTCGCG	1797
Db	1790	ATG	CCCGCTGGGTTCCTGACCGTGCCTTCTCCCGGACCAAGGACTCTAAGGCATTCGGA	1849
Qy	1798	CAG	ATGGGCATTTGATGATTTCCAGCAAGAACAACCGGGGACCCAAAGATGCCTTGAACCCCT	1857
Db	1850	CAG	ATGGGCATTCGATGACTTAGCAAGAAGAACCCGGGTGCCTCAAGATGCTCTGAACCCCT	1909
Qy	1858	GAG	GATCAGCTGGATGAGTTCCTGAGCCGCTGCCATCGATGCCGACGATTTGATCAGCTG	1917
Db	1910	GAG	GATCAGGTGGACGAGTTCTTGGGCCGAGGCATCGATGCCGGAAGCATCGACGACGCTG	1969
Qy	1918	CGA	AGGACCATGTGGCCCGGTTTTTGTCTACCTTCCAGAGAGAGGATTTTTGAGAAAGAAG	1977
Db	1970	CGT	AAGGACCATGTGGCCGCTTCTGCTCACTTCCAGAGGGAGGATCTCGAGAAGAAG	2029
Qy	1978	TAC	TCCCGGAAGTGGATCCCCGCTTCGGAGGCTAGTTTGGTTCCTGTCCTGCTC	2037
Db	2030	TAT	TTCACGGAAGTAGACCCCTCGTTTTCGAGGCTACGTCGCTGTGCCCTCTCTGGTTTTC	2089
Qy	2038	TGCT	TTCATCTGCTTCATCCAGCTTCTAAATTTTCCACACTCCACCTCATGCTCTTGGGATT	2097
Db	2090	TGCT	TTCATCTGTTTATCATCCAGTTCCTCTGATTTCCACACTCGGCCCTGATACTCGGGATT	2149
Qy	2098	TAT	GCCAGCATCTTCTGCTGCTTAATCACCCTGCTGATCTGTGCTGTGCTACTCCTGT	2157
Db	2150	TAT	GCCGGATCTTCTTTTGTGCTGGTCAACGCTGCTCATCTGTGCTGTGCTGCTCCTGT	2209
Qy	2158	GGT	TCTCTGTTCCCTAAGGCCCTGCAACGTCGTCTCCGCGAGGATGTCCGCTCAGGGCA	2217
Db	2210	GGT	GTTTCTTCTTCCCAACGCCCTGCAGCCCTGTCCCGACGATGCTCCGCTCAGCGGTG	2269
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Rattus norvegicus (strain Sprague-Dawley) adult liver, kidney,			

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Rattus.
1 (bases 1 to 4131)
Premont,R.T.
Multiple mechanisms underlying desensitization of the liver
adenylyl cyclase system. Structure and camp regulation of liver
adenylyl cyclases
thesis (1992)
2 (bases 1 to 4131)
Premont,R.T., Chen,J., Ma,H.W., Ponnappalli,M. and Iyengar,R.
Two members of a widely expressed subfamily of hormone-stimulated
adenylyl cyclases
Proc. Natl. Acad. Sci. U.S.A. 89 (20), 9809-9813 (1992)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 6036)  
AUTHORS Krupinski, J., Lehman, T.C., Frankenfield, C.D., Zwaagstra, J.C. and Watson, P.A.  
TITLE Molecular diversity in the adenylyl cyclase family. Evidence for eight forms of the enzyme and cloning of type VI  
JOURNAL J. Biol. Chem. 267 (34), 24858-24862 (1992)  
MEDLINE 93077589  
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Qy	1516	GC	AGAACCGGCTGGCGCATCCACATCACTCGGGAACACTGCAGTACCTGAACGGG	1575
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Db	1555	GAC	TATGAGTGGAGCAGCGCGTGTGTGAACCAATGCGTACCTCAAGSAGCAGTGC	1614
Qy	1636	ATT	CAGACTTCTTCATCTCGGCGCCAGCCAGAACGGAAAGAGAGAAAGGATGCTG	1695
Db	1615	ATT	CAGACTTCTTCATCTGCGCGCCAGCCAAAACGGAAAGAGAGAAAGGATGCTG	1674
Qy	1696	GCA	AGCTGACAGGCACTCGGCGCAACTCCATGGAGGGCTGATCGCGCGATGGTTCCT	1755
Db	1675	GCA	AGCTTCAAGCGACACGGGCGCAACTCCATGGAAAGACTGATGCCCGCTGGGTTCCT	1734
Qy	1756	GAT	CGTGCCTTCTCCCGGACCAAGGACTCCAAAGGCTTCCCGCGAGATGGCATTTGATGAT	1815
Db	1735	GAC	CGTGCCTTCTCCCGGACCAAGGACTCTAAGGCATTCGCCCAGATGGCATTTGATGAT	1794
Qy	1816	TCC	AGCAAGACAAACCGGGGCAACCCAGATGCCCTGAACCTTGAGGATGAGGTGGATGAG	1875
Db	1795	TCT	AGCAAGACAAACCGGGGTGCCAAGATGCTCTGAACCTTGAAGATGAGGTGGATGAG	1854
Qy	1876	TT	CTGAGCGGTGGCATCGATCGCCCGCCAGCATTTGATCAGCTGCGGAAGGACCATGTGCGC	1935
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[illegible]



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Db 3115 ACCTATGACGAGTGGCGCGCTCACACATCAGCGCTGGCTGACTGCTATGCCATCGCGCTC 3174

QY 3196 ATGAGCAGATGAAGCACATCAATGAGCAGCTCCCTTCAACAATTTCCAGATGAAGATTGGG 3255

Db 3175 ATGAGCAGATGAAGCACATCAATGAACACTCTTTCAACAATTTCCAGATGAAGATCGG 3234

QY 3256 CTGACATGGGCCAGTCTGGCAGGTGTCTATCGGGGCTCGGAAGCCACAGATGACATC 3315

Db 3235 TTGAACATGGTCCGGTGTAGCAGCGCTCATTTGGGCGCCGAAAGCCACAGTATGACATC 3294

QY 3316 TGGGGGAACACAGTGAATGTCTCTAGTCGTATGCACAGCAGCGGGGCTCCCGACCGCAATC 3375

Db 3295 TGGGGAATACCGTGAATGTTTCCAGTCGTATGCACAGCACTGGAGTCTCTGACCGAATA 3354

QY 3376 CAGGTGACCGGACCTGTACCAAGTTCCTAGCTGCCAAGGCTACCAAGCTGGAGTGTGGA 3435

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RESULT 15

ARI174472

LOCUS ARI174472 1812 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 3 from patent US 6306830.

ACCESSION ARI174472

VERSION ARI174472.1 GI:17914792

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1812)

AUTHORS Hammond,H.Kirk., Insel,P.A., Ping,P., Post,S.R. and Gao,M.

TITLE Gene therapy for congestive heart failure

JOURNAL Patent: US 6306830-A 3 23-OCT-2001;

FEATURES

source location/Qualifiers

1..1812

/organism="unknown"

BASE COUNT 361 a 539 c 507 g 405 t

ORIGIN

Query Match 51.0%; Score 1808.4; DB 6; Length 1812;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 696 GCGCAGCCCTCTCGGGGCTCTGGTGCCTGTGTCTTTGATATACATCGCATACAGCT 755

Db 63 GCGCAGCCCTCTCGGGGCTCTGGTGCCTGTGTCTTTGATATACATCGCATACAGCT 122

QY 756 CCTCCCATCCGATGGGGTGGCTGCTCAGCGGCTGGGCTCTCCACCTTGCATTT 815

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QY 816 GATCTGGCTGGCAACTTAACCTGGTGTGATGCTCTCTGGAAGCAGCTCGTGCCAA 875

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Db 363 GCATGAGAATCGGCAGAGGAGCGCTGCTGCTGTCGGTATTGCCCCAGCAGCTTGCCAT 422

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Db 423 GGAGATGAAGAAGACATCAACACAAAAAAGAAAGACATGTTCCACAAAGATCTACATACA 482

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Db 483 GAACGATGACAAATGTACGATCCTGTTTGGCAGACATGAGGGCTTCACCAAGCTGGGATC 542

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Db 543 CCAGTGCACCTGCGCAGGAGCTGGTCAAGACCTGAATGAGCTCTTTGGCCCGGTTTGACAA 602

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QY 1296 GTCAGGCTGCCGAGGCCCGCGGACCATGCCACTGCTGTGTGGAGATGGGGGTAGA 1355

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QY 1356 CATGATTGAGGCCATCTCGCTGGTACGTGAGTGCACAGTGTGAATGTGAACATGCGCGT 1415

Db 723 CATGATTGAGGCCATCTCGCTGGTACGTGAGTGCACAGTGTGAATGTGAACATGCGCGT 782

QY 1416 GGGCATCCACAGCGGGCGCTGTCACCTGCGGCTCTTTGGCTTGGGAAATGGCAGTTTCCA 1475

Db 783 GGGCATCCACAGCGGGCGCTGTCACCTGCGGCTCTTTGGCTTGGGAAATGGCAGTTTCCA 842

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Db 963 CCGTGGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGCACATTGAGACTTTCTTCATCCT 1022

QY 1656 GGGCCGACGACAGAAACGGAAGAGGAGGAAAGGATGCTGCCAAGCTGCAGCGGACTCG 1715

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QY 1716 GGCCAACTCCATGGAAGGCTGATGCCGCTGATGGTTCCTGATCGTGCCTTTCTCCCGGAC 1775

Db 1083 GGCCAACTCCATGGAAGGCTGATGCCGCTGATGGTTCCTGATCGTGCCTTTCTCCCGGAC 1142

QY 1776 CAAGGACTTCAAGGCTTCCGCCAGATGGGCTTGTGATGATTCACGAAGAACAAACCGGG 1835

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QY 1956 GAGAGAGATTTTGAAGAAGTACTCCCGGAAGGTGGATCCCGCTTTTCGGAGGCTACGT 2015

Db 1323 GAGAGAGATTTTGAAGAAGTACTCCCGGAAGGTGGATCCCGCTTTTCGGAGGCTACGT 1382

QY 2016 TGCCTGTGCCCTGTGTGCTTCTGCTTCATCTGCTTCATCCAGCTTCTAAATTTCCCA 2075

Db 1383 TGCCTGTGCCCTGTGTGCTTCTGCTTCATCTGCTTCATCCAGCTTCTAAATTTCCCA 1442



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3549	100.0	3549	22	AAD08563 Human cardiac aden
2	3484.8	98.2	3552	22	AAD08567 Human cardiac aden
3	3478.4	98.0	4942	20	AA000461 Human type VI aden
4	3379.2	95.2	3582	22	AAD08568 Human modified car
5	2996.8	84.4	4046	14	AA042525 Cardiac adenyllyl c
6	2765	77.9	5841	24	AB199680 Mouse ischaemic co
7	2751.2	77.5	4131	21	AA053923 Type VI adenyllyl c
8	1808.4	51.0	1812	22	AAD08562 Human partial card
9	1808.4	51.0	2127	19	AAV23246 Human adenyllylcyl

10	1703.4	48.0	4523	20	AA000462 Human type V adeny
11	1690	47.6	4356	16	AA095540 Cardiac adenyllyl c
12	1688.4	47.6	4356	14	AA037543 Cardiac adenyllyl c
13	1648.2	46.4	3924	21	AA053922 Type V adenyllyl cy
14	843	23.8	3137	24	AAD28058 Human adenyllyl and
15	595	16.8	3978	21	AA053918 Adenyllyl cyclase t
16	586	16.5	837	22	AAD30177 DNA encoding rena
17	545	15.4	3811	24	AAD28061 Human adenyllyl and
18	529.6	14.9	915	22	AA030223 DNA encoding rena
19	529.6	14.9	915	22	AA030223 DNA encoding nove
20	505.2	14.2	3518	22	AA02694 Human adenylate cy
21	495.8	14.0	6470	24	AAD31191 Human adenylate cy
22	494.2	13.9	4011	22	AAD06820 Human adenylate cy
23	475.2	13.4	5873	24	AAD31190 Human adenylate cy
24	463.6	13.1	4601	21	AA053925 Type VIII adenyllyl
25	460.2	13.0	3769	24	AAD28057 Human adenyllyl and
26	459	12.9	4008	17	AA014528 Rat adenyllyl cycla
27	459	12.9	4008	21	AA053919 Adenyllyl cyclase t
28	449.4	12.7	4827	23	ABL07501 Drosophila melanog
29	446.6	12.6	3312	24	ABN89298 Human adenylate cy
30	441.6	12.4	4533	21	AA053920 Type III adenyllyl
31	433	12.2	5199	21	AA053924 Type VII adenyllyl
32	428	12.1	3357	21	AA053921 Type IV adenyllyl c
33	412	11.6	4355	24	ABL39754 Human NS cDNA sequ
34	407.6	11.5	3505	24	AAD34078 Human secreted pro
35	395.8	11.2	2601	21	AA053926 Human pancreatic c
36	393.2	11.1	1652	21	AA053926 Adenyllyl cyclase C
37	388.6	10.9	4080	22	AAH16647 Human cDNA sequenc
38	382.2	10.2	7005	23	ABL15355 Drosophila melanog
39	343.8	9.7	3239	22	AAF33100 Human secreted pro
40	295.2	8.3	314	22	AAD08561 Human partial card
41	288.2	8.1	2092	17	AA014529 Human adenyllyl cyc
42	284.4	8.0	1180	22	AAH46933 Human secreted pro
43	277	7.8	5046	23	ABL02755 Drosophila melanog
44	273.6	7.7	320	24	ABL90026 Human polynucleoti
45	267.6	7.5	5201	23	ABL29627 Drosophila melanog

#### ALIGNMENTS

#### RESULT 1

AAD08563 ID AAD08563 standard; DNA; 3549 BP.

XX AC AAD08563;

XX XX 04-SEP-2001 (first entry)

XX XX Human cardiac adenylcyclase VI (ACVI) isoform #1 DNA.

XX DE Human; cardiant; beta-adrenergic signalling protein; beta-ASP;

XX KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;

XX KW adenylcyclase; adenylate cyclase; CAMP synthetase;

XX KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;

XX KW cardiac adenylcyclase VI; ACVI isoform; beta-ASP transgene; ds.

XX OS Homo sapiens.

XX XX

PH Key Location/Qualifiers

FT CDS 1..3504

FT FT /\*\*tag= a

FT FT /product= "Human cardiac adenylcyclase VI isoform #1"

FT FT /EC\_number= "4.6.1.1"

XX XX WO200148164-A2.

PN PN

XX XX 05-JUL-2001.

PD PD

XX XX 26-DEC-2000; 2000WQ-US35411.

PF PF

XX XX 27-DEC-1999; 99US-0472667.

XX XX

PA	(REGC ) UNIV CALIFORNIA.	
XX		
PI	Hammond HK, Gao M;	
XX		
DR	WPI: 2001-418260/44.	
DR	P-PSDB; AAE04310.	
XX		
PT	Novel polynucleotide encoding a modified adenylylcyclase polypeptide	
PT	useful for enhancing cardiac function in mammalian hearts, and for	
PT	treating heart disease, especially congestive heart failure -	
XX		
PS	Example 5; Page 122-129; 153pp; English.	
XX		
CC	The present invention relates to methods and compositions for enhancing	
CC	cardiac function in mammalian hearts by inserting transgenes encoding	
CC	beta-adrenergic signalling proteins (beta-ASP) which increase	
CC	beta-adrenergic responsiveness within the myocardium using in vivo	
CC	gene therapy. The beta-ASPs of the invention include beta-adrenergic	
CC	receptors (beta-AK), adenylylcyclases (also referred as adenylylcyclase,	
CC	adenylylate cyclase and cAMP synthetase) and G-protein receptor kinase	
CC	(GRK) inhibitors. The beta-ASP is used for enhancing cardiac function	
CC	in mammalian hearts and for treating heart disease, especially	
CC	congestive heart failure. The present DNA sequence encodes human	
CC	cardiac adenylylcyclase VI (ACVI) isoform which is used for generating	
CC	a third beta-ASP transgene, used in the exemplification	
CC	of the invention.	
XX		
SQ	Sequence 3549 BP; 699 A; 1025 C; 1061 G; 764 T; 0 other;	
	Query Match 100.0%; Score 3549; DB 22; Length 3549;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 3549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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DB	1 ATGTCATGTTTATGTGCTCTCCCTGTCCTAAAGTGGATGAACGGAAGAGCCTGGGGT	60
QY	61 GAACGCAATGGGCAGAGCGTTCCGGGCGCGTGGCACTCGGGCAGGTGCTTCTGCACG	120
DB	61 GAACGCAATGGGCAGAGCGTTCCGGGCGCGTGGCACTCGGGCAGGTGCTTCTGCACG	120
QY	121 CCCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCACCCCTCGGGCCCC	180
DB	121 CCCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCACCCCTCGGGCCCC	180
QY	181 CCTCGTGGCCCTGGCAGGATGAGCCTTCATCCGGAGGGCGGCCAGCAAGGCAAG	240
DB	181 CCTCGTGGCCCTGGCAGGATGAGCCTTCATCCGGAGGGCGGCCAGCAAGGCAAG	240
QY	241 GAGCTGGGGTGGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACGACAGCG	300
DB	241 GAGCTGGGGTGGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACGACAGCG	300
QY	301 GCGCGACGCGTCAGTGGCGCCGACGCGGTGCCAGAGTGGCGATCCTGCTGGCGC	360
DB	301 GCGCGACGCGTCAGTGGCGCCGACGCGGTGCCAGAGTGGCGATCCTGCTGGCGC	360
QY	361 CGTTTGGTCAGGTGTTCCAGTCAAGACAGTTCCTTTCGGCCCAAGCTGGAGCGCCTGTAC	420
DB	361 CGTTTGGTCAGGTGTTCCAGTCAAGACAGTTCCTTTCGGCCCAAGCTGGAGCGCCTGTAC	420
QY	421 CAGCGGTACTTTTCCAGATGAACACAGAGCGCTTACCGTGTGCTGGGGTGGTGGTG	480
DB	421 CAGCGGTACTTTTCCAGATGAACACAGAGCGCTTACCGTGTGCTGGGGTGGTGGTG	480
QY	481 CTGCTCACAGCGTGTGCTGGCTTTTCCAGCGCACCCGCCCTCAGCCTGCTTAT	540
DB	481 CTGCTCACAGCGTGTGCTGGCTTTTCCAGCGCACCCGCCCTCAGCCTGCTTAT	540
QY	541 GTGGCACTGTGGCCTGTGCGCGCCCTGTTCTGGGGTCTATGTTGTTGTAACCGG	600
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QY	601 CATAGCTTCGCCAGGACTCCATGTGGTGGTGAGTAACGTGTGGTGGCATCTCTGGCG	660
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QY	661 GCAGTGCAGTTCGGGGCGCTTTTCGACGACAGACCCGGCAGCCCTCTGCGGGCTCTGG	720
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QY	901 GTCATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG	960
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DB	1321 GACCATGCCACTGCTGTGTGGAGATGGGGTAGACATGATGAGGCCATCTCGTGGTA	1380
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QY	1621 CTCAGGAGCAGCACATTTGAGACTTTTCTCATCTTGGGGCCAGCCAGAAACGGAAGAG	1680
DB	1621 CTCAGGAGCAGCACATTTGAGACTTTTCTCATCTTGGGGCCAGCCAGAAACGGAAGAG	1680
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Db	1681		GAGAAAGGCATGCTGCCAAGCTGCAGCGGACTCGGGCCAATCCATGGAAAGGCGT	1740
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Db	1801	ATGGGCAATGATGATTCACAGCAAGACAAACCGGGGACCCCAAGATGCCCTGAAACCTTGAG	1860	
Qy	1861	GATGAGGTGGATCAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTCGGG	1920	
Db	1861	GATGAGGTGGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTGATCAGCTCGGG	1920	
Qy	1921	AAGGACCATGTGCGCGGTTCCTGCTCACTTCCACAGACAGAGATTTTGAGAAGAAGTAC	1980	
Db	1921	AAGGACCATGTGCGCGGTTCCTGCTCACTTCCACAGACAGAGATTTTGAGAAGAAGTAC	1980	
Qy	1981	TCCCGGAAGTGGATCCCGGCTTCGGAGCCTACGTTGCCCTGTGCCCTTGTGGTCTTCCTGC	2040	
Db	1981	TCCCGGAAGTGGATCCCGGCTTCGGAGCCTACGTTGCCCTGTGCCCTTGTGGTCTTCCTGC	2040	
Qy	2041	TTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCTTGATGCTTGGATTTAT	2100	
Db	2041	TTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCTTGATGCTTGGATTTAT	2100	
Qy	2101	GCCAGCATCTTCTGCTGCTGCTAATCAACGCTGCTGATCTCTGCTGTGTACTCCCTGTGGT	2160	
Db	2101	GCCAGCATCTTCTGCTGCTGCTAATCAACGCTGCTGATCTCTGCTGTGTACTCCCTGTGGT	2160	
Qy	2161	TCTCTGTTCCCTTAAGGCCCTGCAAGCTCTGTCCCGCAGCATTTGCCCTCACGGGCACAT	2220	
Db	2161	TCTCTGTTCCCTTAAGGCCCTGCAAGCTCTGTCCCGCAGCATTTGCCCTCACGGGCACAT	2220	
Qy	2221	AGCACCGCAGTTGGGATCTTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTTGCCAATG	2280	
Db	2221	AGCACCGCAGTTGGGATCTTTTCCGTCCTGCTTGTGTTTACTTCTGCCATTTGCCAATG	2280	
Qy	2281	TTTCACTGTAAACACACACCCCATACGGAGCTGTGCAGCCGGATGCTGAATTTAAACACCT	2340	
Db	2281	TTTCACTGTAAACACACACCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAAACACCT	2340	
Qy	2341	GCTGACATCACTGCCCTGCCACCTGCAGCAGCTCAATTACTCTCGGCCCTGGATGCTCCC	2400	
Db	2341	GCTGACATCACTGCCCTGCCACCTGCAGCAGCTCAATTACTCTCGGCCCTGGATGCTCCC	2400	
Qy	2401	CTGTGTGAGGGACACATGCCACCTGCAGCTTTCCTGAGTGTCCATCGGGAACATGCTG	2460	
Db	2401	CTGTGTGAGGGACACATGCCACCTGCAGCTTTCCTGAGTGTCCATCGGGAACATGCTG	2460	
Qy	2461	CTGAGTCTCTTGCGCAGCTCTGCTTCTCTGCACATCAGCAGCATCGGGAAGTTGGCCCATG	2520	
Db	2461	CTGAGTCTCTTGCGCAGCTCTGCTTCTCTGCACATCAGCAGCATCGGGAAGTTGGCCCATG	2520	
Qy	2521	ATCTTTTGTCTTGCGGCTCATCTAATTTGGTGTGCTTCTGCTGGGTCCCGCAGCGCCATC	2580	
Db	2521	ATCTTTTGTCTTGCGGCTCATCTAATTTGGTGTGCTTCTGCTGGGTCCCGCAGCGCCATC	2580	
Qy	2581	TTTGACAACATGACCTACTGCTTGGGTGCCATGCGCTTGGCTTCTTCCAATGAGACCTTT	2640	
Db	2581	TTTGACAACATGACCTACTGCTTGGGTGCCATGCGCTTGGCTTCTTCCAATGAGACCTTT	2640	
Qy	2641	GATGGGCTGGACTGTCACCTGCAGGGAGGTGGCCCTCAATATATGACCCCTGTGATT	2700	
Db	2641	GATGGGCTGGACTGTCACCTGCAGGGAGGTGGCCCTCAATATATGACCCCTGTGATT	2700	
Qy	2701	CTGCTGGTGTTCGCTGGCGTGTATCTGCAATGCTCAGCAGGTGGAATCGACCTGCCCG	2760	
Db	2701	CTGCTGGTGTTCGCTGGCGTGTATCTGCAATGCTCAGCAGGTGGAATCGACCTGCCCG	2760	
Qy	2761	CTAAACTTCTCTGGAACCTACAGGCAACAGGGGAAAAAGAGAGATGGAGAGCTACAG	2820	

Db	2761	CTAAACTTCTCTGGAAACTACAGGCAACAGGGGAAAAAGAGGAGATGGAGGAGCTACAG	2820
Qy	2821	GCATACAACCGGAGGCTGCTGCATACAACTTCTGCCAAAGGACGTGGCGGCCCACTTCCCTG	2880
Db	2821	GCATACAACCGGAGGCTGCTGCATACAACTTCTGCCAAAGGACGTGGCGGCCCACTTCCCTG	2880
Qy	2881	GCCGGGAGGCGCGCAATGATGAATCTCTACTACTATCAGTCGCTGTGTGGCTGTATTG	2940
Db	2881	GCCGGGAGGCGCGCAATGATGAATCTCTACTACTATCAGTCGCTGTGTGGCTGTATTG	2940
Qy	2941	TTTGGCCTCCAACTGCCCAACTTCTCTCAGTTCATGTAGAGCTGGAGGCAACAATGAGGGT	3000
Db	2941	TTTGGCCTCCAACTGCCCAACTTCTCTCAGTTCATGTAGAGCTGGAGGCAACAATGAGGGT	3000
Qy	3001	GCCGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGTATGAGATTATCAGCGAG	3060
Db	3001	GCCGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGTATGAGATTATCAGCGAG	3060
Qy	3061	GAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGTTAGCACCTACATGGCTGCCTCA	3120
Db	3061	GAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGTTAGCACCTACATGGCTGCCTCA	3120
Qy	3121	GGCTGAACCCAGCAGCTTACGATCAGGTGGGCGCCTCCCACATCACTGCCCTGGCTGAC	3180
Db	3121	GGCTGAACCCAGCAGCTTACGATCAGGTGGGCGCCTCCCACATCACTGCCCTGGCTGAC	3180
Qy	3181	TAGCCCATGGCGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCCTTCAACAATTTC	3240
Db	3181	TAGCCCATGGCGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCCTTCAACAATTTC	3240
Qy	3241	CAGATGAAGATTGGGCTGAACATGGGCCCGACGTGGCAGGTGTCATCGGGGCTCGGAAG	3300
Db	3241	CAGATGAAGATTGGGCTGAACATGGGCCCGACGTGGCAGGTGTCATCGGGGCTCGGAAG	3300
Qy	3301	CCACAGTATCACATCTGGGGGAACACAGTGAATGCTCTAGTCGTATGGACAGCAGCGGG	3360
Db	3301	CCACAGTATCACATCTGGGGGAACACAGTGAATGCTCTAGTCGTATGGACAGCAGCGGG	3360
Qy	3361	GTCCCCGACCGAATCCAGGTGACACGGGACCTGTACCAGTTCTAGCTGCCAAGGGCTAC	3420
Db	3361	GTCCCCGACCGAATCCAGGTGACACGGGACCTGTACCAGTTCTAGCTGCCAAGGGCTAC	3420
Qy	3421	CAGCTGGAGTGTGCGAGGGTGGTCAAGGTGAAGGCAAGGGGAGATGACCACCTACTTC	3480
Db	3421	CAGCTGGAGTGTGCGAGGGTGGTCAAGGTGAAGGCAAGGGGAGATGACCACCTACTTC	3480
Qy	3481	CTCAATGGGGGCCCCAGCAGTTAACAGGCCCCAGCCACAATTCAGCTGAAGGAGCAACAAG	3540
Db	3481	CTCAATGGGGGCCCCAGCAGTTAACAGGCCCCAGCCACAATTCAGCTGAAGGAGCAACAAG	3540
Qy	3541	GTGGGCACT 3549	
Db	3541	GTGGGCACT 3549	
RESULT 2			
AAD08567			
ID	AAD08567 standard; DNA; 3552 BP.		
XX	AAD08567;		
AC			
XX			
XX			
DT	04-SEP-2001 (first entry)		
DE	Human cardiac adenylylase VI (ACVI) isoform #2 DNA.		
XX			
KW	Human; cardiant; beta-adrenergic signalling protein; beta-ASP;		
KW	myocardium; gene therapy; beta-adrenergic receptor; beta-AR;		
KW	adenylylase; adenylylase; adenylylase; adenylylase; adenylylase;		
KW	G-protein receptor kinase; GRK; heart disease; congestive heart failure;		
XX	cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ds.		
OS	Homo sapiens.		
XX			













|||||  
Db 3565 TACCAGCTGGAGTGTCTGAGGGTGGTCAAGGTGAAGGCAAGGGGAGATGACACCTAC 3624  
QY 3478 TTCTCTCAATGGGGCCCCCAGCAGTTAACAGGCGCCAGCCACAAATTCAGCTGAAGGACC 3537  
Db 3625 TTCTCTCAATGGGGCCCCCAGCAGTTAACAGGCGCCAGCCACAAATTCAGCTGAAGGACC 3684  
QY 3538 AAGGTGGGCACT 3549  
Db 3685 AAGGTGGCATT 3696  
|||||  
RESULT 4  
AAD08568  
ID AAD08568 standard; cDNA; 3582 BP.  
XX  
AC AAD08568;  
XX  
DT 04-SEP-2001 (first entry)  
XX  
Human modified cardiac adenylylase VI (ACVI) isoform cDNA.  
DE  
XX  
KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;  
KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
KW adenylylase; adenylylase; adenylylase; cAMP synthetase;  
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key  
FT CDS  
FT Location/Qualifiers  
FT 22..3525  
FT /\*tag= a  
FT /product= "Human modified cardiac ACVI isoform"  
XX  
PN W0200148164-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US35411.  
XX  
PR 27-DEC-1999; 99US-0472667.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Hammond HK, Gao M;  
XX  
DR WPI; 2001-418260/44.  
DR P-PSDB; AAE04312.  
XX  
PT Novel polynucleotide encoding a modified adenylylase polypeptide  
PT useful for enhancing cardiac function in mammalian hearts, and for  
PT treating heart disease, especially congestive heart failure -  
XX  
PS Claim 4; Page 143-150; 153pp; English.  
XX  
CC The present invention relates to methods and compositions for enhancing  
CC cardiac function in mammalian hearts by inserting transgenes encoding  
CC beta-adrenergic signalling proteins (beta-ASP) which increase  
CC beta-adrenergic responsiveness within the myocardium using in vivo  
CC gene therapy. The beta-ASPs of the invention include beta-adrenergic  
CC receptors (beta-AR), adenylylases (also referred to as adenylylase,  
CC adenylylase and cAMP synthetase) and G-protein receptor kinase  
CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
CC in mammalian hearts and for treating heart disease, especially  
CC congestive heart failure. The present cDNA sequence encodes human  
CC modified cardiac adenylylase VI (ACVI) isoform which is used for  
CC generating a beta-ASP transgene, used in the exemplification of the  
CC invention.  
XX  
SQ Sequence 3582 BP; 703 A; 1036 C; 1067 G; 776 T; 0 other;

Query Match 95.2%; Score 3379.2; DB 22; Length 3582;  
Best Local Similarity 97.4%; Pred. No. 0;  
Matches 3458; Conservative 0; Mismatches 88; Indels 6; Gaps 2;  
QY 1 ATGTCATGGTTTGTAGTGGCTTCTGGTCCCTAAAGTGGATGAACGAAACAGCCTGGGGT 60  
Db 22 ATGTCATGGTTTGTAGTGGCTTCTGGTCCCTAAAGTGGATGAACGAAACAGCCTGGGGT 81  
QY 61 GAACGCAATGGCAGAGCGTTCCGCGCGCGTGGCACTCGGCAGGTGCTTCTGCACG 120  
Db 82 GAACGCAATGGCAGAGCGTTCCGCGCGCGTGGCACTCGGCAGGTGCTTCTGCACG 141  
QY 121 CCCCCTATATAGCTCCCTCCCGGATGACAGCCACCCAGCCGCCCTGGGGCCCC 180  
Db 142 CCCCCTATATAGCTCCCTCCCGGATGACAGCCACCCAGCCGCCCTGGGGCCCC 201  
QY 181 CCTCGGTGCCCCCTGGCAGGATGACGCTTCATCCGAGGGGGGCCAGGGAAG 240  
Db 202 CCTCGGTGCCCCCTGGCAGGATGACGCTTCATCCGAGGGGGGCCAGGGAAG 261  
QY 241 GAGCTGGGGCTGGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGTGACAACGACAGCG 300  
Db 262 GAGCTGGGGCTGGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGTGACAACGACAGCG 321  
QY 301 GCGGGACGCGCTGAGGTGGCGCCCGCAGCGGTGCCAGAGTGGGGCATCTGCTGGCGC 360  
Db 322 GCGGGACGCGCTGAGGTGGCGCCCGCAGCGGTGCCAGAGTGGGGCATCTGCTGGCGC 381  
QY 361 CGTTTGGTGCAGGTGTTCCAGTGAAGCAGTTCGTTTGGGCCAAGTGGAGCGCTGTAC 420  
Db 382 CGTCTGGTGCAGGTGTTCCAGTGAAGCAGTTCGTTTGGGCCAAGTGGAGCGCTGTAC 441  
QY 421 CAGCGTACTTTTCCAGATGAACGAGCAGCTGACGCTGTGGTGGCGGTGCTGGTG 480  
Db 442 CAGCGTACTTTTCCAGATGAACGAGCAGCTGACGCTGTGGTGGCGGTGCTGGTG 501  
QY 481 CTGCTCACAGCGTGTGCTGGCTTTCCAAAGCGCGCACCCCGCCGCCCTCAGCCTGCCTAT 540  
Db 502 CTGCTCACAGCGTGTGCTGGCTTTCCAGCGCGCACCCCGCCGCCCTCAGCCTGCCTAT 561  
QY 541 GTGGCACTGTGGCTGTGCGCGCGCCCTGTTGTTGGGGCTCATGTGTGTGTAAACCG 600  
Db 562 GTGGCACTGTGGCTGTGCGCGCGCCCTGTTGTTGGGGCTCATGTGTGTGTAAACCG 621  
QY 601 CATAGCTTCCGCGCAGACTCCATGTGGTGGTGAAGTAACTGGTGGCATCTCTGGCG 660  
Db 622 CATAGCTTCCGCGCAGACTCCATGTGGTGGTGAAGTAACTGGTGGCATCTCTGGCG 681  
QY 661 GCAGTGCAGTGGGGGGCGCTTTTCGAGCAGACCCCGCGCAGCCCTCTGGGGGGCTCTGG 720  
Db 682 GCAGTGCAGTGGGGGGCGCTTTCGAGCAGACCCCGCGCAGCCCTCTGGGGGGCTCTGG 741  
QY 721 TGGCCCTGTGTTCTTTGTATATACATGCGATACACGCTCTCCCCATCGGCATCGGGGCTGCC 780  
Db 742 TGGCCCTGTGTTCTTTGTATATACATGCGATACACGCTCTCCCCATCGGCATCGGGGCTGCC 801  
QY 781 GTCTCTCAGCGGCTGGGCGCTTCCACCTTTCATTTGATCTTGGCTGGCAACTTAAACCGT 840  
Db 802 GTCTCTCAGCGGCTGGGCGCTTCCACCTTTCATTTGATCTTGGCCCTGGCAACTTAAACCGT 861  
QY 841 GGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTGTCTCTGCACCAAC 900  
Db 862 GGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTGTCTCTGCACCAAC 921  
QY 901 GTCATTAGCATGTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 960  
Db 922 GTCATTTGGCATGTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 981  
QY 961 ACCCGGAGTTACATCCAGGCGCGGCTCCACCTCAGCATGAGATCGGAGAGGAGCGG 1020  
Db 982 ACCCGGAGTTACATCCAGGCGCGGCTCCACCTCAGCATGAGATCGGAGAGGAGCGG 1041  
QY 1021 CTGCTGCTGTGGGTATTGGCCCGCAGCAGCTTGGCATGGAGATGAAGAAGACATCAACACA 1080



QY 3238 TTCAGATGAAGATTGGCTGAACATGGGCCAGTCTGGCAGGTGTCATCGGGCTCGG 3297  
|||||  
Db 3259 TTCAGATGAAGATTGGCTGAACATGGGCCAGTCTGGCAGGTGTCATCGGGCTCGG 3318  
|||||  
QY 3298 AAGCCAGATGACATCTCGGGGAACACAGTGAATGCTCTAGTCTGTATGGACAGCAG 3357  
|||||  
Db 3319 AAGCCAGATGACATCTCGGGGAACACAGTGAATGCTCTAGTCTGTATGGACAGCAG 3378  
|||||  
QY 3358 GGGTCCCCCAGCAATCCAGGTGACACAGGACCTGTACCAGTTCTAGTGTGCAAGGGC 3417  
|||||  
Db 3379 GGGTCCCCCAGCAATCCAGGTGACACAGGACCTGTACCAGTTCTAGTGTGCAAGGGC 3438  
|||||  
QY 3418 TACCAGTGGAGTGTCTGAGGGGTGGTCAAGGTGAAGGGCAAGGGAGATGACACACCTAC 3477  
|||||  
Db 3439 TACCAGTGGAGTGTCTGAGGGGTGGTCAAGGTGAAGGGCAAGGGAGATGACACACCTAC 3498  
|||||  
QY 3478 TTCTCAATGGGGCCCCCAGAGTTACAGGGCCCCAGCCACAAATTACAGTGAAGGGACC 3537  
|||||  
Db 3499 TTCTCAATGGGGCCCCCAGAGTTACAGGGCCCCAGCCACAAATTACAGTGAAGGGACC 3558  
|||||  
QY 3538 AAGTGGGCACT 3549  
|||||  
Db 3559 AAGTGGGCACT 3570  
|||||

RESULT 5

ID AAQ42525 standard; DNA; 4046 BP.  
XX AAQ42525;

XX AC AAQ42525;  
XX XX

DT 14-SEP-1993 (first entry)  
XX Cardiac adenyl cyclase gene.

DE Regulation; cardiac function; heart; heart failure; ss.  
XX Canis familiaris.

OS Canis familiaris.  
XX Key Location/Qualifiers

FT CDS 131..3627  
FT /\*tag= a

XX EP543137-A.  
XX 26-MAY-1993.

XX 12-OCT-1992; 92EP-0117374.  
XX 18-NOV-1991; 91US-0793961.

XX (AMCY ) AMERICAN CYANAMID CO.  
XX Ishikawa Y;

PI WPI; 1993-168873/21.  
XX P-PSDB; AAR37309.

DR Purified DNA encoding cardiac adenyl cyclase - useful to screen  
XX for cpds. which stimulate activity of the cyclase

PT Claim 1; Fig 2; 34pp; English.  
XX

XX A canine heart cDNA library was constructed in lambda gt10 and was  
CC screened with a 970 bp AatI-HincII fragment from type I adenyl cyclase cDNA probe (encodes the first cytoplasmic domain of adenyl cyclase, which has significant homology to other previously known types of adenyl cyclase). One positive clone, of 5.4 kb was obtd.

CC Positive colonies were subcloned into pUC18 and further subcloned  
CC and sequenced bidirectionally. The 5.4 kb clone was used to  
CC rescreen the library and on overlapping clone contg. the 5' end of  
CC the gene was isolated. Together the two clones cover the complete

CC canine cardiac adenyl cyclase gene. The gene is suspected of  
CC being involved in the regulation of cardiac function and it is thought  
CC that decreased activity of adenyl cyclase in the heart may be a  
CC major factor in the development of heart failure. Thus the adenyl  
CC cyclase gene is useful to screen cpds. which stimulate the activity  
XX of the cyclase.  
SQ Sequence 4046 BP; 743 A; 1206 C; 1254 G; 843 T; 0 other;

Query Match 84.4%; Score 2996.8; DB 14; Length 4046;  
Best Local Similarity 91.0%; Pred. No. 0;  
Matches 3233; Conservative 0; Mismatches 307; Indels 12; Gaps 4;

QY 1 ATGTCATGTTTGTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAACAGCTGGGGT 60  
|||||  
Db 131 ATGTCGTTGTTTGTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAACAGCTGGGGT 190  
|||||  
QY 61 GAACGCAATGGGAGAGCGTTTCGGCGCCGCTGGCACTCGGCACTGGCTTCTGCAAG 120  
|||||  
Db 191 GAACGCAATGGGAGAGCGT---CCACGCCCGGGGACTCGGACCACTGGCTTCTGCAAG 247  
|||||  
QY 121 CCCCCTATATGAGTGCCTCCGGGATGACAGCCACCCAGCCCTCGGGGCCCC 180  
|||||  
Db 248 CCCCCTATATGAGTGCCTCCGGGATGACAGCCACCCAGCCCTCGGGGCCCC 307  
|||||  
QY 181 CCTCGTGGCCCTGGCAGGATGACGGCTTCATCCGAGGGGGCGCCAGGCAAG 240  
|||||  
Db 308 CCTCGTGGCCCTGGCAGGATGAGGCTTCATCCGAGAGAGCGCCGGCAAGGCAAG 367  
|||||  
QY 241 GAGCTGGGGTGGCGGAGTGGCCCTGGGCTTCAGAGATACCGAGGTGACAGACAGCG 300  
|||||  
Db 368 GAGCTGGGGTGGCGGAGTGGCCCTGGGCTTCGAGACACTGAGG---CCATGTCAGCG 424  
|||||  
QY 301 GCGGGACCGCTGAGTGGCGCCGAGCGCTGCCAGGAGTGGCGATCCTGCTGGCGC 360  
|||||  
Db 425 GTTGGGCGACTGGAGTGGCCCTGACCTGACCCCGGAGTAGGGGATCCTGCTGGCGC 484  
|||||  
QY 361 CGTTTGTGTCAGTGTTCAGTGAAGCAGCTTCGTTTCGCCCAAGTGGAGCCCTGTATC 420  
|||||  
Db 485 CGTCTGGCCCGAGGTGTTCCAGTGAAGCAGCTTCGCTCGGCCAAGCTGGAGCCCTGTATC 544  
|||||  
QY 421 CAGCGGTACTTTTTCAGATGAACAGAGAGCGCTGACGCTGCTGGTGGCGGTGCTGGTG 480  
|||||  
Db 545 CAGCGGTACTTTTTCAGATGAACAGAGAGCGCTGACGCTGCTGGTGGCGGTGCTGGTG 604  
|||||  
QY 481 CTGCTCACAGCGGTGCTGCTGGCTTTCCAAAGCCGACCCGCCCTCAGCTGAGCTGCTAT 540  
|||||  
Db 605 CTGCTCACAGCGGTGCTGCTGGCTTTCCAAAGCCGACCCGCCCTCAGCTGAGCTGCTAT 664  
|||||  
QY 541 GTGGCAGTGTGGCTGTGCGCCGCCCTGTTGCTGGGGCTCATGTTGTTGTTGTAACCGG 600  
|||||  
Db 665 GTGGCAGTGTGGCTGTGCGCCGCCCTGTTGCTGGGGCTCATGTTGTTGTTGTAACCGG 724  
|||||  
QY 601 CATAGCTTCGGCAGGACTCCATGTGGTGGTGAAGTAACTGTTGTTGTTGTTGTTGTTG 660  
|||||  
Db 725 CACAGCTTTTCGCCAGGACTCCATGTGGTGGTGAAGTAACTGTTGTTGTTGTTGTTGTTG 784  
|||||  
QY 661 GCAGTGCAGTTCGGGGCGCTTTTCGAGCAGACCCCGGAGCCCTCTGCGGGCTCTGG 720  
|||||  
Db 785 GCGGTTTCAGGTTGGGGTGGCCCTGGGAGCAACCCCGGAGCCCTCTGTTGGGCCCTCTGG 844  
|||||  
QY 721 TGGCCCTGTGTTTGTATATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 780  
|||||  
Db 845 TGGCCCTGTGTTTGTATATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 904  
|||||  
QY 781 GTCTTCAGCGGCTCGGGCTCTCCACCTTGATCTGATCTGTTGGCTGGCAACTTAACCGT 840  
|||||  
Db 905 GTCTTCAGTGGCTCGGGCTCTCCACCTTGATCTGATCTGTTGGCTGGCAACTTAACCGT 964  
|||||  
QY 841 GGTGATGCTCTCTGGAAGAGAGCTCGGTGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 900  
|||||  
Db 965 GGTGATGCTCTCTGGAAGAGAGCTCGGTGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 1024  
|||||



Db 3182 GAGAGCGGTTCCGGCAGCTGGAGAAATCAAGACGATCGGTAGCAGTACATGGCTGCG 3241  
QY 3118 TCAGGGCTGAACCCAGCAGCTACGATCAGGTGGCGCTGCCACATCACTGCGCCCTGGCT 3177  
Db 3242 TCGGGCTGAACCCAGCAGCTACGATCAGCGCGCGCTCCACATCACTGCGCCCTGGCC 3301  
QY 3178 GACTAGCCCATGGCTCATGAGCAGATGAAGCAGCATCAATGAGCAGCTCTTCAACAAT 3237  
Db 3302 GACTATGCCATGGCTCATGGAGCAGATGAACACATCAACGAGCAGCTCTTCAACAAC 3361  
QY 3238 TTCAGATGAAGATTGGCTGAACATGGGCGCCAGTCGTGGCAGGTGTATCGGGGCTCGG 3297  
Db 3362 TTCAGATGAAGATTGGCTGAACATGGGCGCCAGTTGTGGCAGCGCTCATTTGGGGCTCGG 3421  
QY 3298 AAGCCAGTATGACATCTGGGGGAACACAGTGAATGCTCTAGTGTGATGGACAGCAGC 3357  
Db 3422 AAGCCAGTATGACATCTGGGGGAACACAGTGAATGCTCTAGTGTGATGGACAGCAGC 3481  
QY 3358 GGGGTCCCGACCGAATCCAGGTGACACCGGACCTGTACCAGTTCTAGCTGCCAAGGC 3417  
Db 3482 GGGGTCTCTGACCGAATCCAGGTGACACCGGACTTGTACCAGTTCTAGCTGCCAAGGC 3541  
QY 3418 TACCAGCTGAGTGTGAGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACCACTTAC 3477  
Db 3542 TACCAGCTGAGTGTGAGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACCACTTAC 3601  
QY 3478 TTCTCTCAATGGGGGCCCCAGCAGTTAACAGGGGCCAGCCACAAATTCAGCTGAAGGGACC 3537  
Db 3602 TTCTCTCAATGGGGGCCCCAGCAGTTAGCAGACGCCAGCTACAGTTTCAGCTGCAGGACC 3661  
QY 3538 AAGGTGGGCACT 3549  
Db 3662 AAGGTGGGCACT 3673

RESULT 6

ABI99680  
ID ABI99680 standard; cDNA; 5841 BP.  
XX  
AC ABI99680;  
XX  
XX  
DT 07-MAR-2002 (first entry)  
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:716.  
XX  
XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;  
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.  
XX  
OS Mus musculus.  
XX  
XX WO200188188-A2.  
XX  
XX 22-NOV-2001.  
XX  
XX 18-MAY-2001; 2001WO-JP04192.  
XX  
XX 18-MAY-2000; 2000JP-0145977.  
XX  
XX (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
XX  
XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;  
PI  
XX  
XX WPI; 2002-034733/04.  
DR P-PSDB; ABB57257.  
XX  
XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
PT expression levels of particular genes defined in the specification or  
PT by determining the expression profile of a gene group comprising these  
PT genes -  
XX  
XX Claim 2; Page 1771-1780; 2690pp; English.  
XX  
XX The present invention describes a method for examining ischaemic

CC conditions, comprising measuring the expression levels of particular  
CC genes (I) in a test sample or determining the expression profile of a  
CC gene group in the sample comprising genes selected from (I). The method  
CC is useful for examining the ischaemic condition (e.g. compressive  
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring  
CC expression levels of particular genes (ABI99202 to ABI99912, encoding  
CC the protein sequences in ABB57020 to ABB57374) or by determining the  
CC expression profile of a gene group comprising these genes. The  
CC expression levels or expression profiles produced by these genes are  
CC used as an indicator when screening for ischaemic condition-improving  
CC drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914  
CC represent PCR primers for a mouse ischaemic condition related sequence,  
CC which are used in the exemplification of the present invention.  
XX  
QY Sequence 5841 BP; 1214 A; 1558 C; 1673 G; 1396 T; 0 other;  
Query Match 77.9%; Score 2765; DB 24; Length 5841;  
Best Local Similarity 87.1%; Pred. No. 0;  
Matches 3095; Conservative 0; Mismatches 445; Indels 13; Gaps 5;  
QY 1 ATGTCATGTTTGTAGTGGCCCTCTGTCCTTAAAGTGGATGAACGAAACAGCTTGGGGT 60  
Db 96 ATGTCATGTTTGTAGTGGCCCTCTGTCCTTAAAGTGGATGAACGAAACAGCTTGGGGT 155  
QY 61 GAACGCAATGGGCGAGAGCGTTCCCGCGCCGCTGGCACTCGGCGAGGTGCTTTCGACG 120  
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Db 1803 TGAGGTGTC 1812

RESULT 9
AAV23246
ID AAV23246 standard; cDNA; 2127 BP.
XX
AC AAV23246;
XX
DT 17-JUL-1998 (first entry)
XX
DE Human adenylylase isoform VI encoding cDNA.
XX
KW Human; adenylylase VI; AC-VI; beta-adrenergic signalling protein;
transgene; gene therapy; congestive heart failure; cardiac function;
adenovirus; ss.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
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/transl_except= (pos:229..231,aa:Xaa)
/transl_except= (pos:315..317,aa:Xaa)
/feature= "no stop codon given; Xaa = unknown"
FT misc_difference 315
/feature= b
/feature= "n indicates a gap of about 0.5 kb"
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WO9810085-A2.
XX
PD 12-MAR-1998.
XX
PF 05-SEP-1997; 97MO-US15610.
XX
PR 16-JUN-1997; 97US-0048933.
XX
PR 05-SEP-1996; 96US-0708661.
XX
(COLL-) COLLATERAL THERAPEUTICS.
PA (REGC ) UNIV CALIFORNIA.
PI Gao M, Hammond HK, Insel PA, Ping P, Post SR;
XX
WPI: 1998-193633/17.
DR P-FSDB; AAW53345.
XX
Vectors containing transgene(s) encoding beta-adrenergic signalling
```

proteins - useful for gene therapy of congestive heart failure

Claim 60; Fig 12A; 114pp; English.

The present sequence encodes human adenylylcyclase isoform VI (AC-VI) from the present invention. The present invention describes a recombinant replication-defective viral particle (I) comprising a gene encoding a beta-adrenergic signalling protein (beta-ASP) operably linked to a promoter. Also described are: (1) a recombinant pro-viral plasmid (Ia) comprising a gene encoding a beta-ASP, as above, operably linked to a promoter and further comprising a replication-defective viral genome; (2) a (mammalian) cell transfected with (I) or (Ia); (3) an isolated polynucleotide comprising a sequence encoding a human adenylylcyclase isoform VI (AC-VI), or a variant having AC activity; (4) a human AC-VI encoded by (3); (5) an isolated polynucleotide sequence which hybridises at high stringency to (3); and (6) a vector comprising the polynucleotide of (3). (I) can be used to form a filtered adenovirus particle preparation. (I) is used to enhance cardiac function in mammals.

XX SQ Sequence 2127 BP; 421 A; 637 C; 615 G; 452 T; 2 other;

Query Match 51.0%; Score 1808.4; DB 19; Length 2127;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	636	TAACGTGGTCTGGGCATCTCGCGCAGTGCAGGTGCGGGGCGCTTTCGACGACAGCC	695
DB	318	TAACGTGGTCTGGGCATCTCGCGCAGTGCAGGTGCGGGGCGCTTTCGACGACAGCC	377
QY	696	GCGCAGCCCTCTGCGGGCCTCTGGTCCCTGTGTTCTTTGTATACATCGCATACAGCCT	755
DB	378	GCGCAGCCCTCTGCGGGCCTCTGGTCCCTGTGTTCTTTGTATACATCGCATACAGCCT	437
QY	756	CTTCCCATCCGATCGGGCTGCGGCTCAGCGGCTGCGGCTCTCCACCTTGCAATTT	815
DB	438	CTTCCCATCCGATCGGGCTGCGGCTCAGCGGCTGCGGCTCTCCACCTTGCAATTT	497
QY	816	GATCTTGGCTGGCACTTAACCGTGTGTATGCTTCTCTGGAAGCAGCTCGGTGCAAA	875
DB	498	GATCTTGGCTGGCACTTAACCGTGTGTATGCTTCTCTGGAAGCAGCTCGGTGCAAA	557
QY	876	TGTGCTGCTTCTCTGCAACCAACGTATAGCATCTGCACACACTATCCAGCAGAGT	935
DB	558	TGTGCTGCTTCTCTGCAACCAACGTATAGCATCTGCACACACTATCCAGCAGAGT	617
QY	936	GTCTCAGCGCCAGGCTTTTCAGAGACCCCGCAGTTACATCCAGGCCGGCTCCACCTGCA	995
DB	618	GTCTCAGCGCCAGGCTTTTCAGAGACCCCGCAGTTACATCCAGGCCGGCTCCACCTGCA	677
QY	996	GCATGAGAATCGGCAGCAGGCGGCTGCTGCTGCGGTATTCGCCAGCAGCTTGCCAT	1055
DB	678	GCATGAGAATCGGCAGCAGGCGGCTGCTGCTGCGGTATTCGCCAGCAGCTTGCCAT	737
QY	1056	GGAGATGAAGAGACATCAACACAAAAAAGAGACATGTTCCACAAGATCTACATACA	1115
DB	738	GGAGATGAAGAAGACATCAACACAAAAAAGAGACATGTTCCACAAGATCTACATACA	797
QY	1116	GAAGCATGAACATCTCAGCATCTGTTTTCAGACATTTAGGGCTTCACAGCCTGGCATC	1175
DB	798	GAAGCATGAACATCTCAGCATCTGTTTTCAGACATTTAGGGCTTCACAGCCTGGCATC	857
QY	1176	CCAGTGACATCGGCAGGAGCTGCTATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAA	1235
DB	858	CCAGTGACATCGGCAGGAGCTGCTATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAA	917
QY	1236	GCTGGCTGCGGAGATCACTGCTGAGGATCAAGATCTTGGGGAGCTGTTTACTGTGT	1295
DB	918	GCTGGCTGCGGAGATCACTGCTGAGGATCAAGATCTTGGGGAGCTGTTTACTGTGT	977
QY	1296	GTACGGCTGCCGGAGGCCCGGCCGACCATGCCCACTGCTGTGTGGAGATGGGGTAGA	1355
DB	978	GTACGGCTGCCGGAGGCCCGGCCGACCATGCCCACTGCTGTGTGGAGATGGGGTAGA	1037

QY	1356	CATGATTGAGGCCATCTCGCTGTGTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGT	1415
DB	1038	CATGATTGAGGCCATCTCGCTGTGTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGT	1097
QY	1416	GGGCATCCACAGCGGGCGGTGCACTCGCGGCTCTTTGGCTTGGGAAATGGCATTTGCA	1475
DB	1098	GGGCATCCACAGCGGGCGGTGCACTCGCGGCTCTTTGGCTTGGGAAATGGCATTTGCA	1157
QY	1476	TGTGTGTCAATGATGTGACCCCTGGCCAAACCACATGGAAGCAGGAAGCGGGCTGCGCG	1535
DB	1158	TGTGTGTCAATGATGTGACCCCTGGCCAAACCACATGGAAGCAGGAAGCGGGCTGCGCG	1217
QY	1536	CATCCACATCACTCGGGCAACACTGCACTGAGTACCTGAACGGGACTACGAAGTGGAGCCAGG	1595
DB	1218	CATCCACATCACTCGGGCAACACTGCACTGAGTACCTGAACGGGACTACGAAGTGGAGCCAGG	1277
QY	1596	CCGTGTGGCAAGCGCAACCGGTACCTCAAGGAGCAGACATTTGAGACTTTCTTCATCCT	1655
DB	1278	CCGTGTGGCAAGCGCAACCGGTACCTCAAGGAGCAGACATTTGAGACTTTCTTCATCCT	1337
QY	1656	GGCGCCAGCCAGAAACGAAAGAGGAGAAAGCATCTGCCCAAGCTGCAGCGGACTCG	1715
DB	1338	GGCGCCAGCCAGAAACGAAAGAGGAGAAAGCATCTGCCCAAGCTGCAGCGGACTCG	1397
QY	1716	GGCCAACTCCATGGAAGGGCTGATGCCGCGATGGGTTCTCTGATCGTCCCTTCTCCCGGAC	1775
DB	1398	GGCCAACTCCATGGAAGGGCTGATGCCGCGATGGGTTCTCTGATCGTCCCTTCTCCCGGAC	1457
QY	1776	CAAGGACTCCAAGCCCTCCGCCAGATGGGATTTGATTTCCAGCAAGACACACCGGGG	1835
DB	1458	CAAGGACTCCAAGCCCTCCGCCAGATGGGATTTGATTTCCAGCAAGACACACCGGGG	1517
QY	1836	CACCAAGATGCCCTGAACCTGAGGATGAGGTGATGAGTTCTGAGCGGTGCATTCGA	1895
DB	1518	CACCAAGATGCCCTGAACCTGAGGATGAGGTGATGAGTTCTGAGCGGTGCATTCGA	1577
QY	1896	TGCCCGCAGCATTTGATCAGCTGCGGAAGACCATGTGCGCGGTTTGTGCTACCTTTCCA	1955
DB	1578	TGCCCGCAGCATTTGATCAGCTGCGGAAGACCATGTGCGCGGTTTGTGCTACCTTTCCA	1637
QY	1956	GAGAGAGATTTTGAGAAGAAGTACTCCCGGAAGGTGGATCCCGCTTCGGAGCCTACGT	2015
DB	1638	GAGAGAGATTTTGAGAAGAAGTACTCCCGGAAGGTGGATCCCGCTTCGGAGCCTACGT	1697
QY	2016	TGCTGTGCCCTGTGTGCTTCTGCTTCACTGCTTCACTCAGCTTCTAAATTTTCCACA	2075
DB	1698	TGCTGTGCCCTGTGTGCTTCTGCTTCACTGCTTCACTCAGCTTCTAAATTTTCCACA	1757
QY	2076	CTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTAATCAGCGTGT	2135
DB	1758	CTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTAATCAGCGTGT	1817
QY	2136	GATCTGTGCTGTGTACTTCTGTTTCTGTTCCCTTAAGGCCCTGCAACGCTGTGCTCCG	2195
DB	1818	GATCTGTGCTGTGTACTTCTGTTTCTGTTTCTGTTCCCTTAAGGCCCTGCAACGCTGTGCTCCG	1877
QY	2196	CAGCATTTGCGCTCAGCGGCACATAGCAGCATGTTGGCATCTTTTCCGCTGCTGTGT	2255
DB	1878	CAGCATTTGCGCTCAGCGGCACATAGCAGCATGTTGGCATCTTTTCCGCTGCTGTGT	1937
QY	2256	GTTTACTTCTGCCATTTGCCAACATGTTTCACTGTAAACACACACCCCATACGGAGCTGTGC	2315
DB	1938	GTTTACTTCTGCCATTTGCCAACATGTTTCACTGTAAACACACACCCCATACGGAGCTGTGC	1997
QY	2316	AGCCCGGATGCTGAATTTAACCTGCTGACATCAGTGTGCTGCGCCTGACAGAGCTCAA	2375
DB	1998	AGCCCGGATGCTGAATTTAACCTGCTGACATCAGTGTGCTGCGCCTGACAGAGCTCAA	2057
QY	2376	TTACTCTCTGGGCTGTGCTCCCTGTGTGAGGGCAGCATGCCACCTGCGAGCTTTC	2435
DB	2058	TTACTCTCTGGGCTGTGCTCCCTGTGTGAGGGCAGCATGCCACCTGCGAGCTTTC	2117

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QY 2436 TGAGGTGTCC 2445
DB 2118 TGAGGTGTTC 2127

RESULT 10
AAX00462
XX ID AAX00462 standard; DNA; 4523 BP.
XX AC AAX00462;
XX
XX 25-MAY-1999 (first entry)
XX DE Human type V adenylyl cyclase coding sequence.
XX KW Type V adenylyl cyclase; human; hAC5; heart disease; brain;
XX KW therapy; diagnosis; ds.
XX OS Homo sapiens.
XX PN WO9901546-A1.
XX PD 14-JAN-1999.
XX PF 01-JUL-1998; 98WO-US13540.
XX PR 01-JUL-1997; 97US-0886362.
XX PR 01-JUL-1997; 97US-0070901.
XX PA (CORT-) COR THERAPEUTICS INC.
XX
XX Tomlinson JA;
XX WPI: 1999-106048/09.
XX P-PSDB; AAW30600.
XX
XX Newly isolated and purified human type V adenylyl cyclase (hAC5)
XX polypeptide - useful for identifying potential therapeutic agents
XX that modulate hAC5 activity, and for the diagnosis of
XX hAC5-associated diseases and disorders
XX
XX Claim 3; Fig 1a-h; 40pp; English.
XX
XX This sequence encodes the human type V adenylyl cyclase (hAC5) of the
XX invention. hAC5 has a similar putative structure to other adenylyl
XX cyclase isoforms but, like type VI, is distinguishable in that it has a
XX larger N-terminus and a relatively shorter C-terminus as it lacks the
XX C2b region. The hAC5 polypeptides are useful in assays that screen for
XX potential therapeutic agents, which modulate hAC5 activity. These
XX polypeptides are also useful in assays for the diagnosis of diseases and
XX disorders. Agonists of hAC5 are useful control agents in such assays, and
XX they may have useful effects in vivo for treating disease. Antibodies
XX acting as (ant)agonists have diagnostic and therapeutic effects, and are
XX useful in immunoassays for hAC5. (Ant)agonists are particularly useful in
XX treating diseases caused by abnormal hAC5 activity (e.g. in the heart and
XX brain), and in diseases, which are alleviated by modulating hAC5
XX activity. The oligonucleotides are useful in methods that inhibit or
XX regulate hAC5 expression in vivo and in vitro. The cloning of the human
XX isotype of AC5 enables the development of tissue-specific and selective
XX pharmacological agents for use in treating particular human diseases
XX associated with hAC5.
XX
XX Sequence 4523 BP; 840 A; 1419 C; 1428 G; 836 T; 0 other;

Query Match 48.0%; Score 1703.4; DB 20; Length 4523;
Best Local Similarity 71.3%; Pred. No. 0;
Matches 2356; Conservative 0; Mismatches 911; Indels 36; Gaps 7;

QY 214 CGAGGGGCGGCCCAAGGCAAGGCTGGGGCTCGGGCAGTGGCCCTGGGCTTC 273
DB 625 CGGCGGGCAAGGGCGCGGCCCGCAGAGCTGGAGGGCGGCCGCTGAGGGCGCGAG 684
QY 274 GAGGATACCGAGGTGACACGACAGCGGGCGGGACGGCTGAGGTGGCGCGCGGCTG 333

685 GGGTCCGGGATGCGCGGAGCTCGGCGGACTCGGGCTCGGGCGCGGGCGCGCGGTG 744
334 CCCAGAGTGGCGGATCCTGCTGGCGCGCTTTGGTGGCAGTGTCTCAGTCGAAGCAGTTC 393
745 C---TGTCCCTGGGCGCTGCTGCTGGGCTTGCAGATATTCGCTCCCAAGAGTTC 801
394 CTTTCGGCCAAAGCTGGAGCGCTGTACCAGCGGTACTTTTCCAGATGAACAGACAGCAGC 453
802 CGGTCGACAAACTGAGGGGCTGTACCAGCGCTACTTCTTCGCTGAACAGCAGCAGC 861
454 CTGACGCTGCTGGTGGCGGTGCTGTGCTCAGAGCGGTGCTGCTGCTTTTCCAAGCC 513
862 CTCACCATGCTCATGGCGGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 921
514 GCACCGCGCGCCCTCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 573
922 GCGCGCGCGCCCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 981
574 GTGGGCTCATGGTGTGTGTAAACCGGATAGCTTCCGCCAGGACTTCCATGTGGTGTG 633
982 CTCATCATGGCTGTGCTTTGCAACCGCGCGCTTCCACAGGACCATGGGCTGGCC 1041
634 AGTAAGCTGGTGTGCTGGGATCCTGCGGCGAGTGCAGGTGCGGGGCGCTTTTCGACAGAC 693
1042 TGCTATGGCTCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1101
694 CGGCGAGCGCCCTGCGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 753
1102 CCACGAGCGCTCTGAGGGCATCTGGTGGACCGTGTCTTCTATCTACACCATCTACACG 1161
754 CTCCTCCGCATCCGCATCGGGCTGCCCTCCCTCAGCGGCTGGGCTCTCCACCTTGCAT 813
1162 CTGCTGCCGCTGGCATGGGCGCGAGTGTCTCAGGGGTGCTCTCTGCTCCGCTCCAC 1221
814 TTGATCTTGGCTGGCAACTTAACCGTGGTGTGCTGCTCTCTGGAAGCAGCTCGGTGCC 873
1222 CTGGCATCTGCCCTGCGCACCAACGCCAGGACGATGCTCTGCTGAAGCAGCTGTGCTCC 1281
874 AATGCTGCTGCTTCTCTGCAACACGTCATTAGCATCTGCACACATCTACACGAG 933
1282 AATGTTCTCAATTTCTCTCTGCAACACATCTGTTGGGTGCTGCAACCATCTATCCGGCTAG 1341
934 GTGCTCAGCGCGAGCGCTTTTCAGGAGCGCGCAGTTACATCAGCGCGCGCTCCACCTG 993
1342 GTCTCCAGACAGAGCTTTCCAGGAGACCGAGAGTGCATCCAGCGCGCGCTCCACTCG 1401
994 CAGCATGAGATCGGCGAGGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1053
1402 CAGCGGGAGAACACGAGCAGGAGCGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1461
1054 ATGGAGATCAAGAGACATCAACACAAAGAGAC--ATGTTCCACAGATCTAC 1110
1462 ATGGAGATGAAGAGACATCAACGCCAAGCAGGAGGATATGATGTTTCCATGAATTTAC 1521
1111 ATACAGAGCATGACAATGTCAGCATCTCTGTTTGGAGACATTTGAGGGCTTCCACCGCTG 1170
1522 ATCCAGAAACATGACACGTGAGCATCTCTGTTTGTGACATCGAGGGCTTCCAGCGCTG 1581
1171 GCATCCCAGTGCATCGCGAGGAGTGTGTCATGACCTGAATGAGTCTTTTCCCGCGTTT 1230
1582 GGTCTCCAGTGCATCGACGAACTGTTGTCATGACCTCAAGGAGCTCTTCGCGCGCTTT 1641
1231 GACAAGCTGGCTGGGAGAAATCACTGCCCTGAGGATCAAGATCTTGGGGAGCTGTTACTAC 1290
1642 GACAAGCTGGCGGAGAAATCACTGTTTACGTATTAAGATCTTGGGGAGTGTATTATAC 1701
1291 TGTGTGTAGGGCTGCGGAGGCGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1350
1702 TCGTCTCGGGCTGCTGAGCAAGGGCTGACACGCGCCACTGCTGTGTGAGATGGCG 1761
1351 GTAGACATGATTTAGGGCCATCTCGTGTGTGCTGAGGTGACAGGTGTGAATGTGAACATG 1410

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Db 1762 ATGGACATGATGAGGGCCATCTCGTTGGTCCGGAGGTGACAGGGGTGAACGTGAACATG 1821  
QY 1411 CGCGTGGGCATCACAGCGGCGGTGCACCTGCGGCGCTCTTGCTTGGCGGAATATGCGAG 1470  
Db 1822 CGTGTGGGAATTCACAGCGGCGGAGTACACTGCGGTGCTCTTGGTCTCAGGAAGTGGCAG 1881  
QY 1471 TTCGATGTGTGGTCCCAATGATGATGACCCCTGGCCAAACACATGGAAGCAGGAAGCGGGCT 1530  
Db 1882 TTCGACGTCTGGTCTAACAGATGTCACGCTAGCCCAAGCAGATGAGGCTGCGGCAAGGCA 1941  
QY 1531 GGCGGCATCCACATCACTCGGGCAACACTGCAGTACCTGTAACGGGGACTACGGAAGTGGAG 1590  
Db 1942 GGACGCATCCACATCACCAAGAGTACACTCAACTACCTGAATGGAGTACGAGGTGGAG 2001  
QY 1591 CCAGGCGGTGGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGCACATTTAGACTTTCCCTC 1650  
Db 2002 CCAGGCTGTGGGGGAGCGCCACGCGCTACCTCAAGGAGCAGATATCGAGACCTTCCTC 2061  
QY 1651 ATCTTGGGCGCCAGCCAGAAACGAGAAAGAGGAGAAAGCATGCTGGCCAAAGCTGCAAGCGG 1710  
Db 2062 ATCTCGGCTGCAACCAAGAGCGGAAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2121  
QY 1711 ACTCGGCGCAACTCCATGGAAGGCTGATGCGCGGATGGGTTCTGATCGTGGCTTCCTC 1770  
Db 2122 CAGAGAACCAACTCCATCGGGCAACCCACACACTGGGGGGCTGAGCGCCCTTCCTAC 2181  
QY 1771 -----CGGACCAAGGACTCCAAGGCGCTTCGCGCAGATGGGCATTGATGATTC 1818  
Db 2182 AACCACTGGGTGGCAACCAAGGTCTCCAGGAGATGAAGCGGATGGGCTTGAAGACCC 2241  
QY 1819 AGCAGACAAACCGGGCGCCAGAGATGCCCCGTAACCCCTGAGGATGAGGTGAGTTC 1878  
Db 2242 A-----AGGACAGAAACCGCCAGGAGAGTCCGAACCCCTGAGGATGAAGTGAAGTTC 2295  
QY 1879 CTGAGCGTCCCATCGATGCGCGCAGCATTTGATCAGCTGCGGAAGGACCATGTCGCGCGG 1938  
Db 2296 CTGGCGCTGCCATGACGCGCAGAGCATTTGATAGGTTCCGGTCTGAGCAGCTCCCGAAG 2355  
QY 1939 TTTTGTCTACCTTCCAGAGAGAGGATTTTGAAGAAGTACTCCCGGAAGTGGATCCC 1998  
Db 2356 TTCTCTCGACCTTCAGGGAGCGCTGACTTAGAGAAGAAGTACTCCAAGCAGGTAGACGAC 2415  
QY 1999 CGCTTCGGAGCCTACGTGTGCGCTGTGCGCTGTGGTCTTCTGCTTCATCTGCTCATCCAG 2058  
Db 2416 CGATTTGGTGCCTATGTGGGTGTGCGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 2475  
QY 2059 CTTCCTAATTTTCCACACTCCACCCTGATGCTGGGATTTATGCCAGCATCTTCCTGCTG 2118  
Db 2476 ATCACCATCGTGGCCCACTCCATATTCTCATGCTCAGCTCTACCTGACCTGTTCCCTGCTG 2535  
QY 2119 CTGCTAATCACCCTGCTGATCTGTGCTGTACTCTCTGTTGTTCTCTGTTCCCTAAGGCC 2178  
Db 2536 CTGACCTTGGTGGTGTGTGCTGTGATCTACTCTGCTGCTAAAGCTCTTCCCTTCCCA 2595  
QY 2179 CTGCAAGCTGTGCCGAGCATTTGCCGTCAAGGAGCAGATGAGCAGGCGAGTGGCATC 2238  
Db 2596 CTGCAGACCTCTCCAGGAAGATGTCGCGCTCAAGATGAAGCAGCCTGTTGGGGTG 2655  
QY 2239 TTTTCCGTCTGCTGTGTTTACTTCTGCCATTTGCCAGATGTTCACTCTGTAACCAACC 2298  
Db 2656 TTCACCATCACCCTGGTGTGTTTCTGGGGCTTTTGTCAACATGTTTCAAGTGAACCTCCAGG 2715  
QY 2299 CCCATACGAGCTGTGAGCGCGGATGCTCAATTTTAAACCTGCTGATCATCACTGCTGCTG 2358  
Db 2716 GACCTGCTGGGCTGTGGCAGAGGACCAACATCAGCGCGGAGGCTCAAGCGTGT 2775  
QY 2359 CACCTGCAGCAG-----CTCAATTAATCTCTGGGCGTGGATGCTCCCTCTGTGTAGGGC 2412  
Db 2776 CACGTGGCGGAGTCGGCGCTCAACTACAGCCTGGCGCATCAGCAGGGCTTCTGTGGCAGC 2835  
QY 2413 ACCATGCCCACTGACGCTTTCTGTAGGTGTCCATCGGGAACATGCTGTGAGTCTCTTG 2472  
Db 2836 CCCTGGCCCAACTGCAACTTCCCGGAGTACTTCACTTACAGCGTGTGCTGCTGAGCCTGCTG

QY 2473 GCCAGCTCTGCTTCTTCCATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGTCTTG 2532  
Db 2896 GCCTGCTCCGTGTTCTTGCAGATCAGTGCATCGGGAAGCTGGTGCATGCTGCGCCATC 2955  
QY 2533 GGGCTCATCTATTGTTGGTGTCTTCTGCTGGGTCCGCCAGCGGCCATCTTTGACAACTAT 2592  
Db 2956 GAGCTCATCTA--CGTGTCTCATGTGGAGGTGCAGGTGTCAAGCTTCTCGACAAGGCC 3012  
QY 2593 GACCTACTGCTTGGCGCCATGGCTTGGCTTCTTCCAATGAGACCTTTGATGGGCTGGAC 2652  
Db 3013 GACCTGCTGTGTCACCGCAAGCCCATAGACTTCTTCA---ACAACGGGAGCTTCCAGTGC 3069  
QY 2653 TGTCCAGCTCAGGAGGTTGGCCCTCAAAATATATGATACCCCTGTGATTTCTGCTGGTGT 2712  
Db 3070 CCTGAGCATGCACCAAGGTGGCATTTGAAGTGGTGAGGCCCATCATCATCTCACTCTT 3129  
QY 2713 GCGCTGGCGTGTATCTGTCATGTCAGCAGTGGAAATGAGTGCCTCCGCCCTAAACTTCCTC 2772  
Db 3130 GTGCTGGCCCTGTACTTGCACGCGCCAGCAGTGGAGTCCACTGCGCCGCTCGACTTCCTC 3189  
QY 2773 TGGAACTCAGCAACAGGGGAAAGAGAGATGAGGAGCTACAGGAGTACAAGCATACAACGG 2832  
Db 3190 TGGAACTGCAAGCCACAGAGGAGAAAGAGAGATGAGGAGCTGCAAGGCTTACAACCGG 3249  
QY 2833 AGGCTGTGTCATAAATCTTCCCAAGAGCTGGCGGCCCACTTCTTGGCCCGGAGCGC 2892  
Db 3250 CGGCTGCTGCACAACATCTTCCCAAGSAGCTGGCCGCTCACTTCTTGGCCCGGAGCGG 3309  
QY 2893 CGCAATGATGAATCTACTATCAGTCTGTGAGTGTGTGGTGTATGTTGTTGCTTCCAT 2952  
Db 3310 CGCAATGATGAGCTTACTATCAGTCTGTGAGTGTGTGGCGGTCACTGTTGCTGCTCCATC 3369  
QY 2953 GCCAACTTCTGAGTTCTATGTGGAGCTGGAGCAACAATAGGCTGCGGAGTGCCTG 3012  
Db 3370 GCCAACTTCTCCAGTTCTACGTTGAGCTGGAGCCCAACAGAGGTGTGAGTGGCTG 3429  
QY 3013 CGGCTCAACAGATCATCGCTGACTTTTGTAGATTTATCAGCAGGAGCGCTTCCCGG 3072  
Db 3430 CGGCTACTCAATGAGATCATCGCTGACTTTGTAGATCATCATCAGCAGGATCGGTTCCGG 3489  
QY 3073 CAGCTGAAAAGATCAAGACGATTTGGTAGCACTACATGCTGCTGCTGACTACGCCATCGG 3132  
Db 3490 CAGCTGGAGAAGATCAAGACCATCGGAGCAGCTTACATGCTGCTCCGCCCTCAACGAC 3549  
QY 3133 AGCACTTACATCAGTGGCGCGCTCCACATCACTGCCCTGGCTGACTACGCCATCGG 3192  
Db 3550 TCTACCTTACGACAGGTGGGCAAGACCCATCAAGGCACTGGCCGACTTTGCCATGAAG 3609  
QY 3193 CTGATGAGCAGATGAAGCAGCATCAATGAGCACTCTCTTCAACAATTTCCAGATGAAGATT 3252  
Db 3610 CTGATGAGCAGATGAAGTACATCAATCAGCACTCTCTTCAACAATTTCCAGATGAAGATC 3669  
QY 3253 GGGCTGAACATGGGCCAGCTGTTGGCAGGTGTCTATCGGGCTCGGAAGCAGCAGATGAC 3312  
Db 3670 GGGCTAACTCGGCCCGTGGTGGCGGGTGTATAGGGCAGCAAGAAAGCTCTCACTAGAC 3729  
QY 3313 ATCTGGGGGAACACAGATGATGCTCTAGTCTGTATGACAGCAGCGGGTCCCGGACCGA 3372  
Db 3730 ATCTGGGGCAATACCGTGAACGTTGGCCAGCGCATGAGACAGCCGCTGTACCGGACCGC 3789  
QY 3373 ATCAGGTGACCAAGGAGCTGTACAGGTTCTAGCTGCCAAGGCTTACCAGCTGGAGTGT 3432  
Db 3790 ATCCAGTCCACACAGACATGTACCAGTGTGCTGGCTGCCAAGCAGTACCAGCTGGAGTGC 3849  
QY 3433 CGAGGGTGTCTAAGGTGAAGGCAAGGGGAGATGACCACTTCTTCTCAATGAGGGG 3492  
Db 3850 CGGGGCTGTCTAAGGTCAAGGGCAAGGGCAGATGATGACTTCTTCTTCAATGGAGG 3909  
QY 3493 CCC 3495  
Db 3910 CCC 3912



Qy	583	ATGTTGTGTGTTAAACGGCATAGCTTCCGCCAGGACTCAATGTGGTGTTGGTAGTAACGTG	644
Db	766	GCGTGTCTGTTCGAACCGCGCGCTTCCACACAGAACCATGGCGCTGGCCTGTCTACGCG	825
Qy	643	GTGCTGGCATCTCTGGCGCAGTGCAGSTCGGGGGCGCTTTCCGACGACAGACCCGCGCAGC	702
Db	826	CTCATCGCGTGTGTGGCCGTGTGACAGTGTGGGCGTGTCTGCTCCCCACGCGCGCAGC	885
Qy	703	CCCTCTCGGGCCCTCTGGTGCCTGTGTCTTTGTATACATCGCATACACGCTCTCTCCCC	762
Db	886	GCCTCCGAGGSCATCTGGTGGACCGTGTCTTCATCTACACCATCTACACGCTGCTGCC	945
Qy	763	ATCGCATGCGGGCTGCGGTCTCTCACGGCGCTGGGCGCTCTCCACCTTGCATTGATTTG	822
Db	946	GTGCGCATGCGGCGCGCGCTCTCTCACGGGAGTGTCTCTGCGGCGCTCGCATGTGCCCATC	1005
Qy	823	GCCTGGCAACTTAACCGTGTGTATGCTTCCCTCTGGAAGCAGCTCGGTGCCAATGTGCTG	882
Db	1006	GCCCTGGCGCCAAAGCCCAAGHACCGGTTCCTGTCTCAAGCAGCTCGTCTCAATGTCTCT	1065
Qy	883	CTGTTCTCTTGCAACCAAGCTCATTAGCATCTGCACACACTATCCACGACAGAGTGTCTCAG	942
Db	1066	ATTTTCTCTGCAACAACATCTGTGGTGTCTGTACCCACTACCGGCTGACGTCTCCAG	1125
Qy	943	CGCAGGCGCTTTCCAGGAGACCCGCACTTACATCCAGGCCGGCTCCACCTCGACGATGAG	1002
Db	1126	AGACAGCCCTTCCAAGAGACCCGGGAGTGCATCCAGGACAGCGCTCCACTCGCAACGGGAG	1185
Qy	1003	AATCGCAGCAGCAGCGGCTGTCTGTCTGGGTATATGCCCCAGCAGCTTGGCATGGAGATG	1062
Db	1186	AACGACAACAGGAGCGGCTCTGTCTGTCTGTCTGCCCCGACAGCTTGGCATGGAGATG	1245
Qy	1063	AAAGAACAATCAACCAAAAAAGAGA---CATGTCTCCACAAGATCTACATACAGAAAG	1119
Db	1246	AAAGCAGACATCAATGCCAAGCAGGAGATATGATGTCTCCATAAGATTACATCCAGAAA	1305
Qy	1120	CATGACAATCTGACATCTCTGTTTTCAGACATTTAGAGGGCTTCCACGCGCTGCATCCCG	1179
Db	1306	CATGACAACCTGAGCATCTCTGTTGCTGACATCGAGGGCTTCCACGAGCTTGGCATCCCG	1365
Qy	1180	TGCACTCGCAGGAGCTGGTTCATGACCCCTGAATGAGCTCTTTTGGCCGGTTTTGACAAGCTG	1239
Db	1366	TGCACTGCCACAGAGCTGTCTATGACCGCTCAATGAGCTCTTCCGCCCGCTTCGACAAGCTG	1425
Qy	1240	GCTCGCGAGAATCACTGSCCTGAGGATCAAGATCTTTGGGGAGCTTTACTACTGTGTGTCA	1299
Db	1426	GCTCGGAGAATCACTGTGTTTACGTATTAAGATCTTGGGGAGTTGTATTACTGTCTCTCT	1485
Qy	1300	GGGCTGCCGAGGCGCCGGCCGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATG	1359
Db	1486	GGGCTGCTTGAAGCAGAGGCGCGACACGCGCCACTGCTGGCTGGAGATGGGATGGACATG	1545
Qy	1360	ATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTCAAGCATCGCGTGGCG	1419
Db	1546	ATTGAGGCCATCTCGTTGGTCCGGAGGTGACAGGGGTGAACGTGAACATCGCGCTGGGA	1605
Qy	1420	ATCCACAGCGGGCGGTGCATCTCGCGGCTCTTGGCTTGGCGAAATGGCAGTTGCATGTG	1479
Db	1606	ATTCAACAGCGGGCGAGTACACTGCGGTGTCTTGGTCTTCAGGAAGTGGCAGTTTCACGCTC	1665
Qy	1480	TGTTCCAATCATCTGACCCCTGGCCCAACCATGGAGCAGGAAGCGCGCTTGGCCGCATC	1539
Db	1666	TGGTCTTAATCAGCTCAGCTTGGCCCAACCATATGGAAGCTTGGAGGCAAGCTTGGGCGCATC	1725
Qy	1540	CACATCACTCGGGCAACACTTGCAGTACCTGAAACGGGAGCTACGAAGTGGAGCAGGCGGT	1599
Db	1726	CACATCAACAAAGCCACACTCAGCTACCTTGAACGGTGTACTAGAGGTGGAGCCAGGCTG	1785
Qy	1600	GTTGGCAAGCGCAACCGGTACCTCAAGGAGCAGCACATTTGAGACTTTTCTCATCTCGTGGC	1659
Db	1786	GGGGCGGAGCGCAACGCCCTACCTCAAGGAGCAGCATGTTCGAGACCCCTTCTCATCTCGTGGC	1845

[illegible]

Db	2923	CTGCATCCCGACGAAGTGGAGTCCACCGCCGCCCTCGACTTCCTCTGGAATCGCAGGCC	2982
Qy	2788	ACAGGGAAAAAGAGGAGATGGAGGAGCTACAGGCATACAACCGGAGGCTGCTGCATAAC	2847
Db	2993	ACGAGAGAGAGGAGAGATGGAGGAGCTGCGAGGCTTACAAACCGCGGCTGCTGCACAC	3042
Qy	2848	ATTCTGCCCAAGGACGTGGCGGCCCACTTCCTTGGCCGGAGCGCGCAATGATGAATC	2907
Db	3043	ATCTGCCCCAAGGACGTGGCTGCCCACTTCCTGGCCCGTGGAGCAGCAACGACGAGCTC	3102
Qy	2908	TACTATCAGTCGTGTAGTGTGTGCTGTATTATGTGTTTGCCCTCCATTGCCAACTTCTCTG	2967
Db	3103	TACTACCAGTCGTGCGAGTCGTGGGTGTATGTTGCGCTCCATGCCAACTTCTCCGAG	3162
Qy	2968	TTCTATGTGAGCTGGAGGCAACAATGAGGGTGCCGAGTGCTCGCGCTGCTCAACGAG	3027
Db	3163	TTTCAGCTGGAGCTTGAGGCCACAATGAGGGTGTGAGTGGCTGCTCAATGAG	3222
Qy	3028	ATCATCGCTGACTTTGATGAGATTATCAGCGAGAGCGGTTCGCCAGCTGSAAAAGATC	3087
Db	3223	ATCATCGCTGACTTTGATGAGATCATCAGCAGGATCGGTTTCAGGCAGCTGGAGAAGATC	3282
Qy	3088	AAGACGATTGGTAGCCACTTACATGGCTTGCGCTCAGGCTGAAGCCAGCACCTACGATCAG	3147
Db	3283	AAGACCATTTGGCAGCACTTACATGGCGGCTCAGGGCTTCAATGACTCTACATACGACAAG	3342
Qy	3148	GTGGCGCGCTCCACATCATCTGCCCTGGCTGACTACGCCATCGGCTCATGAGCAGATG	3207
Db	3343	GTGGCAAGACCCACATCAAAAGCCCTGGCTGACTTTGCCCATGAAGCTCATGACCAATG	3402
Qy	3208	AAGCACATCAATGACGACTCCTTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGCC	3267
Db	3403	AAGTACATCAATGACGACTCCTTCAACAACACTCCAGATGAAGATCGGCTCAACATCGC	3462
Qy	3268	CCAGTCGTGGCAGGTTCATCGGGGCTCGGAAGCCACAGATATGACATCTGGGGGAACACA	3327
Db	3463	CCCGTGGTGGCCGGGTGTATCGGGGCTCGCAAGCCCTCAGTACGACATCTGGGGCAATACG	3522
Qy	3328	GTGAATGTCCTAGTCGTATGGACACGCGGGTCCCGACCGAATCCAGGTGACCAACG	3387
Db	3523	GTGAATGTGGCCAGCCGCATGGACAGCCGGCGTCCGGAGCCGATCCAGTCAACCAG	3582
Qy	3388	GACCTGTACCAGGTTCTAGCTGCTGCCAAGGGCTACCCAGCTGGAGTGTGCGGGGTGCTCAAG	3447
Db	3593	GACATGTACCAGGTGTTGGCTGCCACACGTAACAGCTACAGCTCGAGTGGAGGGTGTGTCAG	3642
Qy	3448	GTGAAGGGCAAGGGGAGATGACCACTTCTTCTCAATGGGGGGCCCC	3495
Db	3643	GTCAAGGGCAAAAGCGAGATGATGACCTACTTCTCTCAACGGTGGGGCCCC	3690
RESULT 12			
AAQ37543			
ID	AAQ37543 standard; cDNA; 4356 BP.		
XX			
AC	AAQ37543;		
XX			
DT	17-JUN-1993 (first entry)		
XX			
DE	Cardiac adenylyl cyclase type V gene.		
XX			
KW	CACV; therapy; diagnostic; cardiac function; cyclic AMP; CAMP; heart;		
KW	failure; ss.		
XX			
OS	Canis familiaris.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	148..3702	
FT	/*tag= a		
XX			
PN	EP529622-A.		
XX			



PD 03-MAR-1993.  
XX PF 27-AUG-1992; 92EP-0114637.  
XX PR 29-AUG-1991; 91US-0751460.  
XX PA (AMCY ) AMERICAN CYANAMID CO.  
XX PI Ishikawa Y, Konski AF;  
XX WPI; 1993-068688/09.  
DR P-PSDB; AAR32882.  
XX  
PT Isolated nucleic acid mol. encoding Cardiac adenyllyl cyclase type  
PT V - useful for determining and modifying cardiac function  
XX  
XX Claim 1; Page 15-27; 38pp; English.  
XX  
CC Left ventricular tissue of canine heart was used as a source of mRNA.  
CC A cDNA library was prep'd. in lambda gt10 phage. A 970 bp Aat-HincII  
CC fragment from type I adenyllyl cyclase cDNA was used as probe. The  
CC clones isolated were used to obtain cDNA encoding CACV. This probe  
CC may also be used to screen a human cardiac cDNA library to obtain  
CC the cDNA encoding human CACV. CACV, its analogues and antibodies  
CC are useful in therapy or diagnostic assays, e.g. in modifying and  
CC determining cardiac function. A decrease in CACV content of the  
CC heart contributes to impaired cAMP prodn. and in heart failure. The  
CC CACV can also be used to screen for cpds. which stimulate or inhibit  
CC the activity of the cyclase.  
XX  
SQ Sequence 4356 BP; 837 A; 1367 C; 1377 G; 775 T; 0 other;

Query Match 47.6%; Score 1688.4; DB 14; Length 4356;  
Best Local Similarity 70.1%; Pred. No. 0;  
Matches 2347; Conservative 0; Mismatches 981; Indels 20; Gaps 5;

Qy 165 CACCCCTCGGGGCGCCCTCGGTCGCCCTGGCAGGATGACGCCCTTCATCCGGAGGGCGG 224  
Db 346 CGCCCTCGGGGCGGCG 405  
Qy 225 CCGAGGCAAGGGCAAGAGCTGGGGCTGGGGCAGTGGCCCTGGGCTTCGAGGATACGGA 284  
Db 406 CTCGGTGGAGCTGGGCTGGACGAGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 465  
Qy 285 GGTGACACGACACGCGGCGGCGGCTGAGGTGGCGCGCGCGCGCGCGCGCGCGCGCG 342  
Db 466 GGCGAGCG 525  
Qy 343 GGCGATCCTGCTGGCGCGCGCTTGGTGCAGGTGTTCCAGTGCAGACGATTCGTTCCGCC 402  
Db 526 CCGCGCGCTGCTGCCGCGCGCTGCTGCAGATCTTCGCTCCAGAAAGTTCGCGTGGGAC 585  
Qy 403 AAGCTGAGCGCTGTACCGCGGTACTTTTCCAGATGAACGAGCAGCGCTCACGCTG 462  
Db 586 AAGCTGAGCGGTGTACCGCGGTACTTTTCCGCTGGAACGAGCAGCGCTCACCATG 645  
Qy 463 CTGTCGCGGTGCTGCTCTCACAGCGGTGCTGCTGGCTTTCGAGCGCGCACCGCC 522  
Db 646 CTATGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 705  
Qy 523 CGCCCTCAGCGCTGCTATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 582  
Db 706 CCGTGGCGGTGCGCCACCTGGCGCGTGTGCGCGCGCGGTGCTGCTGCTGCTGCTGCTG 765  
Qy 583 ATGTTGTTGTATACCGGATAGCTTCGGCAGGACTCCATGTGGTGGTGGTGGTGGTGGT 642  
Db 766 GCGGTGCTGTCGAAACCGCGCGCTTCACCGAGGACACATGSGGCTGGCTGCTGCTG 825  
Qy 643 GTGCTGGGATCCTCGCGGAGTGCAGGTGGGGCGCTTTCGAGGAGACCGCGCGAGC 702  
Db 826 CTATGCGCGTGTGTCGCGCTGAGTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 885  
Qy 703 CCTCTCGGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 762

Db 886 GCCTCCGAGGGCATCTGCTGGACCGTGTCTTCTATCTACACCATCTACACGCTGCTGCC 945  
Qy 763 ATCCGATGCGGGCTGCGCTCTCAGCGCGCTGGCGCTCTCCACCTTCGATTTGATCTTG 822  
Db 946 GTGCGATGCGGGGCGCGCTCTCAGCGGAGTGCTCTGTGCGGCTGACCTGGCCATC 1005  
Qy 823 GCCTGGCAACTTAACCGTGGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTG 882  
Db 1006 GCCCTGCGGCCAAGCGCCAGGACCGGTCTCTGCTCAAGCAGCTGCTCTCAATGTCTCT 1065  
Qy 883 CTGTTCTCTGCACCAACGTCATTAGCATCTGCACACACTATCCAGCAGAGAGTGTCTCAG 942  
Db 1066 ATTTTCTCTGCACCAACATCGTGGTGTCTGTACCCACTACCCGCTGAGGTCTCCAG 1125  
Qy 943 CGCCAGGCTTTTCAGGAGACCGCAGTTACATCCAGCCCGCTCCACCTGCAGCATGAG 1002  
Db 1126 AGCAGGCTTTCCAGAGACCGCGGAGTGCATCCAGGACGCTCCATCCGCAAGCGGAG 1185  
Qy 1003 AATCGGACGAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1062  
Db 1186 AACCAGCAACGAGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1245  
Qy 1063 AAAGAAGACATCAACACAAAAAAGA---CATGTTCCACAAGATCTACATACAGAG 1119  
Db 1246 AAGCAGACATCAATGCCAAGCAGGAGATATGATGTTCCATAAGATTTACATCCAGAAA 1305  
Qy 1120 CATGACATGTCAGCATCCTGTTTCGACACATGAGGGCTTCACGAGCTGCATCCAG 1179  
Db 1306 CATGACACGTCAGCATCCTGTTTGTGACATCGAGGCTTCACGAGTTCGATCCAG 1365  
Qy 1180 TGCACCTGCGGAGGAGTGTGTCATGACCTGAATGAGCTTTTGGCCGGTTTGCACAGCTG 1239  
Db 1366 TGCACCTGCGGAGGAGTGTGTCATGACCTGAATGAGCTTTTGGCCGGTTTGCACAGCTG 1425  
Qy 1240 GCTCGGAGATCACTGCTGAGGATCAAGATCTTTGGGGAGCTGTACTACTGTGTGTC 1299  
Db 1426 GCTCGGAGATCACTGTTTACGTTAAGATCTTGGGGAGTGTATTACTGTGTCTCT 1485  
Qy 1300 GGGTCTCGGAGGCG 1359  
Db 1486 GGGTCTCGTGAAGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1545  
Qy 1360 ATTGAGGCGATCTCTGCTGAGTGCAGGTGACAGGTGTAATGTGAACATGCGCGTGGCG 1419  
Db 1546 ATTGAGGCGATCTCTGTTGTCGGGAGTGACAGGSGTGAACGTGAACATGCGCGTGGGA 1605  
Qy 1420 ATCCACAGCGGCGGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1479  
Db 1606 ATTACAGCGGCGGAGTACACTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1665  
Qy 1480 TGGTCCATGATGTGACCTTGGCCCAACACATGGAAGCAGGAGCGCGGCTGCGCGCATC 1539  
Db 1666 TGGTCTAATGAGTCACTGCTGCGCAACCATATGGAAGCTGGAAGCAGGCTGCGCGCATC 1725  
Qy 1540 CACATCACTCGGCAACACTGCGAGTACCTGAACCGGAGCTACGAGTGGAGCAGCGCGT 1599  
Db 1726 CCAATCAACAGGCGACACTCAGCTACCTGAACGCTGACTACGAGTGGAGCGAGCTGCG 1785  
Qy 1600 GGTGCAAGCGCAACGCTGCTCAAGGAGCAGCACTGAGACTTTCTCTCATCTCTGGGC 1659  
Db 1786 GGGGCGAGCGCAACGCTTACTCAAGGAGCAGATATCGAGACCTTCTCTCATCTCTGCGC 1845  
Qy 1660 GCCACGAGAAACGGAAG 1719  
Db 1846 TGCACCCAGAGAGCGGAAAG 1905  
Qy 1720 AACTCCATGGAAGGCTGATGCGCGATGGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1779  
Db 1906 AACTCCATGGGCAACCGCGCGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1965  
Qy 1780 GACTCCAAAGGCTTCCCGCAGATGGGCTGATGATTCAGCAAGAGAGAGAGAGAGAGAG 1837

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Db 1966 GGAGGCACACGAGTGTCCCAAGGAGATGAAGCGCATGGGCTTCGAAGACCCCAAGGACAAG 2025
QY 1838 -----CCCAAGATGCCCTGAACCCCTGAGGATCAGGTGATGAGTTCCTGAGCCCTGCCCATC 1893
Db 2026 AACGCCACGAAAGTGCACCCCTGAGGATGAAGTGGATGAATTTCTGGGCCGCGCCATT 2085
QY 1894 GATGCCCGCAGCATATGATCAGTCGCGGAAGACCATATGTCGCGCGTTTTCCTGCATCCATTC 1953
Db 2086 GAGGCCAGGAGCATCGACAGCTCGGTCGAGCAGCACCTCGCAAGTTTCCTCCTGACCTTC 2145
QY 1954 CAGAGAGAGATTTTGAGAGAGAGTACTCCCGGAAGTGGATCCCCCTTCGGAGCCTAC 2013
Db 2146 AGGAGCCTGACTTAGAAAAGAGTACTCCAAGCAGGTGATGACCATTCGGTGCCTAC 2205
QY 2014 GTTGCCCTGTGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCCTAAATTTTCCCA 2073
Db 2206 GTGGCATGTCCCTCGCTGTCTTCTTCTTCCATCTGCTTTTCCAGATCACCATCGTACC 2265
QY 2074 CACTCCACCCTGATGCTTTGGGATTTATGCCAGCATCTTCCTGCTGCTGCTGCTGCTGCTG 2133
Db 2266 CACTCCGTTGTCATGTTGAGTTTCTACTTGACCTGTTTCTGCTGCTGCTGCTGCTGCTGCTG 2325
QY 2134 CTGATCTGCTGTGTACTCTCTGTTGTTCTCTGTTCCCTAAGCCCTGCAACGTCCTGCTC 2193
Db 2326 TTTGTGTCCTGATCTATTCTCTGCTGAAGCTCTTCCCGGCCGCTCCAGAGCCTCTCG 2385
QY 2194 CGCAGCATTTGTCGCTCACCGGCACATAGCACCGCAGTTGGCATCTTTTCCGCTCCTGTT 2253
Db 2386 AGNAGATCTGCGCTCCAGACCAACAGCACCTGTGCGGGGTGTTCCACCATCACCTG 2445
QY 2254 GTGTTTACTTCTGCCATTTGCCAATGTTTCCACTGTCAACACACACCCCATACGAGAGTGT 2313
Db 2446 GTGTTCTGTCGGCTTTCGTCAACATGTTTCATGTGAACCTCGAGGACCTGTTGGGCTC 2505
QY 2314 GCAGCCGGATGCTGAATTTAAACCTGCTGACATCACTGCTGCCACCT-----CGAG 2367
Db 2506 CTGGCGCAGCAGCACACATCAGCACACAGCCGGGTCAACCGGTGCCACGTGGCGGGCTG 2565
QY 2368 CAGTCAATTTACTCTCTGGGCCCTGGATGCTCCCTCTGTGAGGCGACCATGCCACCTGTC 2427
Db 2566 GCGGCCAACCCTAGCCTGGCGGACGAGCAGGGCTTCTGCGGCACGCCCTGGCCCGAGTGC 2625
QY 2428 AGCTTTCTCAGGTGTCATCGGGAACATGCTGCTGAGTCTCTTGGCCAGCTCTGTGCTTC 2487
Db 2626 AACTTCCCGAGTACTTCACGTACAGGCTGCTGCTCAGCCTGCTGCTGCTGCTGCTGCTGCTG 2685
QY 2488 CTCACATCAGCAGCATCGGSAAGTTTGGCCATGATCTTTCTTGGGGCTCATCTATTG 2547
Db 2686 CTCGATCAGCTGCACTGGGAAGCTGGTCTCATGCTGGCCATTTGAGCTCATATA--C 2742
QY 2548 GTGCTGCTTCTGCTGGTCCCGCAGCCGCCATCTTTGACAACTATGACCTACTGCTTGGC 2607
Db 2743 GTGCTGCTGCTGAGGTGCCCGGGTCACACTGTTTGACAACTGACCTGCTGGTCAAC 2802
QY 2608 GTCCATGGCTTGGCTTCTTCCATGAGACCTTTGATGGGTGAGCTTCCAGCTGCAAGG 2667
Db 2803 GCCAACCCATAGACTTCAACAACAACAACGGGACCTTCGAGTGCCTGAGCAGCGAC 2862
QY 2668 AGGTGGCCCTCAAAATATATGACCCCTGTGATTTCTGCTGCTGTTTGGCTGGCGCTGAT 2727
Db 2863 AAGTGGCGCTGAAGTGTGAGCCCATCATCATCTCCGCTCTCTGCTGGCCCTGTAC 2922
QY 2728 CTCGATGCTCAGCAGGTGGAATGACTGCCCGCTTAACTTCTCTGGAACCTACAGGCA 2787
Db 2923 CTCGATGCCAGCAAGTGGAGTCCACGCCCGCTCGACTTCTCTGGAACCTGCAAGCC 2982
QY 2788 ACAGGGAAAAGAGAGATGGAGAGCTACAGGCATACAAACCGGAGGCTGCTGCATAAC 2847
Db 2983 ACGGAGGAGAGGAGAGATGGAGAGCTGCAAGCCCTTACAAACCGCGGCTGCTGCAAC 3042
QY 2848 ATTCTGCCCAAGGACGTGGCGGCCACTTCTTGGCCGGGAGCGCGCAATGATGACTC 2907
Db 3043 ATCTGCCCCAAGACGTGGCTGCCCACTTCTTGGCCGCTGAGCGACGCAACGAGAGCTC 3102
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QY 2908 TACTATCAGTCGTGTGAGTGTGGCTGTATATGTTTCCCTCCATTGCCAACTTCTCTGAG 2967
Db 3103 TACTACAGTCGTGCGAGTGCCTGGCTGTCATGTTGCGCTCCATCGCAACTTCTCCGAG 3162
QY 2968 TTCTATGTGAGCTGGAGGCAACAATGAGGTCGCCAGTGCCCTGCGGCTGCTCAACGAG 3027
Db 3163 TTCTACGTGGAGCTTGAGGCCACAATGAGGTCGAGTGCCTGCGCTGCTCAATGAG 3222
QY 3028 ATCATCCCTGACTTTTATGATGATTTATCAGCGAGGAGCGGTTCCGCGAGCTGGAAGAATC 3087
Db 3223 ATCATCCTGACTTTTATGATGATCATCAGCGAGGATCGGTTTCAGCGAGCTGGAAGAATC 3282
QY 3088 AAGACCATTTGGTAGCCTACATGGCTGCCTCAGGGCTGAACGCCAGCACCTACGATCAG 3147
Db 3283 AAGACCATTTGGCAGCACCCTACATGGCCGCTCAGGCCCTCAATGACTCTACATACGACAAG 3342
QY 3148 GTGGCCGCTCCACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3207
Db 3343 GTGGCAGAACCCACATCAAGGCCCTGGCTGACTTTGCCATGAAGCTCATGGACCAATG 3402
QY 3208 AAGCACATCAATGAGCACTCTTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGC 3267
Db 3403 AAGTACATCAATGAGCACTCTTCAACAATTTCCAGATGAAGATCGGGCTCAACATGGC 3462
QY 3268 CCAGTCTGTCAGGTCATCGGGGCTCGGAAGCCACAGATGATGATGATGATGATGATGATG 3327
Db 3463 CCCGTGCTGCCGGGTGATCGGGGCTCGCAAGCTCAGTACGACATCTGGGGCAATACG 3522
QY 3328 GTGAATGTCCTGATGCTATGAGCAGCAGCGGGGTGCCCGACCAATCCAGGTGACCAAG 3387
Db 3523 GTGAATGTGCCAGCCGATGGCAGCAGCGGGCTGCCGACCCATCCAGTCCAGTCCACAG 3582
QY 3388 GACCTGTACCAGCTTCTAGCTGCCAAGGCTACAGCTGGAGTCTCAGGGGTGCTCAAG 3447
Db 3583 GACATGTACCAGGTTTGGCTGCCAACACAGTACCAGCTGGAGTGCAGGGGTGCTCAAG 3642
QY 3448 GTGAAGGCCAAGGGGAGATGACCACCTACTTCTCTCAATGGGGGCCCC 3495
Db 3643 GTCAAGGCCAAGGCGAGATGATGACCTACTTCTCTCAACGTTGGGCC 3690

RESULT 13
AAA53922
ID AAA53922 standard; cDNA; 3924 BP.
XX
AC AAA53922;
XX
DT 03-JAN-2001 (first entry)
XX
Type V adenyllyl cyclase coding sequence.
DE
XX
XX Adenyllyl cyclase; type I; type II; recombinant; enzyme; CAMP;
KW cyclic AMP; adenosine monophosphate; screening; stimulation;
KW inhibition; treatment; cholera; pituitary tumour; heart failure;
KW ischaemia; endocrine disorder; cell necrosis;
KW pseudohypoparathyroidism; endocrine deficiency; human; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 3..3329
FT FT /*tag= a
FT FT /product= Type V adenyllyl cyclase
XX
PN US6107076-A.
XX
XX 22-AUG-2000.
XX
XX 04-OCT-1996; 96US-0726214.
XX
XX 04-OCT-1995; 95US-0005498.
XX
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Qy	2010	CTACGTTGCCGTGGCCCTGTTGGTCTTCCTGCCTTCATCTGCCTTCATCCAGCCTCTCAATTTT	2069
Dy	1802	CTATGTGGCCTGTGGCTCGCCTTGTTTTTTCCTCTCATCTGCTTTGTCCAGATCACCATGT	1861
Qy	2070	CCCACATCCACCCTGATGCTTGGGATTATGCCAGCATCTTCCTGCTGCTGCTAAATCAC	2129
Dy	1862	GCCCCATCCCTGTTATGCTGACTGAGCTTCACCTGTGTTTCCTGCTACTGCGCTTGGT	1921
Qy	2130	CGTGCTGATCTGTGCTGTGTAFTCTCTGGTCTCTGTTTCCCTAAGCGCCTGCAAGGCT	2189
Dy	1922	GGTGTTTATATCTGTGATCTACGCCCTGTGTGAAGCTCTTCCTCTACTCCCTGCGACACT	1981
Qy	2190	GTCOCGAGCATTTGTCOGCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCOGTCT	2249
Dy	1982	CTCCAGGAAGATAGTGGATCCAGAAGAACAAGCACGCCCTGGTCGGSGTGTTCACCATCAC	2041
Qy	2250	GCTTGTGTTTACTTCTGCCATTCGCCAACATGTTTCACTGTAAACACACCCCCATACGGAG	2309
Dy	2042	CCTGGTGTCTCTCGGCTTTTGTCAACATGTTTGTATGTGCAACTCTAAGAAACCTGGTGG	2101
Qy	2310	CTGTGCAGCCGGATGCTGAATTTAAACCTGCTGACATCACTGCTGCCACCTGCACGCA	2369
Dy	2102	TTGCTGCGAGAGAGCAACAATACAGGTGAACAGGTGAACGATGTCATGTGATGGA	2161
Qy	2370	G-----CTCAATTACTCTCTGGGCCCTGGATGCTCCCTGTGTGAGGCGACCATGCCAC	2423
Dy	2162	GTCGGCTTCAACTACAGCTGGCGACGACGAGGCTTCTGTGGCAGCCCCGATCCA	2221
Qy	2424	CTGCAGCTTTCCTGAGGTGTCCATCGGGAACATGTCTGTAGTCTTCTTWGGCAGCTCTGT	2483
Dy	2222	CTGCAACTTCCCAGAGTACTTCACTTACAGCTGTCTGCAGCCTGCTGGCTGCTCGCT	2281
Qy	2484	CTTCTGCACATCAGCAGCATCGGAAGTTGGCCATGATCTTGTCTTWGGGCTCACTCA	2543
Dy	2282	GTTCCTGCAGATCAGCTGCATCGGGAAGCTGGTGCTCATGTGGCCATCGAGCTCATCTA	2341
Qy	2544	TTTGGTGCTGCTTCTGCTGGTGCCCCAGCCGCCCATCTTTGACAACTATGACCTACTGCT	2603
Dy	2342	---CGTGCTCATGTAAGGTGGCCGCTGTCACTCTTTGACAACTGACCTTCTGCT	2398
Qy	2604	TGGGTCCATGGCTTGGCTTCTTCCAATCAGACCTTTGATGGGCTGGACTGTCCAGCTGC	2663
Dy	2399	CACGBCAAATGCCATAG---ACTTCAGCAACAACGGGACCTCCCACTGCTGAGCATGC	2455
Qy	2664	AGGAGGCTGGCCCTCAAAATATATACCCCTGTGATCTCTGTGGTGTWTGGCTGGCGCT	2723
Dy	2456	GACCAAGTGGCGCTGAGGTGGTGAGCGCCATCATCTCTGTCTTCTGTGCTGGCTCT	2515
Qy	2724	GTATCTGCATGCTCAGCAGTGGATPCGACTGCCCGCCTAACTTCCCTCTGGAACATA	2783
Dy	2516	GTATCTGCATGCTCAGCAGTGGATPCCACTGCTCGCTTGACTTCCCTCTGGAACATGCA	2575
Qy	2784	GGCAACAGGGAAAAGAGAGAGATGGAGAGCTACAGGATACAAACGGAGGCTGCTGCA	2843
Dy	2576	GGCCACAAGAGAGAGAGAGATGGAGAGCTGACGGCCTACAAACCGGCTTGTCTGCA	2635
Qy	2844	TAACTTCTCCCAAGAGCTGGCGGCCACTTCTGCGCGGAGCGCCGAATGATGA	2903
Dy	2636	CAACTTCTCCCAAGAGCTGGCTGCCACATCTCTGCGCGGAGCGGCGCAATGATGA	2695
Qy	2904	ACTCTACTATCACTGCTGTGAGTGTGGCTGTTATGTTGGCTTCCATTTGCCAACTCTC	2963
Dy	2696	ACTGTACTACCAATCTCGAGTGGCTGTGATGTTTGGCTTCCATCGCCAACTTCTC	2755
Qy	2964	TGAGTTCTATGTGGAGCTGGAGGCAACAANTGAGGCTGCCAGTGCCTTGGGCTGCTCAA	3023
Dy	2756	CGAATTTCTAGTGGAGCTAGAGGCCAACAAATGAGGGCTTTGAATGCCCTACGGCTGCTCAA	2815
Qy	3024	CGAGATCATCGCTGACTTTGATGAGATTATCAGCAGAGCGGTTTCGGCAGCTGGAAAA	3083
Dy	2816	TGAGATCATCGACACTTTGATGAGATCATCAGTAGAGATCGGTTTCAGGAGCTGGAAAA	2875
Qy	3084	GATCAAGAGCAATTGTPAGCACCTACATGCTGCCCTCAGGGGTGAACGCCAGCAGCTACGA	3143

Db	2876	GATCAAGACCATAGGTAGCACCTACATGGCTGCTCTGGCCCTCAAGGACTCCACCTATGA	2935
Qy	3144	TCAGGTGGCCCGCTCCACATCAGTCCCTGGCTGACTAGCCATGGGCTCATGGAGCA	3203
Db	2936	CAAGCAGGCAAGACCCACATCAAGGCTCTTCAGACTTCGCCATGAAGCTGATGACCA	2995
Qy	3204	GATGAAGCACATCAATGAGCACTCCCTTCAACAATTTCCAGATGAAGATTGGGCTGAACAT	3263
Db	2996	AATGAAGTACATCATGAGCACTCTTCAACAACTTCCAGATGAAGATCGGCTTACAT	3055
Qy	3264	GGCCCAAGTCGTGGCAGGTGTATCGGGCTCGGAAGCCACAGTATGACATCTGGGGGAA	3323
Db	3056	TGGACCTGTAGTGGCTGGGGTCATTGGGGCTCGCAAGCCCTCAGTATGACATCTGGGGCAA	3115
Qy	3324	CACAGTGAATGTCTCTAGTCTGATGGACAGCAGGGGGTCCCGGACCCGAATCCAGGTGAC	3383
Db	3116	TACAGTAATGTGGCCAGCCGTATGGACAGCAGTGGGGTCCCTGACCCGATCCAGGTTAC	3175
Qy	3384	CACGACCTGTACCAAGGTCTAGCTGCCAAGGCTACCAGCTGGAGTGTGAGGGGCTGGT	3443
Db	3176	TACAGATATGTACCAAGGTCTGGCCGCCAACACATACCAGCTGGAGTGGCGGGTGTGGT	3235
Qy	3444	CAAGGTGAAGGCAAGGGGAGATGACCACTACTTCTCTCAATGGGGGCC	3494
Db	3236	CAAGGTCAAGGCAAGGGTGAGATGATGACCTACTTCTCAATGGAGGCC	3286
RESULT 14			
AAD28058			
ID	AAD28058	standard; cDNA; 3137 BP.	
XX			
AC	AAD28058;		
XX			
DT	22-APR-2002	(first entry)	
XX			
DE	Human adenyl and guanylyl cyclase (ADGUC)-2 cDNA.		
XX			
KW	Human; adenyl and guanylyl cyclase; ADGUC-2; cardiovascular disorder;		
KW	angina pectoris; myocardial infarction; vision disorder; keratitis;		
KW	iritis; cataract; neurological disorder; epilepsy; Alzheimer's disease;		
KW	Pick's disease; stroke; mental disorder; mood and anxiety disorder;		
KW	reproductive disorder; infertility; endometriosis; impotence; asthma;		
KW	smooth muscle disorder; migraine; bacterial infection; gene therapy;		
KW	transgenic animal; vaccine; enzyme; ss.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	1..2514	
FT		/*tag= a	
FT		/product= "Human ADGUC-2 protein"	
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PN	WO200202757-A2.		
XX			
PD	10-JAN-2002.		
XX			
PF	26-JUN-2001; 2001WO-US20491.		
XX			
PR	29-JUN-2000; 2000US-215476P.		
PR	04-AUG-2000; 2000US-223545P.		
PR	31-AUG-2000; 2000US-229876P.		
PR	22-SEP-2000; 2000US-234838P.		
PR	29-SEP-2000; 2000US-236483P.		
XX			
PA	(INCY-) INCYTE GENOMICS INC.		
XX			
PI	Gandhi AR, Tribouley C, Ding L, Lu DAM, Lee EA, Yue H, Yang J;		
PI	Baughn MR, Thornton M, Yao MG, Wallia NK, Tang YT, Elliott VS;		
PI	Lu Y;		
XX			
WPI	2002-154740/20.		
DR	P-PSDB: AAE17130.		







Db 919 CTGGCTCGGAATGTTGGCATGGAGATGAAGGAGGACTTCCTGGAAGCCCTTGAGAGGATT 978  
Qy 1096 TTCCAAAGATCTACATACAGAAGCATGACAATGTACGATCCTGTGTCAGACATTCAG 1155  
Db 979 TTCCAAAGATTTATACATCCAGCGCATGACAACGTGAGCATCCTTTTGGAGACATCGTG 1038  
Qy 1156 GCGTTACACCGCTGGGATCCAGTGCATCTCGGAGGAGGTGGTCATGACCCCTGAATGAG 1215  
Db 1039 GCGTTACAGGCTTGGGCTCAAGTGCACGCGCCAGGAGCTGGTGAACACTCCTCAATGAG 1098  
Qy 1216 CTCCTTGGCCGGTTTGACAAGCTGGCTGCGGAGATCACTGCTGAGGATCAAGATCTTG 1275  
Db 1099 CTCCTGGGAAGTTTGACAGCTGGCCACAGAACCACTCCGCCGCATCAAGATCCTG 1158  
Qy 1276 GGGAGCTGTTACTACTGTGTGTCAGGGCTGCCGAGGCGCGGCGGCGACATGCGCCACTGC 1335  
Db 1159 GGAGATTGCTACTACTGCTGTGGCTCACTGACGCCAAGACTGACCCAGCCGACATGC 1218  
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Db 1771 AACGTTGTCCAAACCAACCCCGGCACACAGTGTCAACAGGTACATCGGCGGCTCCTGGAA 1830  
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Qy 2056 CAGCTTCTAATTTTCCACACTCAACCTGATGCTTGGGATTTATGCCAGCATCTTCCTG 2115  
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Qy 2176 GCCCTGCAACGTCCTGTCGCCGACGCAATGTTCGCTCACGGGCACATAGCACCGCACTGGC 2235  
Db 2008 AGTGTGGCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2067  
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Db 2068 TACCTACACATCACCCGGT-----CCAGTGTTCAGGGTGCCTGACCATCC 2116  
Qy 2296 ACCCCATACGAGCTGTCGACCCCGGATGCTGAATTTAAACACCTGCTCAGATCACTGCC 2355  
Db 2117 AGATCCGACCCGTTGTGCACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2175  
Qy 2356 TGCCACCTGCAAGAGCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2415  
Db 2176 -----TGTGTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2227  
Qy 2416 ATGCCCACTGAGCTTTCTGAGGTGCTGCTGAGGACATGCTGCTGCTGCTGCTGCTGCTG 2475  
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Db 2347 GTCTCTCTTGGCCAAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2406  
Qy 2596 CTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2655  
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Db 2437 GGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2496  
Qy 2716 CTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2775  
Db 2497 TGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2556  
Qy 2776 AAATACAGGCAACAGGGAAGAGAGATGGAGGAGTACAGGATACAGGAGGAGG 2835  
Db 2557 GCGGCCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2616  
Qy 2836 CTGCTGATAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2895  
Db 2617 ATTCTCTCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2676  
Qy 2896 AATGATGAACCTCTACTATCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2955  
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Db 2857 CTAGAGAAGATCAAGACCATTTGGGAGCAGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2916  
Qy 3133 -----AGCACCTAGCATCAGGTGGCGCTGCCACATCACTGCTGCTGCTGCTGCTGCTGCTG 3186  
Db 2917 GCTGGGACCAAGGCTTAAGAAGTGCATCTCTCCACCTCAGCACGCTTGGCAGATTTGGC 2976  
Qy 3187 ATCGGCTCATGAGCAGATGAAGCAGATCAATGAGCATCTCTTCAACAATTTCCAGATG 3246  
Db 2977 ATCGAGATGTTTGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3036





GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 22:08:18 ; Search time 116.945 Seconds  
(without alignments)  
9306.902 Million cell updates/sec

Title: US-09-750-240-5

Perfect score: 3549

Sequence: 1 atgtcatgttttagtgacct.....aaggaccgaagtgggcaact 3549

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Capext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*

2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*

3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*

4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*

5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3549	100.0	3549	4	US-09-008-097-5
2	3478.4	98.0	4942	4	US-09-474-076-1
3	2990.4	84.3	4046	1	US-07-793-961A-1
4	2990.4	84.3	4046	1	US-08-240-357-1
5	2751.2	77.5	4131	3	US-08-726-214-11
6	1808.4	51.0	1812	4	US-09-008-097-3
7	1703.4	48.0	4523	4	US-09-473-716-1
8	1648.2	46.4	3924	3	US-08-726-214-9
9	595	16.8	3978	3	US-08-726-214-1
10	505.2	14.2	3518	4	US-09-412-210-2
11	463.6	13.1	4601	3	US-08-726-214-15
12	459	12.9	4008	3	US-08-307-896-5
13	459	12.9	4008	3	US-08-726-214-3
14	459	12.9	4008	5	PCT-US95-11808-5
15	441.6	12.4	4533	3	US-08-726-214-5
16	433	12.2	5199	3	US-08-726-214-13
17	428	12.1	3357	3	US-08-726-214-7
18	393.2	11.1	1652	4	US-08-726-214-17
19	295.2	8.3	314	4	US-09-008-097-1
20	288.2	8.1	2092	3	US-08-307-896-6
21	288.2	8.1	2092	5	PCT-US95-11808-6
22	216.8	6.1	4473	3	US-08-894-173-1
23	216.8	6.1	4473	4	US-09-398-193-1
24	209.4	5.9	4985	4	US-09-473-717-1
25	207.8	5.9	5515	4	US-09-398-193-98
26	73	2.1	7218	1	US-08-232-463-14
27	64.4	1.8	1259	2	US-08-997-080-123

Sequence 123, App  
Sequence 123, App  
Sequence 123, App  
Sequence 122, App  
Sequence 176, App  
Sequence 176, App  
Sequence 176, App  
Sequence 176, App  
Sequence 173, App  
Sequence 173, App  
Sequence 173, App  
Sequence 173, App  
Sequence 44, Appl  
Sequence 44, Appl  
Sequence 44, Appl  
Sequence 44, Appl

## ALIGNMENTS

RESULT 1  
US-09-008-097-5  
; Sequence 5, Application US/09008097  
; Patent No. 6306830  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. Kirk  
; APPLICANT: Insel, Paul A.  
; APPLICANT: Ping, Peipei  
; APPLICANT: Post, Steven R.  
; APPLICANT: Gao, Meihua  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE  
; TITLE OF INVENTION: HEART FAILURE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/008.097  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dylan, Tyler M  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 22000-20567.21  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3549 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1...3501  
; OTHER INFORMATION:

US-09-008-097-5

Query Match 100.0%; Score 3549; DB 4; Length 3549;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGTCATGTTT	AGTGGCCCT	CTCTGGTCCCT	TAAGTGGAT	GAACGAA	AACAGCCCT	GGGGT	60		
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DB	61	GAACGCAAT	GGGCAGAAC	GTTCGGCGCGCT	TGCACT	TCGGGCAGGT	TGGCTT	CTGCACG	120		
QY	121	CCCCGCT	TATATAG	CTCCCT	CCGCGAT	GCAGAGC	CAACCC	AGCCCT	GGGGCCCC	180	
DB	121	CCCCGCT	TATATAG	CTCCCT	CCGCGAT	GCAGAGC	CAACCC	AGCCCT	GGGGCCCC	180	
QY	181	CCTCGGT	GGCCCT	GGCAGAT	GACGCC	TTTTCAT	CCGGAG	GGGGCCCC	AAG	240	
DB	181	CCTCGGT	GGCCCT	GGCAGAT	GACGCC	TTTTCAT	CCGGAG	GGGGCCCC	AAG	240	
QY	241	GAGCTGGGG	CTGGGC	AGTGGCC	TTTCGAGGAT	ACCGAG	GTGACA	CGACAGCG	300		
DB	241	GAGCTGGGG	CTGGGC	AGTGGCC	TTTCGAGGAT	ACCGAG	GTGACA	CGACAGCG	300		
QY	301	GGCGGAC	GGCTGAG	GTGGCG	CCCGAC	CGCGGT	TGCCAG	GGTGGCG	ATCCTT	GGCGC	360
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QY	361	CGTTTGG	TGTCAG	TGTTCC	AGTCCG	AGCAGT	TCCTG	TGCGG	CAAGCT	GTATC	420
DB	361	CGTTTGG	TGTCAG	TGTTCC	AGTCCG	AGCAGT	TCCTG	TGCGG	CAAGCT	GTATC	420
QY	421	CAGCGT	ACTTTT	TCCAGAT	GAAC	CAGAGC	CTTAC	CGCTG	CTG	TGGTGGTG	480
DB	421	CAGCGT	ACTTTT	TCCAGAT	GAAC	CAGAGC	CTTAC	CGCTG	CTG	TGGTGGTG	480
QY	481	CTGCT	CACAGCG	TGCTG	CTGGCT	TTTCC	AAGCGC	ACCCCG	CGCTC	TAGCGCT	540
DB	481	CTGCT	CACAGCG	TGCTG	CTGGCT	TTTCC	AAGCGC	ACCCCG	CGCTC	TAGCGCT	540
QY	541	GTGGCACT	GTGGCCT	GTGGCG	CGCCCT	GTGGT	CGGCT	CTAT	GTGGT	TAACCGG	600
DB	541	GTGGCACT	GTGGCCT	GTGGCG	CGCCCT	GTGGT	CGGCT	CTAT	GTGGT	TAACCGG	600
QY	601	CATAGCT	TCGGC	CAGACT	CCAT	GTGGT	GGTGA	GTGCT	TGGGCAT	CTCTGGCG	660
DB	601	CATAGCT	TCGGC	CAGACT	CCAT	GTGGT	GGTGA	GTGCT	TGGGCAT	CTCTGGCG	660
QY	661	GCAGT	GCAGT	CGGGCG	CTTT	CGCAGC	AGACCC	CGCGC	CTCT	GTGGGCT	720
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QY	721	TGCGCT	GTGTCT	TATATAC	TGCAT	ACACG	CTCT	CCCCAT	CCGCAT	TGCGGGCT	780
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DB	961	ACCCGAG	TTACAT	CCAGG	CCCGCT	CCACCT	CGCAT	GAGAA	TTCG	GAGAGCGG	1020





Db 2485 CCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAATTACTCTCTGGGCTGSAATGCT 2544  
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Qy 2458 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCTGTCACATCAGCAGCATCGGGAAGTTGGCC 2517  
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Qy 2518 ATGATCTTTGCTTTGGGGCTCATCTATTGTTGCTGCTCTTCTGCTGGGTCCCCAGCCGCC 2577  
Db 2665 ATGATCTTTGCTTTGGGGCTCATCTATTGTTGCTGCTCTTCTGCTGGGTCCCCAGCCACC 2724  
Qy 2578 ATCTTTGACAACTATGACCTACTCTTGGGGTCCATGGCTTGGCTTCTTCCAATGAGACC 2637  
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Qy 2638 TTTGATGGCTGAGTCTTCAGCTGCAGGAGGAGGTGGCCCTCAATATATATGACCCCTGTG 2697  
Db 2785 TTTGATGGCTGAGTCTTCAGCTGCAGGAGGAGGTGGCCCTCAATATATATGACCCCTGTG 2844  
Qy 2698 ATTCTGCTGGTGTGTTGGCTGGCCCTGTATCTGCATCTCAGCAGGTGGAATCGACTGCC 2757  
Db 2845 ATTCTGCTGGTGTGTTGGCTGGCCCTGTATCTGCATCTCAGCAGGTGGAATCGACTGCC 2904  
Qy 2758 CGCCTAACTTCTCTGGAACTACAGGCAACAGGGGAAAGAGAGATGGAGAGCTA 2817  
Db 2905 CGCCTAGACTTCTCTGGAACTACAGGCAACAGGGGAGAGAGATGGAGAGCTA 2964  
Qy 2818 CAGGCATACACCGGAGGCTGCTGCATTAACATTTCTGCCCAAGGACGTGGCGGCCACTTC 2877  
Db 2965 CAGGCATACACCGGAGGCTGCTGCATTAACATTTCTGCCCAAGGACGTGGCGGCCACTTC 3024  
Qy 2878 CTGCCCGGAGCGCCCAATGATGAATCTACTATCAGTCGCTGAGTGTGTGCTGTT 2937  
Db 3025 CTGCCCGGAGCGCCCAATGATGAATCTACTATCAGTCGCTGAGTGTGTGCTGTT 3084  
Qy 2938 ATGTTTGCTCCATTGCCAACTTCTCTGAGTTCTATGTGAGCTGGAGCAAAACAATGAG 2997  
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Qy 2998 GGTCCGAGTCCCTGGCGTCTCAAGCAGATCATCGTGACTTTGTATGAGATTAATCAGC 3057  
Db 3145 GGTCTGAGTCCCTGGCGTCTCAAGCAGATCATCGTGACTTTGTATGAGATTAATCAGC 3204  
Qy 3058 GAGCAGCGTTCCGGCAGCTGGAAGATCAAGACGATTGTAGCACCCTACATGCTGCC 3117  
Db 3205 GAGCAGCGTTCCGGCAGCTGGAAGATCAAGACGATTGTAGCACCCTACATGCTGCC 3264  
Qy 3118 TCAGGGTGAACGCCAGCACCCTAGCATCAGGTGGCGCGCTCCACATCACTGCCCTGGCT 3177  
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Qy 3238 TTCCAGATGAAGATTGGCTGAACATGGCCCACTCGTGGCAGGTGTCATCGGGGCTCGG 3297  
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Qy 3298 AAGCACAGTATGACATCTGGGGGAACACAGTGAATGTCTAGTCTGATGCAGCAGCAGC 3357  
Db 3445 AAGCACAGTATGACATCTGGGGGAACACAGTGAATGTCTAGTCTGATGCAGCAGCAGC 3504  
Qy 3358 GGGTTCGCCACCGAATCCAGGTGACCACCGACCTGTACCAAGTCTTACGTGCCAAGGCG 3417  
Db 3505 GGGTTCGCCACCGAATCCAGGTGACCACCGACCTGTACCAAGTCTTACGTGCCAAGGCG 3564  
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Qy 3478 TTCCTCAATGGGGCCCCCAGCAGTTAAACAGGGCCCCAGCCACAAAATTCAGCTGAAGGGACC 3537  
Db 3625 TTCCTCAATGGGGCCCCCAGCAGTTAAACAGGGCCCCAGCCACAAAATTCAGCTGAAGGGACC 3684  
Qy 3538 AAGGTGGGCACT 3549  
Db 3685 AAGGTGGGCACT 3696

RESULT 3  
US-07-793-961A-1  
; Sequence 1, Application US/07793961A  
; Patent No. 5334521  
; GENERAL INFORMATION:  
; APPLICANT: Yoshihiro Ishikawa  
; TITLE OF INVENTION: Cloning and Character-  
; TITLE OF INVENTION: Cloning of a Cardiac Adenylyl Cyclase  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Alan M. Gordon  
; STREET: 1937 West Main Street,  
; STREET: P.O. Box 60  
; CITY: Stamford  
; STATE: Connecticut  
; COUNTRY: USA  
; ZIP: 06904  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC AT  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: ASCII from DNA  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07793,961A  
; FILING DATE: 19911118  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gordon, Alan M.  
; REGISTRATION NUMBER: 30,637  
; REFERENCE/DOCKET NUMBER: 31,705  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 203 321 2719  
; TELEFAX: 203 321 2971  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4046 base pairs listed  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-07-793-961A-1

Query Match 84.3%; Score 2990.4; DB 1; Length 4046;  
Best Local Similarity 90.9%; Pred. No. 0;  
Matches 3229; Conservative 0; Mismatches 311; Indels 12; Gaps 4;  
Qy 1 ATGTCATGTTTGTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACAGCCCTGGGGT 60  
Db 131 ATGTCGTTGTTTGTAGTGGCTCTCTGCTCCCAAGTGGATGAACGGAACACAGCCCTGGGGT 190  
Qy 61 GAACGCAATGGCAGAAAGCGTTTCGGCGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCAGC 120  
Db 191 GAACGCAATGGCAGAAAGCGT---CCACGCGCGCGGAGCTCGGACCACTGGCTTCTGCAGC 247  
Qy 121 CCCGCTATATGAGTGTCTCGGGATGCAGAGCCACCCAGCCGCCCTGCGGGCCCC 180  
Db 248 CCCGCTATATGAGTGTCTCGGGATGCAGAGCCGCCCTGCGGGCTCCC 307

QY 181 CCTCGGTGCCCTGGCAGGATGAGCCCTTCATCCGGAGGGCGCGCCAGGAGGGCAAG 240  
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QY 241 GAGCTGGGGTGGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACAGCAGCG 300  
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; Sequence 1, Application US/08240357  
; Patent No. 5578481  
; GENERAL INFORMATION:  
; APPLICANT: Ishikawa, Yoshihiro  
; TITLE OF INVENTION: Cloning and Characterization of a  
; TITLE OF INVENTION: Cardiac Adenylyl Cyclase  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Cyanamid Plaza  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07470-8426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/240.357  
; FILING DATE: 10-MAY-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gordon, Alan M.  
; REGISTRATION NUMBER: 30,637  
; REFERENCE/DOCKET NUMBER: 31,705-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-831-3244  
; TELEFAX: 201-831-3305  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4046 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 131..3625  
US-08-240-357-1

Query Match 84.3%; Score 2990.4; DB 1; Length 4046;  
Best Local Similarity 90.9%; Pred. No. 0;  
Matches 3229; Conservative 0; Mismatches 311; Indels 12; Gaps 4;  
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RESULT 5  
US-08-726-214-11  
; Sequence 11, Application US/08726214  
; Patent No. 6107076  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Wei-Jen  
; APPLICANT: Gilman, Alfred G.  
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE  
; TITLE OF INVENTION: AND USES THEREFOR  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08726,214  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/005,498  
; FILING DATE: 04-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L.  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: UTSD:450  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4131 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-726-214-11

Query Match 77.5%; Score 2751.2; DB 3; Length 4131;  
Best Local Similarity 86.7%; Pred. No. 0;  
Matches 3080; Conservative 0; Mismatches 463; Indels 11; Gaps 4;  
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Db 1370 GCACCATGCCACTCTCTGTGGAGATGGGGGTAGACATGATCGAGGCCATCTCGCTG 1429

QY 1378 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCTGGGCATCCACAGCGGCGGTG 1437  
Db 1430 GTGCGTGAAGTGAAGGTGTAAATGTGAACATGCGCTGGGCATCCACAGCGGCGGTGA 1489  
QY 1438 CACTGCGGCTGCTTGGCTTTCGGAAATGCGATGTCATGTGTTGGTCCAATGATGTGACC 1497  
Db 1490 CACTGCGGCTGCTTGGCTTTCGGAAATGCGAGTTGATGCTGTGTTCAACAGATGTGACC 1549  
QY 1498 CTGCGCAACACATGGAAGCAGGAGCCGGCTGGCGCATCCACATCACTCGGGCAACA 1557  
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QY 1558 CTGCAGTACCTGAACCGGGACTACGAAGTGGAGCAGCGCGTGTGTCAGCAGCGAACGCG 1617  
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QY 1678 GAGGAGAAAGCATGTGCGCAAGCTGCAGGAGCTCGGGCACTCCATGGAAGGCTG 1737  
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QY 1738 ATGCGCGCATGGGTTCCTGATCGCTTCTCCGAGCAAGGACTCCAAGGCTTCCTCG 1797  
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QY 1858 GAGGATCAGGTGAGTGTCTCAGCGGTGCCATCATGCCGACAGCATGTGACAGCTG 1917  
Db 1910 GAGGATCAGGTGAGGAGTTCTGGCGCGAGCCATCATGCCGAGAGCATCGACAGCTG 1969  
QY 1918 CGAAGGACCATGTGCGCGGTTTTTCTCACCTTCCAGAGAGAGGATTTTGAAGAAG 1977  
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Db 2150 TATGCCGAGATCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2209  
QY 2158 GGTGCTCTGTTCCCTAAGGCGCTGCAACGCTGTGTCGCGAGCATGTCGCTCAGGCGCA 2217  
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QY 2278 ATGTTCACTGTAAACACACCCCATACGAGCTGTGTCAGCCGATGCTGAATTTAACA 2337  
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QY 2338 CCGTCTGACATCACTGCTGCCCTGCCAGCTGCAAGCTCAATTTACTCTCTGGGCTGGATGCT 2397  
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Qy 2458 CTGCTGAGTCTCTTGGCCAGCTCTGTCTCTCTGCACATCAGCAGCATCGGGAAGTTGGCC 2517  
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Qy 2578 ATCTTTGACAACATGACCTACTCTTGGGCTCATCTGCTTGGCTTCTTCCAAATGAGACC 2637  
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Qy 2638 TTTGATGGCTGGACTCTCAGCTGCGAGGAGGTGGCCCTCAATATATGACCCCTGTG 2697  
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Qy 2698 ATTCTGCTGTTGCTGGCTGGCGCTGTATCTGATCTCAGCAGGTGGAATCAGCTGCC 2757  
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Qy 2758 CGCCTAAACTTCTCTGAAACTACAGGCAACAGGGGAAAGAGAGATGGAGGAGCTA 2817  
Db 2810 CGCTGGACTTCTCTGGAACATCGAGCCACAGGGGAGAGAGATGGAGGAGTTG 2869  
Qy 2818 CAGCATACAAACGGAGGCTGCTGCATATCTGCCAAGAGCGTGGCGGCCACTTC 2877  
Db 2870 CAGGCTTACAACCGCGGCTGCTCATATCCTTCCCAAGGAGCTGGCTGCCACTTC 2929  
Qy 2878 CTGCCCCGGAGCGCCCAATGATGAACTCTACTATCAGTCGCTGTGATGCTGGCTGTT 2937  
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Qy 2938 ATGTTTCCCTCCATGTCGAACCTCTCTGAGTTCTATGTGAGCTGGAGGCAACAAATGAG 2997  
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Qy 3058 GAGGAGCGGTTCCGGCAGCTGGAAAGATCAAGACGATTGGTAGCACCCTACATGGCTGCC 3117  
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Qy 3418 TACCAGCTGGAGTGTCCAGGGGTGGTCAAGGTGAAGGCAAGGGGAGATGACCACCTAC 3477  
Db 3470 TACCACTGGAGTGTCCAGGGGTGGTCAAGGTGAAGGGAAGGGGAGATGACCACCTAC 3529  
Qy 3478 TTCTCAATGGGGCCCGCAGCAGTTAACAGGGCCCA--GCCACAAATTTTCACTGAAGGGA 3535  
Db 3530 TTCTCAATGGGGCCCGCAGCAGTTAGCAGAGCCACGAGTGGGAATTTCAACCAAGGGA 3589  
Qy 3536 CCAAGTGGGCACT 3549

Db 3590 CCAAGTGGGCACT 3603  
RESULT 6  
US-09-008-097-3  
: Sequence 3, Application US/09008097  
: Patent No. 6306830  
: GENERAL INFORMATION:  
: APPLICANT: Hammond, H. Kirk  
: APPLICANT: Insel, Paul A.  
: APPLICANT: Ping, Peipei  
: APPLICANT: Post, Steven R.  
: APPLICANT: Gao, Melhua  
: TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE  
: TITLE OF INVENTION: HEART FAILURE  
: NUMBER OF SEQUENCES: 9  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: MORRISON & FOERSTER  
: STREET: 755 PAGE MILL ROAD  
: CITY: PALO ALTO  
: STATE: CA  
: COUNTRY: USA  
: ZIP: 94304-1018  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette  
: COMPUTER: IBM Compatible  
: OPERATING SYSTEM: DOS  
: SOFTWARE: FastSeq for Windows Version 2.0  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/008.097  
: FILING DATE:  
: CLASSIFICATION:  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER:  
: FILING DATE:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Dylan, Tyler M  
: REGISTRATION NUMBER: 37,612  
: REFERENCE/DOCKET NUMBER: 22000-20567.21  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 650-813-5600  
: TELEFAX: 650-494-0792  
: TELEX: 706141  
: INFORMATION FOR SEQ ID NO: 3:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1812 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: double  
: TOPOLOGY: linear  
: FEATURE:  
: NAME/KEY: Coding Sequence  
: LOCATION: 1..1812  
: OTHER INFORMATION:  
US-09-008-097-3

Query Match 51.0%; Score 1808.4; DB 4; Length 1812;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 636 TAACGTGGTGTGGGCACTCTCTGGGGCGAGTCAGGTGCGGGCGCTTTTCGCAGCAGACCC 695  
Db 3 TAACGTGGTGTGGGCACTCTCTGGGGCGAGTCAGGTGCGGGCGCTTTTCGCAGCAGACCC 62  
Qy 696 GCGCAGCCCCCTCTCGGGGCGCTCTGGTGCCTGTGTTCTTTGTATACATCGCATACAGCT 755  
Db 63 GCGCAGCCCCCTCTCGGGGCGCTCTGGTGCCTGTGTTCTTTGTATACATCGCATACAGCT 122  
Qy 756 CCTCCCCATCGCATCGGGGCTGCGCTCTCAGCGGCTGGGCGCTCTCCACCTTCGATTT 815  
Db 123 CCTCCCCATCGCATCGGGGCTGCGCTCTCAGCGGCTGGGCGCTCTCCACCTTCGATTT 182  
Qy 816 GATCTTGGCCCTGGCAACTTAACCCGTGGTGTGATGCCTTCTCTGGAAGCAGCTCGGTGCCAA 875





QY 2413 ACCATGCCACCTGCGACGTTTCTGAGTGTCCATCGGGAAACATGCTGCTGAGTCTCTTG 2472  
DB 2836 CCCTGGCCCAACTGCAACTTCCCGAGTACTTCACTACAGCGTGTGCTCAGCGCTGCTG 2895  
QY 2473 GCCAGCTCTCTCTTCTGTCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTGTCTTG 2532  
DB 2896 GCTTGTCTGCTGCTTCTGTCAGATCAGCTGATCGGGAAGTGTGCTTCATCTGGCCATC 2955  
QY 2533 GGGCTCATCTATTGTTGCTGCTTCTGCTGGTCCCGCCAGCCGCTTCTTGACAACTAT 2592  
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QY 2653 TGTCCAGCTCGAGGGAGGTGGCCCTCAATATATGACCCCTGTGATTCGTGCTGGTGT 2712  
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DB 3190 TGGAACTCGAGGCCACAGAGAGAAAGAGAGATGGAGGAGCTGCAAGGCTACAACCGG 3249  
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DB 3250 CGGCTGCTGCACAACTCTGTCGCAAGGAGTGGCGGCTCATCTTCTGCGCCCGGAGCGG 3309  
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DB 3310 CGCAATGATGAGCTTACTATCATCTGCTGTGAGTGTGTGCGGTGATGTTGCGCTCATC 3369  
QY 2953 GCCAATCTCTGAGTCTATGTTGAGCTGGAGGCAAAATAGGAGTGGCGAGTGCCTG 3012  
DB 3370 GCCAATCTCTCCGAGTCTACGTTGAGTGGAGGCCAAACAGGAGGTGTCGAGTGCCTG 3429  
QY 3013 CGGCTGCTCAACAGATCATCGCTGACTTTGATGAGATATCAGCGAGGAGCGTTCGG 3072  
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QY 3073 CAGCTGAAAGATCAAGAGGATTTGTAGCACCCTACATGCTGCTCCTCAGGCTGAACGCC 3132  
DB 3490 CAGCTGGAGAAGATCAAGACCATCGCAGCACCTACATGCTGCTCCGCTCAACGAC 3549  
QY 3133 AGCACCTACGATCAGGTGGGCGCTCCCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 3192  
DB 3550 TCTTACCTAGCACAAAGTGGGCAAGACCCACATCAAGGCACTGGCCGACTTTGCCATGAAG 3609  
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DB 3730 ATCTGGGGAAATACCGTGAACCTGGCCAGCGCATGGACAGCACCGGCTTACCCGACCG 3789  
QY 3373 ATCCAGGTGACCAAGCAGCTGTACAGGTTCTAGCTGCGCAAGGCTACCAAGCTGAGTGT 3432  
DB 3790 ATCCAGGTGACCAAGCAGATGTACAGGTTCTAGGCTGCGCAAGCAGTACCAAGCTGAGTGT 3849  
QY 3433 CGAGGGGTGCTCAAGGTGAAGGGCAAGGGGAGATGACCACTTCTCTCAATGGGGG 3492  
DB 3850 CGGGGGGTGCTCAAGGTCAAGGGCAAGGGGAGATGATGACCTTCTCTCAATGAGGG 3909

QY 3493 CCC 3495  
DB 3910 CCC 3912  
RESULT 8  
US-08-726-214-9  
; Sequence 9, Application US/08726214  
; Patent No. 6107076  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Wei-Jen  
; APPLICANT: Gilman, Alfred G.  
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE  
; TITLE OF INVENTION: AND USES THEREFOR  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,214  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/005,498  
; FILING DATE: 04-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L.  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: UTSD:450  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3924 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-726-214-9 ;  
Query Match 46.4%; Score 1648.2; DB 3; Length 3924;  
Best Local Similarity 71.4%; Pred. No. 0;  
Matches 2265; Conservative 0; Mismatches 873; Indels 33; Gaps 6;

QY 345 GCATCTGCTGCTGGCGCGCTTGTGTGAGGTTCAGTTCGAAGCAGTTCGCTTCGGCCAA 404  
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QY 405 GCTGGAGCGCTTACAGCGGTACTTTTCCAGATGAACAGAGCAGCTGACGCTGT 464  
DB 188 ACTGGAGCGTCTGTACAGCGCTATTCTTCCGCTTGAACAGAGCAGCTCACCATGCT 247  
QY 465 GGTGGGCTGCTGGTGTGCTGCTACAGCGGTGCTGCTTCCAAAGCGCAGCCGCCCG 524  
DB 248 CATGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 307  
QY 525 CCTTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 584  
DB 308 GCTCCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 367  
QY 585 GGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 644  
DB 368 TGTGCTCTGCAACCGTGCAGCCCTTCCAGGAGGACATGCGGCTGCTGCTGCTGCTGCT 427



[illegible]

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Db	1568	TGGCAACAGGTTGCCAAGGAATGAAGAGATGGCTTGAGGACCCCA-----AGGA	1621
Qy	1830	CCGGGGCACCAAGATGCCCTGAACCCCTGAGGATGAGTGGATTCCTTGAGCGCTGC	1889
Db	1622	CAAGAAATGCCAGGAAAGTGCCAAACCCTGAGGATGAAGTGGACGAGTTCTGGTCCGAGC	1681
Qy	1890	CATCGATCCCGCAGCATTTGATCAGCTCGGGAAGAGACCATGTGCGCGGTTTTGTGCTCAC	1949
Db	1682	CATCGATGCCAGGAGATATTGACAGACTCGCATCCGAACACAGCTCCGAAAGATTCTCTTGAC	1741
Qy	1950	CTTCCAGAGAGAGATTTTGAAACAAGTACTCCCGGAAGTGGATCCCGCTTTCGGAGC	2009
Db	1742	CTTTAGGAGCCCGACTTTAGAGAAGATCTCCAAGCAGGTGGATACCGATTTGGTGC	1801
Qy	2010	CTAGTTGCCCTGTCGCTTGGTCTTCTGCTTCACTCTGCTTCATCCAGCTTCTAATTTT	2069
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Qy	2070	CCCACATCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCTCTGCTGCTGCTATCATC	2129
Db	1862	GCCCCACTCCCTGTTCATGCTGAGCTTCTACCTGTCGTGTTTCTGCTACTGSCCTTGT	1921
Qy	2130	CGTGTGATCTGCTGTGTACTCTGCTGTGTTCTCTGTTCCTAAGGCCCTGCAAGCTCT	2189
Db	1922	GGTGTTTATCTGTGATCTAGCCCTGTGTGAAGCTCTTCCCTACTCCCTCGAGACATCT	1981
Qy	2190	GTCCCGCAGCATTTGCCCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCCGCTCT	2249
Db	1982	CTCCAGGAAGATAGTCGATCCAAGAAGACAGCACCTGGTCGGGTGTTCAACCATCAC	2041
Qy	2250	GCTGTGTTTACTCTGCGCATTGCACATGTTTCACTGTAAACACACCCCAATACGGAG	2309
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Db	2102	TTGCTGCGCAGAGGACACACATCACGGTGAACCAAGTGAACGATGTCATGTGATGGA	2161
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Db	2162	GTCGSCCTTCAACTACAGCCTGGGCGACGAGCAGGCTTCTGTGGCAGCCCCAGTCCAA	2221
Qy	2424	CTGACGCTTTCGTGAGTGTCCATCGGGAACATGCTGCTGAGTCTCTCTGGCAGCTCTGT	2483
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Qy	2484	CTTCTGCACATCACACCATCGGGAAGTTGCCATGATCTTGTCTGGGCTCATCTA	2543
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Db	2342	---CGTGTCTCATGTAGAGGTCCCGGTTGTCACATCTTTGACACGCTGACCTTCTGGT	2398
Qy	2604	TGGCTCCATGGCTTGGCTTCTTCCAATGAGACCTTTGATGGGCTGGACTGTCCAGCTGC	2663
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Qy	2664	AGGAGGCTGGCCCTCAATATATACACCCCTGTATTCTGCTGTGTTTTCGCTGGCGCT	2723
Db	2456	GACCAAGTGGCGCTGAAGTGGTGAACGCCCATCATCATCTCTGTCTTCTGCTGGCTCT	2515
Qy	2724	GTATCTGCATGCTCAGCAGGTGGAATCGACTCCCGCCTAAACTTCTCTGGAACTACA	2783
Db	2516	GTATCTGCATGCTCAGCAGGTGGAATCCACTGCTGCCTTGACTTCTCTCTGGAACCTGCA	2575
Qy	2784	GGCAACAGGGGAAAAAGAGGAGATGGAGGAGCTACAGGCATACAAACGGAGGCTGTGCA	2843





QY	916	ACACATATCCACGAGAGGTGTCTCGCGCCAGGCTTTTCAGGAGACCCCGAGTTACATC	975
Db	799	GTGAGGATCCTGTGCTGAGCGGCCACAGAGAGGCGCTTCTGTGAGCGCCGGAATCGATT	858
QY	976	CAGGCCGGCTCCACCTGCAGCATGAGAAATCGCGAGCAGGAGCGCTGCTGTCTCGGTA	1035
Db	859	GAGGACGGCTGAGGCTGGAGGTGAGATGAGAGAGCAGGAGCGGCTGCTCATGAGCCTC	918
QY	1036	TTGCCCCAGCAGCTTGCCATGGAGATGAAGAAGACATCAACACAAAAAAGAGACATG	1095
Db	919	CTGCCCTCGGAATGTTGCCATGGAGATGAAGGAGGACTTCTCTGAGCGCCCTGAGAGGATT	978
QY	1096	TTCCACAAGATCTACATACAGAAAGCATGACAATGTCAAGCATCTCTGTTTGACAGACATTGAG	1155
Db	979	TTCCACAAGATTACATCCAGCGGATGACAACGTGAGCATCTCTTTTGACAGACATCGTG	1038
QY	1156	GGCTTCCACAGCCTGGCATCCCAAGTGCACTCGCAGAGAGCTGGTCAATGACCCCTGAATGAG	1215
Db	1039	GGCTTCCACAGGCTTGGCGTCAAGTGCAACGCCACAGAGCTGTGTGAATCTTCATGAG	1098
QY	1216	CTCTTTGCCCGGTTTGACAAGCTGGCTCGGAGAAATCACTGCTTGAGGATCAAGATCTTTG	1275
Db	1099	CTCTTCGGGAAGTTTGACGAGCTGGCCACAGAGAAACCACTGCGCCGCGCATCAAGATCCTG	1158
QY	1276	GGGGACTGTTACTACTGTGTGTCAAGGCTGCCGAGGCGCGGGCCGACCATGCGCCACTGC	1335
Db	1159	GGAGATTGCTACTTGTGCTGTGGCTCTACTCAGGCCAAGACTGACACGCGCCACTGC	1218
QY	1336	TGTTGAGATGGGGTAGACATGATTGAGCGCATCTCGCTGGTACGTGAGGTGACAGGT	1395
Db	1219	TGTTGAGATGGGCTGGACATGATCAACACCATCACTGCTGGCTGAGGCCACTGAG	1278
QY	1396	GTGAATGTGAACATGGCGGTGGCATCCACAGCGGGCGGTGCACTGCGGCGTCTTGCG	1455
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QY	1456	TTCCGGAATGCGAGTTGAGTGTGGTCCAATGATGTGACCTTGGCCACACCACTGGAA	1515
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QY	1696	GCCAACTGCAGCGACTCGGGCCAACTCCATGGAAGGCTGTATGCCCGATGGGTTCCT	1755
Db	1573	ATTCTCTCAGACATAAAACCGGCCAAGAGGATGAAGTTCAAGACCGTGTGCTACCTGCTG	1632
QY	1756	GATCGTGCCTTCTCCGGACCAAGACTCCAAGGCTTCCGCCAGATGGGCATTGATGAT	1815
Db	1633	GTGACGCTCATGCATTCGCGGAAGATGTTCAAGCCGAGATTCCTTCTCCAACGTCATG	1692
QY	1816	TCCAGCAAAAGACAACCGGGGCACCAAGATGCGCTGAAACCTGAGGATGAGGTGGATGAG	1875
Db	1693	ACCTGTGAGATGA-----CCACAGCGGAGGCACTGAGAACACGCTTCGGNAAA	1742
QY	1876	TTCTGTGCGCGTGCATCGATCCCGCAGCATTTGATCAGCTGCGGGAAGGACCATGTGCGC	1935
Db	1743	ACTCAGAAACCGCTCGTCTTTCTCTACA-----	1770
QY	1936	CGGTTTTTGTCTACCTTCCAGAGCAGGNATTTTGAGAAGAAGTACTCCCGGAAGGTGGAT	1995
Db	1771	AAGCTTGTCCAAACCAACCCCGGCACAGTGTCAACAGGTACATCGGCGGCTCTCGAA	1830

QY	1996	CCCCGCTTCGGAGCCCTACGTTGCGCTGTGCCCTTGGCTCTCTGCTGTTTCATCTCTGCTTCATC	2055
DB	1831	GGCCCCCAGATGG---AGCTGGAGATGGGAGACCTGAACCTTTCTTCAACCTCGAAGTACAAG	1887
QY	2056	CAGCTTCTAAATTTTCCACACATCCACCCCTGATGCTTTGGATTATTATGCCAGCATCTTCCCTG	2115
DB	1888	CAAGCTGAGCGAGAGGGAAGTACACCACAGCTTCAGGACGAGTATTTTCACGACGGCGGTG	1947
QY	2116	CTGCTGCTAAATCACCGTGTGTACTCTGCTGTGTACTCTGTTGTTCTCTGTTTCCCTAAG	2175
DB	1948	GTTCTGGCTCTCATTTCTGCGCCCTTATTTGGCCCTGTCTACCTTCTAATAATCCACAG	2007
QY	2176	GCCCTGCAACGTCGTGTCGCGACGATGTTCGCTCACGGGCACATAGCACCGCATGTGGC	2235
DB	2008	AGTGTGGGTCTGCTCTGCTGCTGTGTTCTGCACTGCTCTCTGCTGTGGTGGCCCTGTGCTCTG	2067
QY	2236	ATCTTTTTCGCTCTGCTGTGTTTACTTCTGCATATGCCAATGTCACCAATGTTCACTCTAACCAC	2295
DB	2068	TACCTACACATCACCGGGT-----CCAGTGTTTTCCAGGGTGGCTGACCATCC	2116
QY	2296	AGCCCATACGAGAGTGTGCAGCCCGGATGCTGAATTTAAACACCTGCTGACATCACTGCC	2355
DB	2117	AGATCGCACCGCTCTGTGTCATCTCATCTGTGTCTTAATCTACTCTGTGGCCCAAGGC-	2175
QY	2356	TGCCACCTGACAGAGCTCAATTTACTCTCTGGGCGCTGGATGCTGCCCTCTGTGTAGGGCAC	2415
DB	2176	-----TGCTGGTGGCTGCCCTTGGCTTGGTCTGGAGCTCCAGTCCCAACGGGTCCC	2227
QY	2416	ATGCCACCTGCAGCTTTCCTGAGGTGTCCATCGGGAACATGCTGCTGAGTCTCTTGGCC	2475
DB	2228	TGGTGGTCCCTGCTTCTGGGGCGCGGACCGCATGCTGTGCTG-TCCGCGCCCTCGGAGTCT	2286
QY	2476	AGCTCTGTCTTCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGTTCTTGGGG	2535
DB	2287	GGCGCCCATGCCCTGCTGTGGCGCTCTGTGGCACCCCTCCGCTGGCCATATTCTTCGGG	2346
QY	2536	CTCATCTATTTGGTGTCTGCTGGGTGCCCGCCAGCCGCCATCTTTGACAACTATGAC	2595
DB	2347	GTCTCTCTTCCAAAAATGATCTGTCTCGCGCTGCTCACCACTCTTACATCTCTGTC	2406
QY	2596	CTACTGCTTGGGCTCCATGGCTTGGCTTCTTCCAATGAGACCTTTGATGGGCTGGACTGT	2655
DB	2407	CTGGAGCTCAGCG-----GGTACAGGAAGGCCATG	2436
QY	2656	CCAGCTGACGAGGAGGTGGCCCTCAAAATATATGACCCCTGTGATTTCTGCTGGTGTTCGG	2715
DB	2437	GGGGCGGTGCCATCTCAGGGCGCAGCTTCGAGCCCATCATGGCCATCTGCTATTCTCG	2496
QY	2716	CTGGCGCTGTATCTGCATGCTCAGCAGGTGGAATCGACTGCCGCCCTAACTTCTCTG	2775
DB	2497	TGCACGCTGGCCCTGCACCCCGCAGGTGGATGTCAAGCTGCGGTGGACTACCTCTGG	2556
QY	2776	AACTTACAGGCAACAGGGGAAAAGAGAGATGGAGGAGCTACAGGCATACACCCGGAG	2835
DB	2557	GGCGCCCAAGGAGAGAGCGGGATGACATGGAAAAGTGAAGCTGGACAAACAAGAG	2616
QY	2836	CTGCTGCATAAATTTCTGCCAAGGAGCTGGCGGCCACTTCTCTGGCCCGGAGCGCGC	2895
DB	2617	ATTCTCTCAACTCTCTGCCACCCAGTTGCCCCAGCACTTCTAATGTCCAACCTCGC	2676
QY	2896	AATGATGAACCTACTATTCAGTCTGTGAGTGTGGCTGTATGTGTGCGCTCCATTCGC	2955
DB	2677	AAATGGACCTGTATTACAGTCACTCTCGAGGTGGGGTGCATGTTTGCATCCATCCCC	2736
QY	2956	AACTTCTGTAGTTCTATGTGGAGCTGGAGGCAAAAGTAGGGGTGCCGAGTGCCTGCGG	3015
DB	2737	AACTTTCAATGACTTCTACATCGAGCTGGATGGCAACAACATGGGGTGGAAATGCTACGC	2796
QY	3016	CTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGCCAGGAGCGGTTCCCGCAG	3075
DB	2797	CTTCTGAATGAGATCATCGCTGACTTTGATGAGCTCATGGACAAGAGCTTTTACAAGGAC	2856
QY	3076	CTGGAAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCCCTCAGGGCTGAACGCC--	3132

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Db 2917 GCTGGGACCAAGCTAAGAAAGTCATCTCTCCACCTCAGCAGTGTGGCAGATTTTGGC 2976
QY 3187 ATCGGGCTCATGGAGAGATGAAGCACATCAATGAGCACTCTTCAACAATTTTCCAGATG 3246
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QY 3247 AAGATTGGGCTGAACATGGGCCAGTGGTGGCAGGTGTCTAGTCGTATGACACAGCGGGTCCCC 3366
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QY 3307 TATGACATCTGGGGACACAGTGAATGTCTCTAGTCGTATGACACAGCGGGGTTCCCC 3366
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Db 3157 GGCAGGATCAGGTACAGAGGAAGTTTACCGGCTGCTGGCGGGGTTCTTACCGCTTC 3216
QY 3427 GAGTGTGAGGGGTGTCAAGGTGAAGGCAAGGGGAGATGACCACTACTTCTTCAAT 3486
Db 3217 GTGTGCCGAGGCAAGTCAAGTGTCAAGGCAAGGGTGAGATGCTGACATACTTCTCGAA 3276
QY 3487 GGGGGCCCC 3495
Db 3277 GGCAGGACC 3285

RESULT 10
US-09-412-210-2
; Sequence 2, Application US/09412210
; Patent No. 6403358
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE
; FILE REFERENCE: 5800-47
; CURRENT APPLICATION NUMBER: US/09/412,210
; CURRENT FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3518
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 21529 adenylate cyclase
; NAME/KEY: CDS
; LOCATION: (247)...(3480)
US-09-412-210-2

Query Match 14.2%; Score 505.2; DB 4; Length 3518;
Best Local Similarity 50.0%; Pred. No. 1.6e-115;
Matches 1560; Conservative 0; Mismatches 1488; Indels 72; Gaps 9;

QY 435 CCAGATGAACAGAGCAGCGCTGACGTGCTGTGGCGGTGCTGCTGCTACACGCGT 494
Db 318 CCAGAGTACCCGCTGCTGCTGCTGTGGGGATGCTGCTGTGGCGCTCGCGCGCT 377
QY 495 GCT----GCTGGCTTTCCAGCCGCGACCCCGCCGCTCAG--CCTGCCATATGCGCACT 548
Db 378 GCTCGAGTGGCTGGGCCAGCGCGCAGGGAGCTGACCTCAGACCCGAGCTTCTCGACCAC 437
QY 549 GTTGGCTGTGCGCGCCGCTGTTGCTGGGGCTCATGGTGTGTGAACCGGCATAGCTT 608
Db 438 TGTGCTGTGCGCGCTGGCGGCTTTCGCTGCTGCTGCTGGGCTCGCTTCCGGGAGGAGCG 497
QY 609 CGGCCAGGACTCCATGTGGTGTGTGAGTAACGTGGTCTGGGCATCTCTGGCGCAGTGCA 668
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QY 569 GGTCTGGGGGGCGCTTTCGCACAGACACCGCGCAGCCCTCTGCGGGCCTCTGTTGGCCCTGT 728
Db 558 CCACGCGCTTCTCTCTTACCAGGGGGCGGTGGTGAAGCGCTGGGACAGGCTCTATTTTCT 617
QY 729 GTTCTTTGTATACATCGCATACACGCTCCCTCCCATCCGATCGGCTGCCGCTCCCTCAG 788
Db 618 CTTCTGTCATCTTACGGCGTATGCCATGCTGCCCCTTGGGCATCGGGACCGCCGCTGCG 677
QY 789 CGGCTGGGGCTCTCCACCTTGCATTTTGATCTTGGCTGGCAA-----CTTAACC 838
Db 678 GGGCTCGCGCTCTCACTCTCGCATCTGCTGCTGCTCGGCGCTGTATCTTGGGCCACAGCC 737
QY 839 GTGGTGTATGCTTCTCTCTG--GAAGACGCTCGGTGCCAATGTGCTGTGTTCTCTGTCAC 896
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QY 897 CAACGTCATTAGCATCTGCACACACTATCCAGCAGAGGTGCTCAGCGCCAGGCTTTCA 956
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QY 1017 GCGGCTGCTGCTGCTGTTGGCCCCAGCAGCTTGGCATGGATGAGATGAAGAAGACATCAA 1076
Db 918 ACACCTTCTCTTGTCCATCTTCCCTACCTGGGCGGAGAGATGAAGCAGAGATCAT 977
QY 1077 CACAA-----AAAAAGAAAGACATGTTCCACAGAT 1106
Db 978 GGCAGGCTGCAGGACAGAGGGGTACGCGCCAGAGAGCACTTAACAATTTCCACAGCCT 1037
QY 1107 CTACATACAGACATGACAATCTCAGCATCTCTGTTTGGCAGACATTTAGGGCTTTCACAG 1166
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QY 1227 GTTTGACAGCTGGCTGCGGAGAACTCACTGCTGAGGATCAAGATCTTGGGGACTGTTA 1286
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Db 1338 CATGCGGTGGCGGTGCATCAGCAGCGGTACTGTGTGGAGTCTATCGGGCTGCGAAGTG 1397
QY 1467 GCAGTTGCTGATGTGTGTCATGATGTGACCTTGGCCAAACCATGGAAGACGAGGAGCGG 1526
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QY 1527 GGCTGGCCGCATCCATCACTCGGCAACACTGCACTGCACTGCACTGCACTGCACTGCACT 1586
Db 1458 ACCAGCGGAGTGCATCAGAGGGCTACCTGCGGCCCTGCTGGCAGGGGCTTATGCTGT 1517
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QY 916 ACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCCTTTTCAGGAGACCCCGACTTACATC 975  
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Db 859 GAGGACCGGCTGAGGTGGAGGATGAGAAATGAGAAAGAGGCGGTGTCTCATGAGCCTC 918  
QY 1036 TTGCCCCAGCAGCTTGCCATGGAGATGAAGAAGACATCAACACAAAAAAGAGACATG 1095  
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QY 1156 GCGTTCCAGCAGCTGGGATCCCGAGTGCAGTGCAGCAGGAGTGTGTATGACCCCTGAATGAG 1215  
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Db 1099 CTCTTGCGGAAGTTTACAGAGCTGGCCACAGAGAACCACTGCGCCGCATCAAGATCTCTG 1158  
QY 1276 GGGGACTGTACTGTGTGTCAGGCGCTGCCGAGGCGCCGGCGGACCATGCCCCACTGCG 1335  
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QY 1336 TGTGTGAGATGGGGGTAGACATGATTTGAGGCGCATCTGCTGTGTAGTGTGAGGTGACAGGT 1395  
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Db 1279 GTGGACTTGAACATGCTGTGGGCTGACACCGGAGGCTCTCTGCGGGGTCTCTGGGC 1338  
QY 1456 TTGCGGAATGGCAGTTGCTGTCGAATGATGTGACCTGTGGCCACCAACCATGGA 1515  
Db 1339 CTGCGTAAGTGGCAGTATGATGTGTGTCAACGACGTGACCTTGCCCAACGTCATGGAG 1398  
QY 1516 GCAGGAAGCGGCTGCGCGCATCCACATGACATCGGGCAACACTGACGTACCTGAACGGG 1575  
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QY 1576 GACTACGAAGTGAGCAGCGCTGTGTGCAAGCGCAACGCTGACCTCAAGGAGCAGCAC 1635  
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QY 1636 ATTGAGACTTTCTCATCTGCGCGCCAGCCAGAAAGCGGAAAGGAGGATGCTG 1695  
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QY 1756 GATCGTGCCTTCTCCGGACCAAGGACTCCAAGGCGCTTCGCCAGATGGGCATTGATGAT 1815  
Db 1633 GTGAGCTCATGACATGCGCGGAGATGTTCAAGCCGAGATCCCTTTCTCCAAGCTCATG 1692  
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Db 1771 AACGTGTCCAAACCCCGGACACAGTGTCAACAGGTACATCGGCCCGCTCTCTGGAA 1830

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Db 1831 GCCCGCCAGATGG---AGCTGGAGATGGCAGACCTGAACCTTCTCACCCCTGAAGTACAAG 1887  
QY 2056 CAGCTTCTAATTTTCCACACTCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCTG 2115  
Db 1888 CAAGCTCAGCGAGAGCGAAAGTACCACGAGTTCAGGACGAGTATTTCAACGAGCGCGTG 1947  
QY 2116 CTGCTGCTAATCACCGTGTGATCTGCTGTGTACTCTCTGTTCTCTGTTCCCTAAG 2175  
Db 1948 GTTCTGCTCTCATTTCTGGCGGCTTATTCGGGCTTGTCTACCTTCTAATAATCCCAAG 2007  
QY 2176 GCCTGCAACGCTGTGCTCCCGCAGCATTTGCTGCTCAGCGGCACATAGCAGCATTTGGC 2235  
Db 2008 AGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2067  
QY 2236 ATCTTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2295  
Db 2068 TACCTACACATCACCCGGGT-----CCAGTGTGTTTCCAGGCTGCTGACCATCC 2116  
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Db 2228 TGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2286  
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Db 2407 CTGAGCTCAGCG-----GGTACAGGAAGGCCATG 2436  
QY 2656 CCAGCTCAGCGGAGGTGGCCCTCAAAATATATGACCCCTGTGATCTGCTGCTGCTGCTGCTG 2715  
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QY 2776 AAATCAGCAACAGGGGAAAGAGAGATGGAGGCTACAGGCTACAGGCTACAAACGGAGG 2835  
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QY 2836 CTGCTGCTAATCACTCTGCGCAAGGAGCTGGCGGCCCACTTCTGCGCGCGGAGCGCGCG 2895  
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QY 3076 CTGGAAGATCAAGACGATTTGGTAGCACCTTACATGCTGCTGCTGCTGCTGCTGCTGCTG 3132

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RESULT 10
US-09-412-210-2
; Sequence 2, Application US/09412210
; Patent No. 6403358
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE
; FILE REFERENCE: 5800-47
; CURRENT APPLICATION NUMBER: US/09/412,210
; CURRENT FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3518
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 21529 adenylate cyclase
; NAME/KEY: CDS
; LOCATION: (247)...(3480)
US-09-412-210-2
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Query Match 14.2%; Score 505.2; DB 4; Length 3518;
Best Local Similarity 50.0%; Pred. No. 1.6e-115;
Matches 1560; Conservative 0; Mismatches 1488; Indels 72; Gaps 9;

QY 435 CCAGATGAACACAGAGCAGCTGACGCTGCTGTGGGGTGGTGGTGTCTGCTCACAGCGGT 494
Db 318 CCAGCAGTACCCGCTGCTGCTGTGGGATGCTGCTGTGGCGCTCGCGCGCT 377
QY 495 GCT----GCTGGCTTTCCAGCGGCAACCGCCGCCCTCAG--CTGCTATGTGGCACT 548
Db 378 GCTCGCAGTGGCTGGCGCAGGCGGCAAGGAGTGTACCTCAGACCCGAGCTTCTGACCAC 437
QY 549 GTTGGCTGTGGCGCCCTTCTGCTGGGCTCATGGTGGTGTAAACCGGCATAGCTT 608
Db 438 TGTGCTGTGGCGCTGGCGGCTTCTGCTGTGGGCTCGCTTCCGGGAGCAGCG 497
QY 609 CCGCCAGGACTCCATGTGGTGTGTAGTAACGTGGTGTGGGCTACCTGGCGCAGTGCA 668
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QY 729 GTTCTTTGTATAGATCGCATACAGCTCTCTCCCATCCGATCCGAGTCCGCTCCTCAG 788
Db 618 CTTTGTGATCTTTCACGGCGTATGCCATGTGCTTGGCATCGGACCGCCCGCTCGC 677
QY 789 CGSCCTGGGCTCTCCACCTTGCATTTGATCTTGGCTGSCAA-----CTTAACC 838
Db 678 GGGCTCTGCTCTCACTCTCGCATCTGCTGCTCTGGGCTGTATCTTGGGCACAGCC 737
QY 839 GTGGTATGCCCTTCTCTG--GAAGCAGCTCGGTGCAATGTCTGCTGTCTCTCTGCAC 896
Db 738 GGACTCAGGCGCTGCATCTGCTCCGCGTGTGGCAGCAAAACGAGTGTCTTCTGTGCGG 797
QY 897 CAACGTCATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGGCGCAGGCTTCA 956
Db 798 GAACGTGGCAGGAGTGTACCAAGGCGTGTATGGAGCGCGCTCGGGCCACAGTTCCG 857
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QY 1017 GCGGCTGCTGTCTGCTATTTGCCAGCACGTTGCCATGGAGATGAAGAAGACATCAA 1076
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Db 1218 CTACTGTGTCTGCGCTGCCACTCTCACTGCCAGACCATGCCATCAACTGCGTGCAT 1277
QY 1347 GGGGTGAGACATGATTGAGGCCATCTGCTGTGCTGCTGAGTACAGGTGATGATGAA 1406
Db 1278 GGGCCTGGACATGTGCCGGGCCATCAGAAACTGCGGGCAGCCACTGGCTGGACATCAA 1337
QY 1407 CATGCGCTGGGATCCACAGCGCGCTGCACTCGGCGTCTTGGCTTGGCGAAATG 1466
Db 1338 CATGCTGTGGGCGTCACTGAGGAGCGTACTGTGTGGAGTCACTGGCTGCGCAAGTG 1397
QY 1467 GCAGTTCGATGTGTGCTCAATGATGTACCTTGGCCAAACCATGGAAGCAGGAGCCG 1526
Db 1398 GCAGTACGAGCTTGTGTCACATGATGTACACTGGCTTACCATGAGGAGCGCGGTGT 1457
QY 1527 GGTGCGCGCATCCACATCACTCGGCAACACTGCACTACCTGAACGGGAGCTTACGAAGT 1586
Db 1458 ACCAGGCGAGTGCATCAGAGGGCTACCTGCGCCCTGCTGGCAGGCGCTTATGCTGT 1517
QY 1587 GGAGCCAGCCCTGCTGCAAGCGCAACGCTACCTCAAGAGCAGCACCACATTCAGACTTT 1646
Db 1518 GGAGGACGAGCATGAGGATCGGAGCCCTTACCTTCGGGAGCTAGGGAGGCTTACCTA 1577
QY 1647 CTTCTTCTGGCGCCAGCAGAAACGGAAGAGGAGGAGGATGCTGCGCAAGTGCA 1706
```



[illegible]



Db	3306	GTGTCAGTATTTCTTCGGGCTTAACTCTGCTCTGAAGCTGGCTGTGCTGCTCATATTATGATC	3365
Qy	2536	CTCATCTATTTTGGTGTGCTTCTGCTGGGTCCCCAGCGCCATCTTTTGACAACATGAC	2595
Db	3366	GCCATCT-----AC	3374
Qy	2596	CTACTGCTTGGGTCATGGCTTGGCTTCTTCCATGAGACCTTTGATGGCGTGGACTGT	2655
Db	3375	GCCTCTGACAGAGACCATCTATCGAGGTCTCTTCTGAGTTATGACAACCTTGAACAC	3434
Qy	2656	CCAGCTGCAGGAGGGTGGCCCTCAAATATATGACCCCTGTGATCTGCTGGTGTGTTGGC	2715
Db	3435	AGTGGAGAAGATTTCTGGGGACCAAGGAGGCATCAGCTACTGATGGCCATTCCCTT	3494
Qy	2716	CTGGCGCTGTATCTGCATGCTCAGCAGGTGGAAATCGACTGCCCGCTTAAACTTCCCTCGG	2775
Db	3495	CTTGTGCTATTTACCATGACAGCAGCTGGAGTACACAGCCCGCTAGATTTTCCCTGTGG	3554
Qy	2776	AAACTACAGGCAACAGGGAAAAAGAGGATGGAGGAGCTACAGGCATACAACCGCAGG	2835
Db	3555	CGAGTACAGCCCAAGAGGAGATCAACGATGAGGACTTGGGGACACATGAGAAC	3614
Qy	2836	CTGCTGCATAACATTTCTGCCCAAGACGTGGCGGCCCACTTCTTGGCCCGGAGCGCCG	2895
Db	3615	ATGCTTCGCAATATCTTTACCCGGCCACGTGGCGCCGCCACTTCTCTGGAGAAGACAGAGAC	3674
Qy	2896	AATGATGAACCTCTACTATCAGTCGTGAGTGTGGGTGTATCTTTGCTCCATTTGCC	2955
Db	3675	AATGAGAGCTGTATTTCTCAATCCATATGCCGTGGGGTAAATGTTTGGCTTCCATTCCT	3734
Qy	2956	AACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAACAATAGGGTGGCGAGTGCCTCGG	3015
Db	3735	GGATTTGCAGACTTTTACTTCTCAGACAGAAATGAACAACAGGGAGTGGAAATGTCTCGC	3794
Qy	3016	CTGCTCAACGAGATCATCGCTGACTTTGNATGAGATTATACGGAGGAGCGGTTCOCGCGAG	3075
Db	3795	TTGCTGAATGAGATCATCTGCTGACTTTATGAGTTTACTTTGGAGAGGACCGCTTTTCAGGAC	3854
Qy	3076	CTGGAAGAATCAAGACGATTTGGTAGCACCTACATGGCTGCTCAGGGCTCAAGCGCCAGC	3135
Db	3855	ATAGAGAAGATTAAAGACCATTTGGTAGTACATACATGCTGTCTCAGGACTGTCACCAGAG	3914
Qy	3136	ACCTAGCA---TCAGTTGGCGCGCTCCACATCACTGCGCTGGCTGACTAGCCCATGGG	3192
Db	3915	AAACAGCAATGTGAAGATAAATGGGAGCATTTGTGTGCGCTGGCTGACTTCTCTTGGC	3974
Qy	3193	CTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTTCAACAATTTCCAGATCAAGATT	3252
Db	3975	CTGACTGAAGCATACACAGAGATCAACAGCATTCGTTCAACATTTTGAACCTCGTATT	4034
Qy	3253	GGGCTGAACATGGGCCCATGCTGTGGCAGGTGTATCGGGGTTCGGAAGCCACAGATATGAC	3312
Db	4035	GGCATCAGCCATGGCTCAGTGTAGAGGTGTAAATGGCGCTTAAGAAAACCCACAGATATGAC	4094
Qy	3313	ATCTGGGGAAACAGTGAATGTCATCTAGTCTATGGACACAGCGGGTCCCGACCGA	3372
Db	4095	ATTTGGGGTAAAACCTGTGAACCTTGGCAAGCCGAAATGGACAGCACAGGAGTGAGTGGCGCG	4154
Qy	3373	ATCCAGTGAACCAAGCACCTGTACCAGGTTCTTAGCTGCCAAGGGCTACCAGCTGGAGTGT	3432
Db	4155	ATCCAAGTTCTTGAGGAGACCTATCTCATCTCTGAAGGATCAGGGCTTTGGCCTTCGACTAC	4214
Qy	3433	CGAGGGTGGTCAAGGTGAAGGCGAAGGGGA	3464
Db	4215	CGGGGAGAGATATATGTGAAGGGCATCAGCGA	4246

```

: APPLICANT: Iyengar, Srinivas Ravi
: TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND ADENYLYL
: TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
: FILE REFERENCE: 29770
: CURRENT APPLICATION NUMBER: US/08/307,896C
: CURRENT FILING DATE: 1994-09-16
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 5
: LENGTH: 4008
: TYPE: DNA
: ORGANISM: Rattus norvegicus
US-08-307-896-5

Query Match      12.9%;   Score 459;   DB 3;   Length 4008;
Best Local Similarity 50.8%;   Pred. No. 4.9e-104;
Matches 1370;   Conservative 0;   Mismatches 1240;   Indels 87;   Gaps 8;

Qy 852 CCTGTGGAGAGAGCTGGTGGCAATGTGCTGCTCTCTGACACACGTCATTAGCAT 911
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 624 CTTGTTCTGGCAGATACTGGCCAATGTGATCATTTTCTGCGGAACITTTGGCGGAGC 683
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 912 CTGCACACACTATCCAGCAGAGGTGTCACAGCGCAGGCTTTCAGGAGACCCGCGAGTTA 971
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 684 CTACACAAGCACCTCATGGAGCTTGCCCTGCAGCAAACTCATCGGACACGTGTAATTG 743
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 972 CATCAGCGCCGGCTCCACCTCGACGATGAGAATCGGACGAGGCGGCTGCTGCTGTC 1031
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 744 CATCAAGTCCCGGATCAAGCTGGAATTTGAAAACGGCAGCAGGAACGGCTCCTGCTCTC 803
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1032 GGTATTGCCACGACGTTGCCATGGAGATGAAGAAGACATCA----- 1075
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 804 CTTGCTGCCAGCTCATACCTGGCATGGAGATGAAAGCTGAAATCATCTCAGAGGCTGCAGGG 863
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1076 -----ACACAAAAGAGAGATGTTCCACAAGATCTACATACAGAAGCA 1121
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 864 CCCCAACGACGACAGATGGAAAACACAAAACAACCTCCACAATCTGTATGCAACAGACA 923
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1122 TGACAAATGTAGCATPCTGTTTGGACAGATTTGAGGGCTTTCACGAGCCTGGCATCCCACTG 1181
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 924 CACCAACGTGAGCATATTTATACGCTGACATGTTGGCTTCACCCGCCCTTGCAAGCGATTG 983
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1182 CACTCGCAGAGCTGGTCATGACCTGAATGAGCTCTTTGGCCCGTTTGACAAGCTGGC 1241
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 984 CTCGCCCTGGCAACTGGTCCCATGCTGAATGAACCTCTTTGGGAAGTTTGATCAAAATAGC 1043
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1242 TCGCGAGAACTCACTGCCCTGAGATCAAGATCTTGGGGGACTGTTACTACTGTGCTCAGG 1301
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1044 AAGAGAGAACTGAATGCATGAGAAATTTTAGGAGACTGCTATTTACTGTGTTCCGG 1103
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1302 GTCGCGGAGGCGCGCGGCGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGAT 1361
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1104 GCTCCTATATCACTCCCTTAACCATGCCAAGAACTGTGTGAAATGGGATGCGATATGTG 1163
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1362 TGAGGCATCTCGCTGTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGCGAT 1421
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1164 GGAAGCCATGAAGAAAGTGAGGGATGCTACCGGAGTTGATATCAACATCGCGTGTAGGAGT 1223
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1422 CCACAGCGGCGCGTGCACCTCGGGCGTCTTGGCTTCCGGAATGGCAGTTTCGATGTGTG 1481
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1224 GCATTTCTGGGAACGTTCTCTGTGTGTGATTGGTCTCCAGAGTGGCGATGATGATGTGTG 1283
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1482 GTCCAATGATGTACCTCTGGCCAAACCACATGGAAGCAGGAACCGCGGTGCGCGATCCA 1541
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1284 GTCTCATGATGTTACTCTGGCAACACCATGGAAGCTGGAGAGTCCCTGGCGGTGTTCAC 1343
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1542 CATCACTCGGCGCAACACTTCGACTCTGAACGGGGACTACGAAGTGGAGCCAGCCGCTGG 1601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1344 CATTTCTTCAGTCACTCTGGAGCACTTGAATGGGCTTATAAAGTGGAGGAAGGAGATSG 1403
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1602 TGGCAAGCGCAACCGGTACCTCAAGGACGACACATTGAGACTTTTCCTCATCTCTGGGCGC 1661
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1404 TGAGATAAGAGACCCATATTTAAAGCGACACTTGGTGAACACCTACTTTGTAAAT----- 1457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 12  
US-08-307-896-5  
; Sequence 5, Application US/08307896C  
; Patent No. 6034071  
; GENERAL INFORMATION:

QY 1662 CAGCCAGAAACGGAAGAGAGAAAGCATGCTGGCCAAAGCTGACGAGGACTGGGGCAA 1721  
DB 1458 -----CAATCCCAAGGAGAGCGAGTCTCTCAGCATCTCTTCAGACCTCGACACAC 1511  
QY 1722 CTCCATGAAGAGGCTGATCGCGGATGGGTCTCTGATCGTGGCTTCTCCGGACCAAGGA 1781  
DB 1512 TCTGGAGGAGCCAAAGATGAGACATCTGTCG-----CATGACCGGGTACTTGA 1562  
QY 1782 CTCCAAGGCTTCCGCGCAGATGGCATTTGATTTCCAGCAAAAGACAAACCGGGGCCCA 1841  
DB 1563 GTCTGGGAGACCCCAAGCCATTGCGACATCTGACACAGAGATGACACACAGA 1622  
QY 1842 AGATGCCCCGAGCCCTGAGGATGAGTGGATGATTTCTTCCAGCGGTCGCCATCGATGCCCG 1901  
DB 1623 GAATGGGAAGATTAGTACCAAGGATGGCAATGGGTCAACATAATTTTCAAAATCGCAC 1682  
QY 1902 CAGCATTTGATCAGCTGCGGAGGACCATGTGCGCCGGTTTTTGTCTACCTTCCAGAGAGA 1961  
DB 1683 CTTAAGAACTTAAGTCAAGAGAGAGATTGGAAGAAAGAACTGAATGAAGAGATGATCCA 1742  
QY 1962 GGATTTTGAAGAAGTACTCCCGGAAGTGGATCCCGCTTCGGAGCCCTACGTTGCGTG 2021  
DB 1743 AGCAATTTGATGGATCAATCCAGAGCAATGGCTCAAGTCAAGACACATTTCAAAGAAT 1802  
QY 2022 TGCCCTGTTGGTCTTCTGCTTCTGCTTCTATCCAGCTTCTTAATTTTCCCACTCCAC 2081  
DB 1803 CTCCCTGCTTTCTATAAACAAGAAATATAGAAAGAAATACCGAGCTACTGCACTGCCAGC 1862  
QY 2082 CTTGATG---CTTGGGATTTATGCCAGCATCTTCTGCTGCTCTATCATCAGCTGCTGAT 2138  
DB 1863 ATTCAAGTACTAGTGAACCTGCTGCGCTCATCTTCTCTGCTGCTCATTTGATACAGAT 1922  
QY 2139 CTGTGCTGTG-----TACTCTGTGTTCTGCTGTTCC--CTAAGGCCCTGCAACG 2186  
DB 1923 ACTGTATTCCCAAAACGCTCCATCCTTGGCTTCTCTTTGGAGCTGCACTTCTCTCCCT 1982  
QY 2187 TCTGTCGGGAGCATGTCGCTCAGGGGCAATAGACACCGCAGTGGGCATCTTTCCGT 2246  
DB 1983 CATCTTCATCCTCTTGTCTGCTGCTGCGCTGACAGCTTTTGAATGAGCAAAAAGGCTC 2042  
QY 2247 CTTGCTGTGTTTACTTCTGCCATTTGCCAATGTTCAACCTGTAAACACACACCCCATACG 2306  
DB 2043 CACCTCTCATGTGGCTTTTGAATCATCAGGCATCATCGCCACCGCCCATGGCCACG 2102  
QY 2307 GAGCTGTCAGCCGGATGCTGAATTTAACAACCTGTGACATCACTGCTGCCACCTGCA 2366  
DB 2103 GATCTCCCTCACAAATGCTCACACGCTATCATACTAACCATGGCTGTGTTCAACATGTT 2162  
QY 2367 GCAGCTCAATTAATCTCTGGGCTGGATGCTCCCTGTGTGAGGCGACCATGCCACCTG 2426  
DB 2163 TTTCTTGAGCACTCTGAGGAGACACCTTCCCATGTCCTCCCATGACCAATGCAACAGT 2222  
QY 2427 CAGCTTTCTGAGGTGCTCCATCGGGAACATGCTGCTGAGTCTCTTGGCCAGCTGTGCTT 2486  
DB 2223 TTTCTGTCGGGATTAACAGCGCTGATCTTCTATGCTCGAAACTGTTTTCTCCCGTA 2282  
QY 2487 CTGCAACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGTCTTGGGCTCATCTATTT 2546  
DB 2283 CTTTATATACAGCTGATCTGCGCTGTGATCTCTGCTCGTTTTCTGAGGGTGAACATA 2342  
QY 2547 GGTGCTGCTTCTGCTGGTCCCCAGCCGCATCTTTTGACAACTATGACCTACTGCTGG 2606  
DB 2343 TGAGTTAAAAAATTTAATCATGATGTGGCACTCGTGGGTACCAACACCACTTCTACTCCA 2402  
QY 2607 CGTCCATGGCTTGGCTTCTTCCAAATGAGACCTTTTGTGCTGCTGCTGCTGCTGCTGCTG 2666  
DB 2403 CACCCATGCC---CATGTTCTGATGCGTACAGCCAGGTCCTGTTTCAGAGACCAAGCAT 2459  
QY 2667 GAGGTGGGCCCTCAATATATACCCCTGTGATTTCTGCTGGTGTGCTGCTGCTGCTGCTG 2726  
DB 2460 TTGAAAGACCTCAAGACCATGGCTCCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2519

QY 2727 TCTGCATGCTCAGCAGGTGGAATGCAATGCTGCCGCTAAACTTCTCTGGAACCTACAGGC 2786  
DB 2520 GGTTCCTGGGCAGACAGAGTGAATATTACTGTAGTTAGACTTCTTGTGGAAGAACAAGTT 2579  
QY 2787 AACAGGGGAAAAGAGAGATGGAGAGCTACAGGCATACAGGCATACAAAGGAGGTGCTGCATAA 2846  
DB 2580 CAAAAAGAGCGGAGAGATAGAAACCATGGAAGAACCTAAATCGAGTGTGCTGGAGAA 2639  
QY 2847 CATTCGCCCCAAGAGCTGGCGCCCTTCTGCGCCGCGGAGCGCGCAATGATGAAT 2906  
DB 2640 CGTGTCTCTGACACAGTGGCTGAACACTTCTTGGCCAGGAGCTGAAATAATGAGGAGCT 2899  
QY 2907 CTACTATCAGTCTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2866  
DB 2700 GTACCACCACTCTAGACTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2759  
QY 2967 GTTCTATGAGCTGGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3026  
DB 2760 GTTCTACACAGATCAGATGTGAAGGAGGCTTGAATGCTGCGGCTCTGTAATGA 2819  
QY 3027 GATCATCGCTGACTTTGATGAGATTATCAGCAGAGGAGCGGTTCCGGCAGCTGGAAGAAT 3086  
DB 2820 GATCATTTGCTGACTTTGATGATCTGCTTCTAAGCCAAAGTTTCAAGTGGTCTTCAAAAGAT 2879  
QY 3087 CAAGAGATTTGGTAGCACCCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3146  
DB 2880 CAAGACATTTGGGAGCACATACATGCGCAGCGGACTGAGTGCCTATACCCAGCCAGGA 2939  
QY 3147 GGTGGGCC-----GCTCCCACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3188  
DB 2940 GCAGCGCCAGGAACCTGAGGCTGAGTACATGACATAGGCACCATGCTGGAGTTGCATA 2999  
QY 3189 GCGGCTCATTTGAGCAGATGAAGCACATCAATGAGCACTCTTCAACAATTTCCAGATGAA 3248  
DB 3000 TGCCCTGGTGGGAAACTGGATCCCATCAATAGCACTCTTCAACGACTTCAACTGCG 3059  
QY 3249 GATTGGCTGAACATGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3308  
DB 3060 AGTGGGTCAACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3119  
QY 3309 TGACATCTGGGGAACACAGTGAATGCTCTAGTCTGATGAGCAGCAGCGGGGTCCCGGA 3368  
DB 3120 TGACATCTGGGGAACACAGTGAATGCTCTAGTCTGATGAGCAGCAGCGGGGTCCCGGA 3179  
QY 3369 CGAATCTAGGTCAGCAGCAGCTGTACAGGTTCTAGTGTGCAAGGCTTACAGGCTGGA 3428  
DB 3180 CAAAATACAGTGAAGGAGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3239  
QY 3429 GTCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3485  
DB 3240 ATGTCAGGCTATCATCAATGTGAAGGGAAGGGGACCTGAAGACATATTTTGTGAAA 3296

## RESULT 13

US-08-726-214-3

; Sequence 3, Application US/08726214

; Patent No. 6107076

; GENERAL INFORMATION:

; APPLICANT: Tang, Wei-Jen

; APPLICANT: Gilman, Alfred G.

; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White &amp; Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: United States of America

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,214  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/005,498  
FILING DATE: 04-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: USD:450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4008 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-726-214-3

Query Match 12.9%; Score 459; DB 3; Length 4008;

Best Local Similarity 50.8%; Pred. No. 4.9e-104;

Matches 1370; Conservative 0; Mismatches 1240; Indels 87; Gaps 8;

```
QY 852 CTTCTGGAACGACGTCGGTCCCAATGTCGTCTCTCTCGACCAACGCTATTAGCAT 911
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 624 CTTGTTCTGGCAGACTGCGCCCAATGATCTTTTCATTTTGGGAACCTTGGCGGAGC 683
QY 912 CTCACACACTATCCAGCAGAGGTGTCTACGCCAGCGCTTTTCAGGAGACCGCGAGTTA 971
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 684 CTACCACAAGCACTCATGGAGCTTGCCTTTCAGCAAAACCTATCGGACACAGTGTATTG 743
QY 972 CATCCAGGCCGCGCTCCACCTCGCAGCATGAGATCGGCAGCAGAGCGGCTGCTGTGTC 1031
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 744 CATCAAGTCCCGGATCAAGCTGGAATTTGAAACACGCCAGCAGGAACGGCTCTGCTCTC 803
QY 1032 GGTATTGCCCCAGCAGCTTCCCATGGAGATGAAGAGACATCA----- 1075
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 804 CTTGCTGCCAGCTCATCCCATGCCATGAGATGAAGCTGAATCATTCAGAGGCTGCAGGG 863
QY 1076 -----ACACAAAAAAGAGACATGTTCCACAAGATCTACATACAGAAGCA 1121
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 864 CCCCAAGCAGGACAGATGTAACAAACAAACAACTTCCACAATCTGTATCTCAACGACA 923
QY 1122 TGACATGTCAGCATCTCTGTTTCAGACATTTAGGGCTTCACCAGCCTGGCATCCCAAGT 1181
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 924 CACCAAGCTGAGCATATTATACGCTGACATTTGTGGCTTCACCGCGCTTGCAGCGATTG 983
QY 1182 CACTGCGCAGGAGCTGTATGACCTGATGAGCTGTTTGGCCGCTTTCACAAGCTGGC 1241
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 984 CTCCTCGGCAACTGCTCCACATGCTGAATGAACCTTTTGGGAAGTTTGATCAATAGC 1043
QY 1242 TGCAGGAATCACTGCTGAGGATCAAGATCTTTGGGAGCTGTACTACTGTGTGTCAGG 1301
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1044 AAAGGAGAATGAATGATGATGAGATTAATAATTTTAGGAGAGCTGTTACTGTGTTCGG 1103
QY 1302 CTTGCCGGAGCGCGCGCGACCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGAT 1361
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1104 GCTCCCTATATCACTCCCTAACCTAACCAAGAACTGTGTGAAAATGGGATTGGATATGT 1163
QY 1362 TGAGGCCATCTCGTGTAGCTGAGGTGACAGGTGTGAATGTGNACATCGCGTGGGCAT 1421
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1164 CGAAGCCATAAAGAAAGTAGGGATGCTACCGGAGTTGATATCAACATGCGTGTAGAGT 1223
QY 1422 CCACAGCGCGCGCTGTCAGCTGCGCGCTCTTGGCTTCGGAAATGGCAGTTTCGATGTGTG 1481
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1224 GCATCTGGGAACGCTCTCTGTGTGTGATTTGGTCTCCAGAAAGTGGCAGTATGATGTGTG 1283
QY 1482 GTCAAATGATGTGACCTGGCCCAACCAACATGGAAAGCAGGAAGCGGCTGGCCGCATCCA 1541
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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DB 1284 GTCTCATGATGTTTACTCTGGCAAAACCATGGAAGCTGGAGGATCCCTGGCGGTGTCA 1343
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1542 CATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGTGCAGCCAGCCCTGG 1601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1344 CATTTCTTTCAGTCACTCTGGAGCACCTTGAATGGGGCTTATAAAGTGGGAAGAGATGG 1403
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1602 TGGCAAGCGCAACCGCTACCTCAAGGAGCAGCACATTTGAGACTTTTCCTCATCTCTGGCGC 1661
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1404 TGAGATAAGAGACCCATATTTAAAGCAGACTTGGTGAANAACCTACTTTGTAAT----- 1457
QY 1662 CAGCCAGAAACGAAAGAGAGAAAGCATGCTGGCCAAAGTGCAGCGGATCGGGCCAA 1721
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1458 -----CAATCCCAAGGAGAGAGACGGAGTCTCTCAGCATCTCTTTCAGACTCTGACACAC 1511
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1722 CTCCTGGAAGGGCTGATGCCGCGATGGGTTCCCTGATCGTCTTCTCCCGGACCAAGGA 1781
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1512 TCTGGAGCGGAGCAAGATGAGACATCTGTCCG-----CATGACCCGGTACTTGGT 1562
QY 1782 CTCCAAGGCCCTCCGCCAGATGGGCATTTGATTTCCAGCAAAAGACAAACGGGGCACCCA 1841
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1563 GTCTGGGAGCAGCCAAAGCCATTCGCACATCTGCACCACAGAGATAGCATGACCACAGA 1622
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1842 AGATGCCCTCAACCCCTGAGGATGAGTGGATGTTCTCTGAGCGGTGCCATCGATGCCCG 1901
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1623 GAATGGGAAGATTAGTACCACGATGTGCCAATGGGTCAACATAATTTTCAAAATCGCAC 1682
QY 1902 CAGCATTTGATCTGCTGGGAGGACCATGTGCGCGGGTTTTTGGCTCACCTTCCAGAGAGA 1961
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1683 CTTAAGAACTAAGTCACAGAAGAAGATTTGAAGAAGAACTGAATGAAGGATGATCCA 1742
QY 1962 GGATTTTGAAGAAGTACTCCCGGAAGTGGATGCCCGCTTCGGAGCCCTACGTTGGCTG 2021
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1743 AGCAATTTGATGGGATCAATGCACAGAAGCAATGGCTCAAGTCAAGAAGACATTTCAAAGAAT 1802
QY 2022 TGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCCACGCTTCTAATTTTCCACACTCCAC 2081
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1803 CTCCTGCTTTTCTATAACAAGAAATATAGAGAAGAAATACCGAGCTACTGCACCTGCCAGC 1862
QY 2082 CTTGATG- --CTTGGGATTTTCCAGCATCTTCTCTGCTGCTGTAATACCGCTGCTGAT 2138
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1863 ATTCAGTACTAGTGACCTGCTGCTGCTCATCTTCTCTGCTGCTCATTTCTGTACAGAT 1922
QY 2139 CTGTGCTGTG-----TACTCTGTGTTCTCTGTTTCC--CTAAGGCCCTGCAAGC 2186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1923 ACTTGATTTGCCAAAAACGTCATCTTCTCTCTCTGCTTGGAGCTGCATTTCTCTCCCT 1982
QY 2187 TCTGTCCCGCAGCATTTGTCGCTCACGGGCACATAGCACCGCAGTTGGCATCTTTCCGT 2246
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1983 CATCTTTCATCTCTTCTGCTCTGCTGGACAGCTTTTGCAATGCGCAAAAAGGCTC 2042
QY 2247 CTTGCTTGTGTTTACTTCTGCAATTTGCCAACATGTTTCAACCTGTAACACACACCCCATACG 2306
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2043 CACCTCTCTCATGTTGGCTTTTGAANTCATCAGGCATCATGCCAACCGCCCATGCCACG 2102
QY 2307 GAGCTGTGAGCCCGGATGCTGAATTTAACCCTGCTGACATCACTGCCTGCCACCTGCA 2366
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2103 GATCTCCCTCACAATCTCACACCGGCTATCATACTAACCATGCTGTTGTTCAACATGTT 2162
QY 2367 GCAGCTCAATTACTCTCTGGCCCTGGATGCTCCCTGTGTGAGGGCACCATGCCACCTG 2426
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2163 TTTCTCAGCAAACTCTGAGGAGACAAACCTTCCCACCTGCCAATACATCAAAATGCAAAACGT 2222
QY 2427 CAGCTTTCCTGAGGTGTCCATCGGGAACATGCTGCTGAGTCTCTTGCCACAGCTCTGTCTT 2486
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2223 TTTCTCCCCGGAATCAACAGGGTGCATTTCTTCATGCTGGAACCTTGTTTTCTCCCGTA 2282
QY 2487 CTTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGTCTTGGGGCTCATCTATTT 2546
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2283 CTTTCATATACAGTGCATCTCGGCTTGATCTCTCTGCTCCGTTTCTCTGAGGGTGAAC 2342
QY 2547 GGTGCTCTCTCTGCTGGGTCCCCCAGCGGCATCTTTTGACAACATATGACCTACTGCTGG 2606
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 2343 TGAGTTAAATGTTAATCATGATGTTGGCACTCGTGGGGCTACAACACCACTTCTACTCCA 2402
QY 2607 CGTCCATGGCTTGGCTTCTTCCAAATGAGACCTTTGTATGGGCTGGACTGTCCAGCTGCAGG 2666
Db 2403 CACCCATGCC--CATGTTCTGGATGGTACAGCCAGTCTCTTTTCAGAGACCAAGCAT 2459
QY 2667 GAGGTGGCCCTCAATATATAGCCCTGTGANTTCTGCTGGTGTGGTGGCTGGCGGTGTA 2726
Db 2460 TTGGAAGACCTGAAGACCACTGGGCTCCGTGTCTACTCTCCATATTTCTTCACGCTGCT 2519
QY 2727 TCTGCATGCTCAGCAGGTGAATCGACTGCCCGCTTAACCTTCTCTGGAACTACAGGC 2786
Db 2520 GGTTCGGGACAGAGTGAATTACTGTAGTTAGACTTCTGTGGGAAGACAAGTT 2579
QY 2787 AACAGGGGAAAAAGAGAGATGGAGGAGTACAGGCATACAGCCGAGGCTGTGCATAA 2846
Db 2580 CAAAAAGAGCGGAGAGATGAAGAACCATGGAGACCTAAATCGAGTGTCTGGAGAA 2639
QY 2847 CATTCGCCCAAGGACGTGGCGGCCCACTTCTTGCGCCGGAGCGCGCAATGATNACT 2906
Db 2640 CGTGCCTTCTGCAACACGTGGCTGAACACTTCTTGCGCAGAGGCTGAAAATGAGGAGCT 2699
QY 2907 CTACTATCAGTGTGAGTGTGGCTGTATGTTTGCCTTCATTGCCAACTTCTCTGA 2966
Db 2700 GTACCACCACTGTGCTGTCTGTCTGATGTTTGCCTCCATCCGACACTCAAGGA 2759
QY 2967 GTTCTATGTGGAGTGGAGGCAACAATAGAGGTGCGAGTGTGCGGTGTCTCAACGA 3026
Db 2760 GTTCTACACAGATCAGATGTGAACAAGGAGGCTTGGAAATGCTTGGCGCTCTGAATGA 2819
QY 3027 GATCATGCTGACTTTCATCAGATATATCAGCGAGGAGCGGTTCCGGCAGCTGGAAGAAT 3086
Db 2820 GATCATTGTGACTTTCATGATCTGCTTCTTAAGCCAAAGTTTCAAGTGGTGTGAAAAGAT 2879
QY 3087 CAAGACGATTGGTAGCACCTTACATGGCTCAGGCGCTGAAGCGCCAGCACCTACGATCA 3146
Db 2880 CAAGACATTGGGAGCACATACATGGCAGCCAGGAGCTGAGTGCCATACCCAGCCAGGA 2939
QY 3147 GGTGGGCC-----GCTCCACATCACTGCCCCCTGGCTGACTACGCGCAT 3188
Db 2940 GCAGCGCCCAAGAACCTGAGCGTCAGTACATGCACATAGGCACCATGTTGGAGTTTGATA 2999
QY 3189 CGGCTCATGAGCAGATGAAGCACATCAATGAGCACTCTCTCAACAATTTCCAGATGAA 3248
Db 3000 TGCCCTGGTGGGAAACTGGATGCCATCAATAGCACTCTCTTCAACGACTTCAAACTGCG 3059
QY 3249 GATTGGGCTGAACATGGGCCAGTCTGTGGCAGGTGTCTATCGGGGCTCGGAAGCCACAGTA 3308
Db 3060 AGTGGGTATCAACCATGGGCTGTAAATAGCTGGCGCTCATAGGGGCTCAAAAGCCACAGTA 3119
QY 3309 TGACATCTGGGGGAACACAGTGAATGTCTAGTGTATGGAGCAGACGGGGGTCCCCGA 3368
Db 3120 TGACATCTGGGGGAACACTGTCAACGTGGCCAGCAGAATGGACAGACCCGGGTCTCTGA 3179
QY 3369 CCGAATCCAGGTGACCAAGCACTGTACCAAGTTTCTAGCTGCCAAGGCTACCAAGTGA 3428
Db 3180 CAAATACAGGTGACTGAGGAGACAGCCCTCATCTTGCAGACCGCTTGGCTACACGTGTAC 3239
QY 3429 GTCTCGAGGGGTGGTCAAGGTGAAGGCAAGGGGAGATGACCACCTACTTCTCTCAA 3485
Db 3240 ATGTCGAGGTATCATCAATGTGAAGGGGAAGGGAGCTTGAACACATATTTTGTATA 3296
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## RESULT 14

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PCT-US95-11808-5
; Sequence 5, Application PC/TUS9511808
; GENERAL INFORMATION:
; APPLICANT: Iyengar, Srinivas Ravi V.
; TITLE OF INVENTION: MUTANT ACTIVATED GsALPHA AND
; ADENYLYL
; TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Brumbaugh, Graves, Donohue and
; ADDRESSEE: Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.
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; ZIP: 10112-0228
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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
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; FILING DATE:
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; APPLICATION NUMBER: PCT/US95/11808
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; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/307,896
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; FILING DATE: 16-SEP-1994
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; ATTORNEY/AGENT INFORMATION:
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; NAME: Clark, Richard S.
```

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; REGISTRATION NUMBER: 26,154
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```
; REFERENCE/DOCKET NUMBER: 29970 165/28755
```

```
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (212) 408-2500
```

```
; TELEFAX: (212) 765-2519
```

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; TELEX: 650 6111063
```

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; INFORMATION FOR SEQ ID NO: 5:
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; SEQUENCE CHARACTERISTICS:
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; LENGTH: 4008 base pairs
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; TYPE: nucleic acid
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; STRANDEDNESS: single
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```
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: cDNA
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PCT-US95-11808-5
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Query Match
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Best Local Similarity 12.9%; Score 459; DB 5; Length 4008;
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Matches 1370; Conservative 0; Mismatches 1240; Indels 87; Gaps 8;
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QY 852 CTTCTGGAAGCAGCTCGGTGCCAATGTGCTGTCTCTGCACCAACGCTCATTAGCAT 911
Db 624 CTGTTTGGCAGATACTGCCCAATGTGATCATTTTCATTTGGGAACTTGGCGGAGC 683
QY 912 CTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGAGCGCTTTCAGAGACCCGCGATT 971
Db 684 CTACCAACAAGCACCTCATGGAGCTTGCCTTGCAGCAAAACCTATCGGAGACACGTGTAATG 743
QY 972 CATCCAGGCGCGCTCCACCTGCAGCATGAGATCGCAGCAGGAGCGGCTGTCTGTCTC 1031
Db 744 CATCAAGTCCCGGATCAAGCTGGAATTTGAAACACGGCAGCAGGACGGCTCTCTCTC 803
QY 1032 GGTATTGCCCCAGCAGCTTGCCATGGAGATGAAGAAGACATCA----- 1075
Db 804 CTTGCTGCCAGCTCACATCCCATGGAGATGAAGCTGAATCATTCAGAGGCTGCAGG 863
QY 1076 -----ACACAAAAAAGAACATGTTCCACAAGATCTACATACAGAAGCA 1121
Db 864 CCCCCAAGCAGGACAGATGGAAAAACACAAACAACTTCCACAATCTGTATGTCAACGACA 923
QY 1122 TGACATGTGACGATCCTGTTTGCAGACATTTAGGGCTTTCACCAGCTTGCATCCAGTG 1181
Db 924 CACCAAGCTGAGCATATTATACGCTGACATTTTGGCTTTCACCGCTTGCACGCGATTG 983
QY 1182 CACTGCGCAGGAGCTGTGATACCCCTGAATGAGCTTTTGGCCCGTTCACAAAGCTGC 1241
Db 984 CTCCCTTGGCGAACTGGTCCACATGCTGAATGAACTTTTGGGAAGTTTGCATCAATAGC 1043
QY 1242 TGGCGAAGTAATCTGCTGAGGATCAAGATCTTTGGGGAGACTGTACTACTGTGTGTCAG 1301
Db 1044 AAAGGAGAAATGAATGCATGAGAATTTAAATTTTAGGAGACTGCTATTACTGTGTTCCGG 1103
QY 1302 GCTGCGGAGGCGCGCGCCGACCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGAT 1361
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RESULT 15  
US-08-726-214-5  
Sequence 5, Application US/08726214  
Patent No. 6107076  
GENERAL INFORMATION:  
APPLICANT: Tang, Wei-Jen  
APPLICANT: Gilman, Alfred G.  
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE  
TITLE OF INVENTION: AND USES THEREFOR  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,214  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/005,498  
FILING DATE: 04-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: UTSD:450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4533 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-726-214-5

Query Match 12.4%; Score 441.6; DB 3; Length 4533;  
Best Local Similarity 50.1%; Pred. No. 1.1e-99;  
Matches 1359; Conservative 0; Mismatches 1284; Indels 67; Gaps 8;

Qy	853	CTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTCTGCACCAACGCTATTAGCATC	912
Db	1030	CTGCTGAGGGAGATCCTGGCTAACGCTCTTCTACCTGTGCGGCATCATCTGGGGCATC	1089
Qy	913	TGCACACACTATCCACGACAGAGTGCTCTCAGCGCCAGGCTTTTCAGGAGACCCGCGAGTTAC	972
Db	1090	ATGTCCTTACTATCGGACAGACCGTAAAGACCGAAGGCTTCTGAGAGCGCGCCAGTCG	1149
Qy	973	ATCCAGGCCCGCTCCACCTCGACGATGAGANTCGGACGAGGAGCGGCTGCTGCTGTCG	1032
Db	1150	CTGGAGGTGAAGATGAATCTGGAGGACGAGCCAGCAGGAGAAACCTTATGCTTTCC	1209
Qy	1033	GTATTTGCCCCAGCAGCTTGCCATGAGAGTGAAGAAGACATCAACACA-----	1080
Db	1210	ATCTCTGCCAAGCATGTGGCTGACGAGATGTTGAAGGACATGAAGAAAGATGAGAGTCAG	1269
Qy	1081	AAAAAAGAGACATCTCCACAAAGATCTACATACAGAAGCATGACAATGTCAGATCTCTG	1140
Db	1270	AAGGACGACGACGATGAATCAACACCATGTACATGTACCGGCATGAGAATGTACGATCTG	1329
Qy	1141	TTTTCAGACATTTGAGGGTTTACCAGCTGGCATCCCAAGTGGCACTCCGACGAGGCTGTC	1200
Db	1330	TTTTCAGATATTGCGGGCTTTACCCAGGCTGTCTCTGCTTGGCAGTGGCCAGGAGCTCGTG	1389

Qy	1201	ATGACCTGAATGAGCTCTTTGCCCGTTTGACAAGCTGGCTCGGGAGAAATCACTGCCTG	1260
Db	1390	AAGTACTCAACGAGCTCTTTGCCCGTTTGACAAGCTGGCGCCAAATACCAACGAGCTG	1449
Qy	1261	AGGATCAAGATCTTTGGGGGACTGTTACTACTGTGTGTGTCAGGGCTGCGGGAGGCCGGCC	1320
Db	1450	AGGATCAAGATCTAGCGGACTGTTACTACTGCTATCGCGCTGCGCTGACTACCGGGAG	1509
Qy	1321	GACATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTTAGGCGCATCTCGCTGGTA	1380
Db	1510	GACCACCGCTGTCTCCATCTGATGGGCTTGCCATGTGTAGAGGCGCATCTGCTAGCTG	1569
Qy	1381	CGTGAGGTGACAGGTGTGAATGTGAACATCGGTGGGATCCACAGCGGCGCGTGCAC	1440
Db	1570	CGGAGAAAGACCAAGACCGGAGTGGACATCGGTGTGGGGTGCACACAGGCATGTGCTA	1629
Qy	1441	TGGCGCTCTTGGCTTGGGAAATGSCAGTTGCTGTGTGTGTCCTCAATGATGTACCCCTG	1500
Db	1630	GGTGGCTCTTGGCCAGAAAGCGCTGSCAGTATGATGTTGTTACCGATGTCACTGTG	1689
Qy	1501	GCCAAACCATGGAAGCAGGAAGCGGGCTGGCGGCATCCACATCACTCGGGCNAACACTG	1560
Db	1690	GCAACAAGATGGAGGTGGCGCATCCAGGGCGCTGCACATTTCCCAAGACACCATG	1749
Qy	1561	CAGTACCTGAACGGGACTACGAAGTGGAGCGAGCGCTGTGTGCAAGCGCAACGCGTAC	1620
Db	1750	GACTGCTGAAAGGGAGTTGCGATGTGCAACCTGCTGATGTTGTCAGCTGCTGCGACTAC	1809
Qy	1621	CTCAAGGAGCAGCATTTGAGACTTTCTCATCTCTGGCGGCCAGCCAGAAACGAAAGAG	1680
Db	1810	CTAGATGAGAAGGCATCGAAACCTTACTCTATCATTTGCTTCCCAAGC-CAGAGGTGAAGAA	1868
Qy	1681	GAGAAAGCATGCTGGCCCAAGCTCAGCGGACTCGGGCCAACTCCATGGAAGGCTGATG	1740
Db	1869	GACAGCTCAAAATGGCTCAACGGCTCGGGCTGCCAAACGGAGCACCGGCATCCAAGCC	1928
Qy	1741	CCGCGATGGGTTCCCTGATGCTGCTCTTCCCGGACCAAGGACTCCAAGGCTTCCGCGAG	1800
Db	1929	CAGTCCCTTCCCTTATGAGACCAAGGAGCCCAATGGGAGTGCCTCATGCCAGCGGCTC	1988
Qy	1801	ATGGCATTTGATGATCCAGCAAGACAAACCGGGGGACCCAAAGATGCCCTGAACCCCTGAG	1860
Db	1989	CACATCAGAGGAGCTGAAGAACAGAGGCGCCAGGCTGACAACCCCTCGTTCCCAACCC	2048
Qy	1861	GATGAGTGGATGAGT-TCCGTAGCCGCTGCCATCGATCGCCCGCAGCATTTAGTGC	1919
Db	2049	CCGCGGAGGCTGCGCTTCCAGGACCTGGCAGACCGCTGTGTGGACGCTCTGAGGATGA	2108
Qy	1920	GAAGACCATGTGCGCGGTTTGTCTCACCTTCCAGAGAGAGGATTTTGAGAAGAAATA	1979
Db	2109	GCAGAACTGAACAGCTTCTTAACGAGGCCCTGCTGGAGCGGAGTCCGCCAGGCTG	2168
Qy	1980	CTCCCGGAGGTGGATCCCGCTTCCGAGCCCTAGTTCGCTGTGCCCTGTGTTGGTCTCTG	2039
Db	2169	AAAGAAGAGAAACACATTCCTCTCAACGATGAGGTTCATGGACCCAGAGATGGAACACG	2228
Qy	2040	CTTATCTGCTTCACTCCAGCTTCTAATTTCCACACTCCACCTGATGCTTGGGATTTA	2099
Db	2229	CTACTCGGTGAGAGAGGAGAGAGAGTGGGGCTGCGCTTCAGCTGTTCTCTGTGTTGCT	2288
Qy	2100	TGCCAGCATCTTCTGCTGCTGCTAATCACCGTGTGATCTGTGCTGTACTCTCTGTGG	2159
Db	2289	TTTTCGACGCGCATGTTGGAGATGACTTATCGACCCCTGGTTGATGACAAACTACGTGAC	2348
Qy	2160	TTCTCTGTTTCCCTAAGGCCCTGCAACGCTGTGTCCGCGAGCATTTGCCGTCACGGGCA	2219
Db	2349	CTTCGTTGTTGAGAGGTTCTGCTCTTGATCTCTGACCATCTGTTGATGTTGCTCATCTT	2408
Qy	2220	TAGCACCGCAGTTGGCATCTTTTCGTCCTGCTGTTTACTTCTGCTGCAATGCCAACAT	2279
Db	2409	CCCCAGGCGATTTCCTAAGAAGCTCGTGGCCTTCTCATCTTGGATTGACCGACCCGCTG	2468

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QY 2280 GTTACCTGTAAACACACACCCCAATACGGAGC-----TGTGACGCCCGGATGCTGA 2329
Db 2469 GGGCAAAATACCTGGGCAATGTTAGCCATCTTCATCTGTTATGGCCAATGTTGTGGA 2528
QY 2330 ATTTAAACACTGCTGACATCACTGCCTGCCACCTGCACGCTCAATTACTCTCTGGGCC 2389
Db 2529 CATGCTGAGCTGTCTCCAGTACTACATGGACCT--TACAAGTGAACCCGGATAGAGC 2587
QY 2390 TGGATGCTCCCTGTGTGAGGGCACCAATGCCACCTGTCAGCTTTCTCAGGTGTCCATCG 2449
Db 2588 TGGACGGTGGCTGTATGGAGAACCCCAAGTACTACAACATATGTTGCTGTGCTCCCTCA 2647
QY 2450 GGAACATGCTGCTGAGTCTCTTGGCCAGCTCTGCTTCCGACATACAGCA--GCATCGGG 2508
Db 2648 TCGCCACCATCATGCTGCTGAGGTGAGCCACATGGTGAAGCTGACACTCATGCTGCTCG 2707
QY 2509 AAGTTGGCCATGATCTTTGTTCTTGGGGCTCATCTATTTGGTGGCTCTTCTGCTGGGTCCC 2568
Db 2708 TCACAGGGCGGCTGACTGCCATCAACCTGTATGCCCTGGTGTCTTTGATGAATACG 2767
QY 2569 CCAGCGGCCATCTTTGACAACATATGACCTACTGCTTGGCTGCCATGGCTTGGCTTCTTCC 2628
Db 2768 ACCACAAACCGTTTCAGGAAAGGACTCTCCTATGTTGGTGGCTTAGAGAAGATGCAAGTAC 2827
QY 2629 AATGAGACCTTTGATGGGCTGGACTGCTCCAGCTGCAGG--GAGGTGGCCCTCAAAATATA 2686
Db 2828 TTTCCACCCCTGGGCTCAATGGCTACAGACAGGCTGCCCTGGTGGCTTCCAAAGTACT 2887
QY 2687 TGACCCCTGTGATCTGCTGTGTTGGCTGGGCTGTATCTGCTGCTCAGCAGGTGG 2746
Db 2888 CGATGACTGTGATGATGTTGTTATGATGCTGAGCTTTTACTACTTCTCAGCCACGTGG 2947
QY 2747 AATCGACTGCCCGCTAAACTTCTCTGGAACACTACAGCAACACAGGGGAAAAAGAGAGA 2806
Db 2948 AGAAACTGCCCGGACACTGTTCTGTGGAAGATTGAGGTCCATGACCAGAAAGAACGTG 3007
QY 2807 TGGAGGAGCTACAGGCATACAAACGGAGGCTGCTGCATAAATCTGCCCAAGGACGTGG 2866
Db 3008 TGTACGAGATCGCGGTGGACAGGAGGCTTGGTCAACAACATGTTGCCAGAGCAITGTG 3067
QY 2867 CGGCCACTTCTGGCCGGGAGCGCGCAATGATGAATCTACTATCATGCTGCTGAGT 2926
Db 3068 CACGCCATTTCTGGGCTCCAGAGAGAGATGAGGAGCTGTACAGCCAGTCTTATGAGC 3127
QY 2927 GTGTGGCTGTTATGTTGGCTCCATTTGCCAATTTCTCTGAGTTCTTATGTGGAGCTGGAGG 2986
Db 3128 AGATTGGAGTCACTGTTGCCCTCTTGCCCACTTTGCCGACTTCTACACTGAGGAGAGCA 3187
QY 2987 CAACAATGAGGTCGCCAGTGCCTGGGCTGCTCAAGGAGATCATCGCTGACTTTGATG 3046
Db 3188 TCAATAATGGTGGCATCGAGTGTACGCTTCCCTCAATGAGATCATCTCTGATTTGACT 3247
QY 3047 AGATTATCAGCGAGGAGGGTTTCGGCAGCTGGAAAGATCAAGACGATTGGTAGCACCT 3106
Db 3248 CTCCTCTGGACAATCCCAAAATTCGGGTCTACACCAGATCAAAACCATCGGCAGCACCT 3307
QY 3107 ACATGGCTGCTCAGGGGCTGAACGCCACACCTAC----- 3141
Db 3308 ATATGGCAGCTTCTGGAGTCAACCCAGATGTCAACACCAATGGCTTTACAAGCTCCAGCA 3367
QY 3142 -----GATCAGGTGGGCCCTCCACATCACTGCGCTGGCTGACTACGCCA 3187
Db 3368 AGGAGGAAAAGTCAACAAAGAGCGCTGGCAGCAGCTGGCTGACCTGGCAGACTTTGCAC 3427
QY 3188 TGGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCTCTCAACAATTTCCAGATGA 3247
Db 3428 TAGCCATGAAGGACACGCTTACAAACATCAACACCAGTCAATTCAACAACCTTCATGCTGC 3487
QY 3248 AGATTGGGCTGAACATGGGCCAGTCTGTGGCAGGTGTCATCGGGGCTCGGAAGCCACAGT 3307
Db 3488 GCATAGGCATGAACAAAGGAGGAGTTCTGGCTGGAGTCAATTGGAGCCCGGAGCCACACT 3547
QY 3308 ATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCTGATGGACAGACGGGGTCCCGG 3367
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Db 3548 ATGACATCTGGGGAAACACACGGTCAATGTGGCCAGCAGGATGGAATCCACAGGGTCAATGG 3607
QY 3368 ACCGAATCCAGGTGACACAGGACCTGTACCAGGTTCTAGCTCCCAAGGGCTACAGAGCTGG 3427
Db 3608 GCAATATCCAGGTGTAGAAGAGACACAGGTCATCTTCGAGAGTATGGCTTCCGCTTTG 3667
QY 3428 AGTGTCTGAGGGGTGTCGAAGGTGAAGGGCAAGGGGAGATGACCACTACTTCTCTCAATG 3487
Db 3668 TGAGCGAGGACCCCATCTTTGTGAAGGCAAGGGAGCTTCTGACCTTTTCTTTAAAGG 3727
QY 3488 GGGGCCCCAG 3497
Db 3728 GCGGGACAG 3737
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Job time : 166.945 secs



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OM nucleic - nucleic search, using sw model

Run on: February 23, 2003, 02:25:49 ; Search time 186.362 Seconds  
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Title: us-09-750-240-5  
Perfect score: 3549  
Sequence: 1 atgtcatgttagtgacct.....aaggaccaaggtggcgact 3549

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 442118 seqs, 280819700 residues  
Total number of hits satisfying chosen parameters: 884236

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
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2	3484.8	98.2	3552	10	US-09-750-240-10
3	3478.4	98.0	4942	9	US-10-201-000-1
4	3379.2	95.2	3582	10	US-09-750-240-12
5	1808.4	51.0	1812	10	US-09-750-240-3
6	1703.4	48.0	4523	9	US-10-175-158-1
7	586	16.5	837	9	US-09-989-442-23
8	529.6	14.9	915	9	US-09-764-868-181
9	529.6	14.9	915	9	US-09-989-442-69
10	505.2	14.2	3518	9	US-10-121-911-2
11	395.8	11.2	2601	10	US-09-925-297-352
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13	284.4	8.0	1180	10	US-09-915-582-11
14	265.6	7.5	1140	10	US-09-925-297-56
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17	216.8	6.1	4473	10	US-09-751-100B-1
18	209.4	5.9	4985	12	US-10-071-223-1
19	207.8	5.9	5515	10	US-09-751-100B-98

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21	145.8	4.1	449	10	US-09-960-352-13136	Sequence 13136, A
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24	127.4	3.6	630	9	US-09-989-442-66	Sequence 66, Appl
25	124.4	3.5	330	9	US-09-764-868-182	Sequence 182, App
26	124.4	3.5	330	9	US-09-989-442-71	Sequence 71, Appl
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28	94.6	2.7	220	10	US-09-728-445-487	Sequence 487, App
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33	75.2	2.1	2335	10	US-09-917-800A-1569	Sequence 1569, Ap
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35	64.4	1.8	1259	9	US-09-880-505-123	Sequence 123, App
36	64.4	1.8	2013	9	US-10-051-643-176	Sequence 176, App
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c 45	54.4	1.5	3698	9	US-10-038-937-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1  
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; Sequence 5, Application US/09750240  
; Patent No. US20020103147A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammon, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
; TITLE OF INVENTION: FAILURE  
; FILE REFERENCE: 220002056723  
; CURRENT APPLICATION NUMBER: US/09/750,240  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/472,667  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 3549  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-750-240-5

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Best Local Similarity	100.0%;	Pred. No. 0;		
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			Indels	0;
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QY 181 CCTGGTGCCCTCGGCAGGATGAGCCCTTCATCCGAGGGCGGCCACGAGGCAAG 240  
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Db 3541 AAGGTGGGCACT 3552  
RESULT 3  
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; Sequence 1, Application US/10201000  
; Publication No. US20020187540A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, James E.  
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL  
; FILE REFERENCE: 44481-5028-01-US  
; CURRENT FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: US/05/474, 076  
; PRIOR FILING DATE: 1999-12-12  
; PRIOR APPLICATION NUMBER: PCT/US98/13694  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/070, 904  
; PRIOR FILING DATE: 1997-07-01  
; PRIOR APPLICATION NUMBER: 08/886, 550  
; PRIOR FILING DATE: 1997-07-01  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4942  
; TYPE: DNA  
; ORGANISM: human type VI adenylyl cyclase  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (145)..(3648)  
US-10-201-000-1  
Query Match 98.0%; Score 3478.4; DB 9; Length 4942;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 3513; Conservative 0; Mismatches 36; Indels 3; Gaps 1;  
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QY 61 GAACGCAATGGGCAGAGCGTTCCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120  
Db 205 GAACGCAATGGGCAGAGCGTTCCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 264  
QY 121 CCCGCTATATGATCGCTCCGGGATGCAGAGCCAGCCAGCCGCCCTCGGGGCCCC 180  
Db 265 CCCGCTATATGATCGCTCCGGGATGCAGAGCCAGCCAGCCGCCCTCGGGGCCCC 324  
QY 181 CCTCGGTGCCCTTGGCAGGATGACGCCCTTCATCCGAGGGGCGGCCAGGCAAGGCAAG 240  
Db 325 CCTCGGTGCCCTTGGCAGGATGACGCCCTTCATCCGAGGGGCGGCCAGGCAAGGCAAG 384  
QY 241 GAGCTGGGCTCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACAGCG 300  
Db 385 GAGCTGGGCTCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACAGCG 444  
QY 301 GCGGGAGCGCTGAGTGGCGCCCGCAGCGGTGCCAGGAGTGGCGCATCTGCTGGCGC 360  
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QY 421 CAGCGGTACTTTTCCAGATGAACAGAGCAGCCTGACGCTGCTGCTGGCGGTGCTGGTG 480  
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QY 481 CTGCTACAGGGTGTGCTGGCTTTTCCAAGCGCACCGCGCCCTCAGCCTGCCTAT 540  
Db 625 CTGCTACAGGGTGTGCTGGCTTTTCCAAGCGCACCGCGCCCTCAGCCTGCCTAT 684



[illegible]

## RESULT 4

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US-09-750-240-12
; Sequence 12, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723

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; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3582
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified AC-VI
;
US-09-750-240-12

Query Match          95.2%; Score 3379.2; DB 10; Length 3582;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 3458; Conservative 0; Mismatches 88; Indels 6; Gaps 2;

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Qy    361  CGTTTGGTGCAGGTGTTCAGTTCGAAGCAGTTCGGTTTCGGCCAAAGCTGGAGCGCTGTAC 420
Db    382  CGTCTGGTGCAGGTGTTCAGTTCGAAGCAGTTCGGTTTCGGCCAAAGCTGGAGCGCTGTAC 441

Qy    421  CAGCGGTACTTTTCCAGATGAACAGAGCAGCTGAGCTGCTGGTGGCGGTGCTGGTG 480
Db    442  CAGCGGTACTTTTCCAGATGAACAGAGCAGCTGAGCTGCTGGTGGCGGTGCTGGTG 501

Qy    481  CTGCTCAGCGGTGCTGCTGGCTTTCCAAAGCCGACACCCGCCGCCCTCAGCCCTGCCTAT 540
Db    502  CTGCTCAGCGGTGCTGCTGGCTTTCCAAAGCCGACACCCGCCGCCCTCAGCCCTGCCTAT 561

Qy    541  GTGCACTGTTGGCCTGTGCGCGCGCCGCTGTTGCTGGGGCTCATGGTGGTGTGTAACCGG 600
Db    562  GTGCACTGTTGGCCTGTGCGCGCGCCGCTGTTGCTGGGGCTCATGGTGGTGTGTAACCGG 621

Qy    601  CATAGCTTCCGCCAGGACTCCATGCTGGTGGTGAAGTAACTGGTGGCGCATCCTGGCG 660
Db    622  CATAGCTTCCGCCAGGACTCCATGCTGGTGGTGAAGTAACTGGTGGCGCATCCTGGCG 681

Qy    661  GCAGTGCAGGTTCGGGGCGGCTTTCGACAGCAGACCCGGCAGCCCTCTTCGGGGGCTCTGG 720
Db    682  GCAGTGCAGGTTCGGGGCGGCTTTCGACAGCAGACCCGGCAGCCCTCTTCGGGGGCTCTGG 741

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Db 2899 CTGCCCGGAGCGCCCAATGATGAACCTCTACTATCATCGTCGTGTGAGTGTGTGCTGTT 2958
QY 2938 ATGTTTCCCTCCATTGCCAATCTCTCTAGTCTCTATCTGGAGCTGGAGGCAACAATGAG 2997
Db 2959 ATGTTTCCCTCCATTGCCAATCTCTCTAGTCTCTATCTGGAGCTGGAGGCAACAATGAG 3018
QY 2998 GGTCCGAGTGCCTCGCGCTCTCAAGCAGATCATCGCTGACTTTGTATGAGATTATCAGC 3057
Db 3019 GGTCTCAGTGCCTCGCGCTCTCAAGCAGATCATCGCTGACTTTGTATGAGATTATCAGC 3078
QY 3058 GAGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTTGGTAGCACCATACATGGCTGCC 3117
Db 3079 GAGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTTGGTAGCACCATACATGGCTGCC 3138
QY 3118 TCAGGGCTGAACGCGCAGCACCCTACGATCAGGTGGCGCGCTCCACATCATCAGTCCCTGGCT 3177
Db 3139 TCAGGGCTGAACGCGCAGCACCCTACGATCAGGTGGCGCGCTCCACATCATCAGTCCCTGGCT 3198
QY 3178 GACTACGCCATCGCGCTCATGGAGCAGATGAAGCACATCAATGAGCAGTCTCTTCAACAAT 3237
Db 3199 GACTACGCCATCGCGCTCATGGAGCAGATGAAGCACATCAATGAGCAGTCTCTTCAACAAT 3258
QY 3238 TTCCAGATGAAGATTGGCTGAACATGGGCCAGTCTGTCAGTGTGATCGGGGCTCGG 3297
Db 3259 TTCCAGATGAAGATTGGCTGAACATGGGCCAGTCTGTCAGTGTGATCGGGGCTCGG 3318
QY 3298 AAGCCAGATGATCATCTGGGGGAACACAGTGAATGTCTAGTCTATGAGCAGCAGC 3357
Db 3319 AAGCCAGATGATCATCTGGGGGAACACAGTGAATGTCTAGTCTATGAGCAGCAGC 3378
QY 3358 GGGTCCCGACCGAATCCAGGTGACACCGGACCTGTACCAAGTTCCTAGCTGCCAAGGGC 3417
Db 3379 GGGTCCCGACCGAATCCAGGTGACACCGGACCTGTACCAAGTTCCTAGCTGCCAAGGGC 3438
QY 3418 TACCAGCTGGAGTGTGAGGGGTGGTCAAGTGAAGGCGCAAGGGGAGATGACCACTAC 3477
Db 3439 TACCAGCTGGAGTGTGAGGGGTGGTCAAGTGAAGGCGCAAGGGGAGATGACCACTAC 3498
QY 3478 TTCTCTAATGGGGGCCCCAGCAGTTAACAGGGGCCAGCCACAAATTCAGCTGAAGGGACC 3537
Db 3499 TTCTCTAATGGGGGCCCCAGCAGTTAACAGGGGCCAGCCACAAATTCAGCTGAAGGGACC 3558
QY 3538 AAGGTGGGCACT 3549
Db 3559 AAGGTGGGCACT 3570

RESULT 5
US-09-750-240-3
; Sequence 3, Application us/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
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; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-3

Query Match      51.0%; Score 1808.4; DB 10; Length 1812;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 636 TAACGTGTGTCTGGGCATCTCTGGCGCAGTGCAGTGGGGCGCTTTTCGACGACGAGACC 695
Db 3 TAACGTGTGTCTGGGCATCTCTGGCGCAGTGCAGTGGGGCGCTTTTCGACGACGAGACC 62
QY 696 GCGCAGCCCTCTCTGGGCGCTCTGGTGGCCCTGTCTTTGTATATACATCGCATACAGCT 755
Db 63 GCGCAGCCCTCTCTGGGCGCTCTGGTGGCCCTGTCTTTGTATATACATCGCATACAGCT 122
QY 756 CCTCCCATTCGCAATGCGGGCTGCCCTCAGCGGCTGGGCGCTCTCCACCTTTGCATTT 815
Db 123 CCTCCCATTCGCAATGCGGGCTGCCCTCAGCGGCTGGGCGCTCTCCACCTTTGCATTT 182
QY 816 GATCTTGGCCTGGCAACTTAACCGTGTGTATGCGCTTCTCTGSAAGCAGCTCGGTGCCAA 875
Db 183 GATCTTGGCCTGGCAACTTAACCGTGTGTATGCGCTTCTCTGSAAGCAGCTCGGTGCCAA 242
QY 876 TGTGCTGCTTCTCTGCAACAGCTCATAGCATCTGCACACACTATCCAGCAGAGGT 935
Db 243 TGTGCTGCTTCTCTGCAACAGCTCATAGCATCTGCACACACTATCCAGCAGAGGT 302
QY 936 GTCFCAGCGCCAGCGCTTTCAGGAGAGCCGAGTTACATCCAGGCGCGCTCCACCTGCA 995
Db 303 GTCFCAGCGCCAGCGCTTTCAGGAGAGCCGAGTTACATCCAGGCGCGCTCCACCTGCA 362
QY 996 GCATGAGAAATGGCAGCAGGAGCGGCTGCTGCTGCGGTATTGCCCGCAGCAGTTGCCAT 1055
Db 363 GCATGAGAAATGGCAGCAGGAGCGGCTGCTGCTGCGGTATTGCCCGCAGCAGTTGCCAT 422
QY 1056 GGAGATGAAGAAGACATCAACACAAAAGAGACATGTTCCACAGATCTACATACA 1115
Db 423 GGAGATGAAGAAGACATCAACACAAAAGAGACATGTTCCACAGATCTACATACA 482
QY 1116 GAAGCATGACAATGTCAGCATCTCTTTGACAGATTCAGGCGCTTCACAGCCTGGCATC 1175
Db 483 GAAGCATGACAATGTCAGCATCTCTTTGACAGATTCAGGCGCTTCACAGCCTGGCATC 542
QY 1176 CCAGTGACTCGCGCAGGAGCTGATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAA 1235
Db 543 CCAGTGACTCGCGCAGGAGCTGATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAA 602
QY 1236 GCTGCTGCGGAGAAATCACTGCCCTGAGGATCAAGATCTTGGGGACTCTTACTACTGTGT 1295
Db 603 GCTGCTGCGGAGAAATCACTGCCCTGAGGATCAAGATCTTGGGGACTCTTACTACTGTGT 662
QY 1296 GTCAGGCTGCCGAGGCGCGCGCCGACCATGCCACTGCTGTGTGGAGATGGGGGTAGA 1355
Db 663 GTCAGGCTGCCGAGGCGCGCGCCGACCATGCCACTGCTGTGTGGAGATGGGGGTAGA 722
QY 1356 CATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGT 1415
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QY 1416 GGGCATCCACAGCGGCGCGCTGCACTGGCGGCTCTTGGCTTGGGAAATGGCAGTTGCA 1475
Db 783 GGGCATCCACAGCGGCGCGCTGCACTGGCGGCTCTTGGCTTGGGAAATGGCAGTTGCA 842
QY 1476 TGTGTGTGTTCAATGATGTGACCCCTGGCCAAACACATGGAAGCAGGAGCCGGGTGGCGG 1535
Db 843 TGTGTGTGTTCAATGATGTGACCCCTGGCCAAACACATGGAAGCAGGAGCCGGGTGGCGG 902
QY 1536 CATCCACATCACTCGGGGCAACACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1595
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Db 3490 CAGCTGGAGAAGATCAAGACCATCGGCAGCACCTACATGGCTGCTCCGGCTCAACGAC 3549  
Qy 3133 AGCACTTACGATCAGGTGGCCGCTCCACATCACTACTGCCCTGGCTGACTAGGCCATCGGG 3192  
Db 3550 TCTACCTACGACAAGGTGGGCAAGACCCACATCAAGGCACCTTGGCCGACTTTGGCCATGAAG 3609  
Qy 3193 CTCATGGAGCAGATGAAGCAGCATCAATGAGCACCTCTTCAACAATTTCCAGATGAAGATT 3252  
Db 3610 CTGATGGACCAAGATGAAGTACATCAATGAGCACCTCTTCAACAATTTCCAGATGAAGATC 3669  
Qy 3253 GGGCTGAACATGGCCCGCAGTCGTCGGCAGGTGTCATCGGGGCTCGGAAGCCACAGATATGAC 3312  
Db 3670 GGGCTCAACATCGCCCGCTGGTGGCCGGGTGATAGGGGCGACCAAGACCTTCAGTACGAC 3729  
Qy 3313 ATCTGGGGGACACAGTGAATGTCTTAGTCGTATGCACAGCAGCGGGGGTCCCGACCGA 3372  
Db 3730 ATCTGGGGCAATACCGTGAAGTGGCCAGCGCATGGACAGCAGCGGTGTACCGGACCGC 3789  
Qy 3373 ATCCAGGTGACCGGACCTGTACAGGTTCTTAGCTGCCAAGGCTACCACTGGAGTGT 3432  
Db 3790 ATCCAGGTCAACACAGATGTACCAAGTCTGCTGCCCAACAGGTACCACTGGAGTGC 3849  
Qy 3433 CGAGGGGTGTCAGGTGAAGGCAAGGGGAGATGACCACTACTTCTCTCAATGGGGGC 3492  
Db 3850 CGGGCGGTGTCAGGTGAAGGCAAGGGGAGATGATGACCTACTTCTCTCAATGGAGGG 3909  
Qy 3493 CCC 3495  
Db 3910 CCC 3912

RESULT 7  
US-09-989-442-23  
; Sequence 23, Application US/09989442  
; Publication No. US20030013649A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P208  
; CURRENT APPLICATION NUMBER: US/09/989,442  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/214,886  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/217,487  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,758  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,963  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/217,496  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,447  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/218,290  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/225,757  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/226,868  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/216,647  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 60/225,267  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/216,880  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 60/225,270  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/231,869

; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/235,834  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/234,274  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 60/234,223  
; PRIOR FILING DATE: 2000-09-21  
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; PRIOR FILING DATE: 2000-09-29  
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; PRIOR APPLICATION NUMBER: 60/241,809  
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; PRIOR APPLICATION NUMBER: 60/236,327  
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; PRIOR FILING DATE: 2000-10-20  
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; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: 60/225,268  
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; PRIOR FILING DATE: 2000-09-29  
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; PRIOR FILING DATE: 2000-12-08  
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; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/234,997  
; PRIOR FILING DATE: 2000-09-25  
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; PRIOR FILING DATE: 2000-09-29  
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; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,038  
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; PRIOR FILING DATE: 2000-09-29  
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; PRIOR APPLICATION NUMBER: 60/237,037  
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; PRIOR APPLICATION NUMBER: 60/237,040  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/240,960  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/239,935  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/239,937  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/241,787  
; PRIOR FILING DATE: 2000-10-20

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; PRIOR APPLICATION NUMBER: 60/225,214  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/235,836  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/230,438  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/215,135  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/225,266  
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; PRIOR APPLICATION NUMBER: 60/232,399  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,401

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; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/241,808  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,826  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,786  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,221  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/246,475  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/231,243  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/233,065  
; PRIOR FILING DATE: 2000-09-14  
  
Query Match 16.5%; Score 586; DB 9; Length 837;  
Best Local Similarity 85.3%; Pred. No. 2.3e-135;  
Matches 652; Conservative 1; Mismatches 111; Indels 0; Gaps 0;  
  
Qy 2732 ATGCTCAGCAGGTGGAATCGACTGCCCGCCTAAACTTCTCTGGAACACTACAGGCAACAG 2791  
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Qy 2792 GGGAAAAGAGAGATGGAGGAGCTACAGGCATACAAACCGAGGCTGCTGCATAACTTCT 2851  
Db 61 AGGAGATAGAGAGATGGAGGAGCTGAGGCGCTTACAACCGGCGCTGCTGCACAACATCC 120  
  
Qy 2852 TGCCCAAGGACGTGGCGGCCACCTTCTTGCCCGGGAGCGCCGAATGATGAATCTTACT 2911  
Db 121 TGCCCAAGGACGTGGCGGCTCACTTCTTGCCCGCGAGCGCGCAATGATGAGCTTACT 180  
  
Qy 2912 ATCAGTCTGTGAGTGTGTGGCTGTATGTTGCTCATTGCCAACTTCTCTGAGTTCT 2971  
Db 181 ATCAGTCTGTGAGTGTGTGGCGGTGATGTCGCTCCATCGCCAACTTCTCCGAGTTCT 240  
  
Qy 2972 ATGTGGAGCTGGAGGCAACAATGAGGCTGCCGAGTGCCTGCGGCTGCTCAACGAGATCA 3031  
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Qy 3092 CGATTGCTAGCACCTACATGCTGCCCTCAGGCTGAACGCCAGCACCTTACGATCAGGTGG 3151  
Db 361 CCATCGCAGCACCTACATGCTGCCCTCCGCGCTCAACGACTTACCTACGACAAAGTGG 420  
  
Qy 3152 GCCGCTCCACATCACTGCCCTGCTGCTGACTAGCCCATGCGGCTCATGGAGAGATGAAGC 3211  
Db 421 GCAAGACCCACATCAAGGCACTGGCGGACTTTGGCATGAAGCTGATGGACGAGATGAAGT 480  
  
Qy 3212 ACATCAATGAGCACTCTTCAACAATTTCCAGATGAAGATGGGCTGAGCAATGAGGCGCCAG 3271  
Db 481 ACATCAATGAGCACTCTTCAACAATTTCCAGATGAAGATGGGCTGAGCAATGAGGCGCCAG 540  
  
Qy 3272 TCGTGGCAGGTGTCTATCGGGCTCGGAAGCCACAGTATGACATCTGGGGGAACACAGTGA 3331  
Db 541 TGGTGGCGGGGTGATAGGGGCACGAAGCCTCAGTACGACATCTGGGGCAATACCGTGA 600  
  
Qy 3332 ATGTCTCTAGTCGTATGGACAGCAGGGGGTCCCGCCGCAATCAAGTGAACGAGGACC 3391  
Db 601 ACGTGGCCAGCCGCATGGACAGCAGCGGTGTACCCGACCGCATCCAGTCCACCAGACA 660  
  
Qy 3392 TGTACCAGGTTCTAGCTGCCAAGGGCTACAGCTGGAGTTCGAGGGGTGTCGAGGTGA 3451  
Db 661 TGTACCAGGTTCTAGCTGCCAAGGGCTACAGCTGGAGTTCGAGGGGTGTCGAGGTGA 720  
  
Qy 3452 AGGCAAGGGGAGATGATGACCTTCTCAATGGGGGCCCC 3495  
Db 721 AGGCAAGGGGAGATGATGACCTTCTCAATGGAGGGCCC 764

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RESULT 8
US-09-764-868-181
; Sequence 181, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PYZ32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 181
; LENGTH: 915
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (815)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (852)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (878)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (883)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-868-181

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Db	551	ACGTGGCCACCGCATGGACAGCACCGGTGTACCCGACCGCATCCAGGTCCACACAGACA	610
Qy	3392	TGTACCAGGTTCTTAGCTGGCCAAAGGGTACCAGCTGGAGTGTGCGAGGGGTGGTCAAGGTGA	3451
Db	611	TGTACCAGGTGCTGGCTGCCAACACACGTACCAGCTGGAGTGGCCGGCGGTGGTCAAGGTCA	670
Qy	3452	AGGCAAGGGGAGATGACCACTTCTCTCAATGGGGGGCCCC	3495
Db	671	AGGCAAGGCGAGATGATGACCTACTTCTCAATGGAGGGCCC	714

RESULT 9

US-09-989-442-69

; Sequence 69, Application US/09989442

; Publication No. US20030013649A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PJZ08

; CURRENT APPLICATION NUMBER: US/09/989,442

; CURRENT FILING DATE: 2001-11-21

; PRIOR APPLICATION NUMBER: 60/179,065

; PRIOR FILING DATE: 2000-01-31

; PRIOR APPLICATION NUMBER: 60/180,628

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: 60/214,886

; PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/217,487

; PRIOR FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: 60/225,758

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/220,963

; PRIOR FILING DATE: 2000-07-26

; PRIOR APPLICATION NUMBER: 60/217,496

; PRIOR FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: 60/225,447

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/218,290

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: 60/225,757

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/226,868

; PRIOR FILING DATE: 2000-08-22

; PRIOR APPLICATION NUMBER: 60/216,647

; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: 60/225,267

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/216,880

; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: 60/225,270

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/251,869

; PRIOR FILING DATE: 2000-12-08

; PRIOR APPLICATION NUMBER: 60/235,834

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: 60/234,274

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: 60/234,223

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: 60/228,924

; PRIOR FILING DATE: 2000-08-30

; PRIOR APPLICATION NUMBER: 60/224,518

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/236,369

; PRIOR FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: 60/224,519

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/220,964

; PRIOR FILING DATE: 2000-07-26

; PRIOR APPLICATION NUMBER: 60/241,809

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/249,299

;  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/236,327  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/241,785  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/244,617  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: 60/225,268  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/236,368  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/251,856  
; PRIOR FILING DATE: 2000-12-08  
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; PRIOR FILING DATE: 2000-09-01  
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; PRIOR APPLICATION NUMBER: 60/229,343  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/229,345  
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; PRIOR APPLICATION NUMBER: 60/229,513  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/231,413  
; PRIOR FILING DATE: 2000-09-08  
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; PRIOR FILING DATE: 2000-09-29  
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; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,038  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/236,370  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/236,802  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,037  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,040  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/240,960  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/239,935  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/239,937  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/241,787  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/246,474  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/246,532  
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; PRIOR APPLICATION NUMBER: 60/249,216  
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; PRIOR APPLICATION NUMBER: 60/249,210  
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; PRIOR APPLICATION NUMBER: 60/226,681  
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; PRIOR APPLICATION NUMBER: 60/225,759  
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; PRIOR APPLICATION NUMBER: 60/225,213  
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; PRIOR APPLICATION NUMBER: 60/227,182  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,214  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/235,836  
; PRIOR FILING DATE: 2000-09-27

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; PRIOR APPLICATION NUMBER: 60/230,438  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/215,135  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/225,266  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/249,218  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,208  
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; PRIOR FILING DATE: 2000-11-17  
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; PRIOR APPLICATION NUMBER: 60/249,211  
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; PRIOR APPLICATION NUMBER: 60/249,215  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,264  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,214  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,297  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/232,400  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/231,242  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/232,081  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/232,080  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/231,414  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/231,244  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/233,064  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/233,063  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,397  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,399  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,401  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/241,808  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,826  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,786  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,221  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/246,475  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/231,243  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/233,065  
; PRIOR FILING DATE: 2000-09-14

Query Match 14.9% Score 529 6; DB 9; Length 915;  
Best Local Similarity 85.2% Pred. No. 2.2e-121;  
Matches 600; Conservative 2; Mismatches 101; Indels 1; Gaps 1;

QY 2792 GGGAAAAGAGGAGATGAGGAGCTACAGGCATACAGGCATACAAACCGAGGCTGCTGCATAAACATTC 2851  
Db 12 GRAGWAAAGAGGAGATGGAGGAGTGCA-CCCTACAAACCGGCGCTGCTGCACAAACATCC 70  
QY 2852 TGCCCAAGGACGTGGCGGCCACTTCTTGCGCCGGGAGCGCCCAATGATGAACCTCTACT 2911  
Db 71 TGCCCAAGGACGTGGCGGCCACTTCTTGCGCCGGGAGCGCGCAATGATGAGCTCTACT 130  
QY 2912 ATCAGTCTGTGAGTGTGCTGGCTGTTATGTTTGCTCCATTTGCAACTTCTCTGAGTTCT 2971  
Db 131 ATCAGTCTGTGAGTGTGCTGGCTCATGTTGCGCTCCATCGCCAACTTCTCGAGTTCT 190  
QY 2972 ATGTGGAGCTGGAGGCAAAACAATGAGGTCGCGAGTGCCTGCGGCTGCTCAACAGAGATCA 3031  
Db 191 ACCTTGAGCTGGAGGCCCAACAAGAGGCTGTCAGTGCCTGCGGCTACTCAATGAGATCA 250  
QY 3032 TCCTGTACTTTGATGATATATCAGCAGGAGCGGTTCCCGCAGCTGGAAGAATCAAGA 3091  
Db 251 TCCTGTACTTTGATGAGATCATCAGCGAGGATCGGTTCCCGCAGCTGGAGAAGATCAAGA 310  
QY 3092 CGATTGGTAGCACCCTACATGGCTGCTCAGGGCTGAAAGGCTGAAAGCTGCAAGCTGAGGTGG 3151  
Db 311 CCATCGGCACACCTACATGGCTGCTCAGGGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTG 370  
QY 3152 GCGCTCCACATCACTGCGCTGGCTGACTACGCCATGCGGCTCATGGAGCAGATGAAGC 3211  
Db 371 GCAAGACCCACATCAAGGCACTGGCGGACTTTGCCATGAAGCTGATGGACAGATGAAGT 430  
QY 3212 ACATCAATGAGCACTCCTTCAACAATTTCCAGATGAAGATTGGCTGCAAGCTGAGGCGCCAG 3271  
Db 431 ACATCAATGAGCACTCCTTCAACAATTTCCAGATGAAGATTGGCTGCAAGCTGAGGCGCCAG 490  
QY 3272 TCCTGCGAGTGTATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGGAACACAGTGA 3331  
Db 491 TGGTGGCGGGGTGATAGGGGACGAAAGCCTCAGTACGACATCTGGGGCAATACCGTGA 550  
QY 3332 ATGCTCTACTGTATGAGCAGCAGCGGGTCCCGACCGCAATCCAGGTACCCAGCGACC 3391  
Db 551 ACCTGGCCAGCCGATGGACAGCAGCGGTGTACCCGACCGATCCAGGTACCCAGCAGACA 610  
QY 3392 TGTAACAGGTTCTAGCTGCCAAGGGCTTACCAGCTGGAAGTGTGAGGGGCTGCTCAAGTGA 3451  
Db 611 TGTACCAAGTGTGCTGGTGTCCACACAGTACCAGCTGGAGTCCCGGGGCTGCTCAAGTGA 670  
QY 3452 AGGCAAGGGGGAGTACACACCTACTTCTCAATGGGGGCCCC 3495  
Db 671 AGGCAAGGGGGAGTACACCTACTTCTCAATGGAGGGCCCC 714

RESULT 10

US-10-121-911-2  
; Sequence 2, Application US/10121911  
; Patent No. US2002016432A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapeller-Libermann, Rosana  
; TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE  
; FILE REFERENCE: 5800-47  
; CURRENT APPLICATION NUMBER: US/10/121,911  
; PRIOR FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US/09/412,210  
; PRIOR FILING DATE: 1999-10-05  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 3518  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: 21529 adenylate cyclase  
; NAME/KEY: CDS  
; LOCATION: (247)...(3480)

US-10-121-911-2  
Query Match 14.2%; Score 505.2; DB 9; Length 3518;  
Best Local Similarity 50.0%; Pred. No. 4.5e-115;  
Matches 1560; Conservative 0; Mismatches 1488; Indels 72; Gaps 9;  
QY 435 CCAGATGAACAGAGCAGCCTGACGCTGCTGGTGGGGTGTCTGGTGTCTACAGCGGT 494  
Db 318 CCAGCAGTACCGCTGCTGCTGTCTGCTGGGATCGTCTGTGCGCGCGCT 377  
QY 495 GCT----GCTGGCTTTCCAAAGCCGACCCCGCCCTCAG--CCTGCCCTATGTGGCACT 548  
Db 378 GCTCGCAGTGGCTGGCGCAGCGGAGAGCTGACCTCAGACCCGAGCTTCCTTGACCAC 437  
QY 549 GTTGGCCGTGCGCGCGCCCTGTTGCTGGGGCTCATGCTGGTGTGTAACCGCATAGCTTT 608  
Db 438 TGTGCTGTGCGCGCTGGCGGCTTCTCGCTGCTGCTGGGCTCGCTTCCCGGGAGCAG 497  
QY 609 CCGCCAGGACTCCATGTGGGTGTGAGTAACGTGTGCTGGGCATCTTGGCGGAGTGCA 668  
Db 498 ACTGCAGCGCTGGACGCGTCCCTGCTCCGCTTGGTATGGTGTGCGCTGTAGCGCTAGG 557  
QY 669 GGTGGGGGCGCTTCGCACGACAGCCGCGCAGCCCTCTGCGGGCTCTGTGCGCCTGT 728  
Db 558 CCAGCGCTTCTGTTACCGGGGCGTGTGAGCGCTGGGACCAAGTGTCTATTCTTCT 617  
QY 729 GTTCTTTGTATACATGCAATACACGCTCCTCCCATCCGCATCGGGCTCGGCTCCTCAG 788  
Db 618 CTTGCTCATCTTCAGGCGTATGCCATGCTGCTGGCTTGGGCATCGGGACGCCCGCTCG 677  
QY 789 CGGCTTGGGCTCTCCACCTTGCATTTGATCTTGGCTGGCTGSCAA-----CTTAACC 838  
Db 678 GGGCTTGGCTCTCCTCCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 737  
QY 839 GTGCTGATGCTTCTCTCTG--GAAGCAGCTCGGTGCGCAATGCTGCTGCTGCTGCTGCT 896  
Db 738 GGACTACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 797  
QY 897 CAACGCTATTAGCATGTGCACACATATCCAGCAGAGGTGTCTCAGCGCCAGCGCTTTCA 956  
Db 798 GAACGCTGGCAGAGTGTACCAAGCGCTGATGGAGCGCGCTCGCGGCCACGTTCCG 857  
QY 957 GGAGCCCGCAGTTACATCCAGCGCGGCTCCACCTGCAACATGAGATGAGATGAGATGAG 1016  
Db 858 GGAGGCACTCAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 917  
QY 1017 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1076  
Db 918 ACACCTTCTCTTGTCCATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 977  
QY 1077 CACAA-----AAAAAGAGACATGTTCCACAAGAT 1106  
Db 978 GGCACGCGCTGCAGGACAGGAGCGGTGTCAGCGCAGAGAGCATTAAACAATTTCCACAG 1037  
QY 1107 CTACATACAGAAGCATGACAAATGTCAGCATCTGTTTGGCAGACATTCAGGGCTTCACC 1166  
Db 1038 CTATGCAAGAGGACACAGGAGTGCAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1097  
QY 1167 CTTGGCATCCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1226  
Db 1098 GCTGGCCAGCGAGTGTCCCTTAAAGAGCTGGTCTCATCTCAATGAGCTCTTTGGCAA 1157  
QY 1227 GTTTGACAAGCTGGCTGCGGAGAAATCATCTGCTGAGGATCAAGATCTTTGGGGACTG 1286  
Db 1158 GTTCGACCAAGATTGCCAAGAGCATGAATGCATGCGGATCAAGATCTTGGGGGACTGTT 1217  
QY 1287 CTACTGTGTGAGGCTGCGGAGGCGCGGCGGACCATGCCACTGCTGCTGCTGCTGCTG 1346  
Db 1218 CTACTGTGTCTGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1277  
QY 1347 GGGGGTAGACATGATTGAGGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1406  
Db 1278 GGGCTGGACATGTGCGGGGCCATCAGGAACCTGCGGGGAGCCACTGCGGCTGGACATCA 1337

QY	1407	CATGCGGTGGGATCCACAGCGGGCGGTGCACCTGGCGGCTCCTTGGCTTTGGGAAGT	1466
Db	1338	CATGCGGTGGGCGTCACATCAGGCAGGGTA <sup>T</sup> CTGTGTGGAGTCATCGGGTGCGAAGAGT	1397
QY	1467	GCA <sup>TTT</sup> TCGATGTGTGTCTCAATGATGTCA <sup>CC</sup> TGACCCTGGCCAACACATGGAAGCAGGAAGCCG	1526
Db	1398	GCAGTAGACGTTTGGTTCACATGATCTCACACTGGCTAACCAATGAGAGCGAGCGGTGT	1457
QY	1527	GGCTGGCGCATCCACATCACTCGGGCAACACTCGAGTACCTGAACGGGAGTACGAAGT	1586
Db	1458	ACCAGGGCGAGTGCACATCACAGGGGCTACCCTGGCCCTGCTGGCAGGGGCTTATGCTGT	1517
QY	1587	GGAGCCAGGCCGTGGTGGCAACGCCAAACCGGTACCTCAAGGAGCAGCACATTGNAGCTTT	1646
Db	1518	GGAGGACGCAGGCATGGAGCATCTGGGAGCCCTACTCTCGGAGCTAGGGAGGCGCTACCTA	1577
QY	1647	CTCATCTCTGGGCGCCAGCCAGCAAAAGGAGAAGAGCAAGGCATGCTGGCCAAGCTGCA	1706
Db	1578	TCGTGTCATGCATCCAGGGCAGAGAGGAGATGAGAAGGGCACTGCAGGAGGCTTGCT	1637
QY	1707	GCGGACTCGGGCCAACTCCATGGAAGGCTGATGCCGGATGGGTCTCTGATGTGCTT	1766
Db	1638	GTCTCGCTTGAGGGCCTCAAGATCGTCCATCACTGCTGATGACCGGCTTACCTGGAGTC	1697
QY	1767	CTCCCGGACCAAGGACTCCAAGGCCCTTCGGCCAGATGGGCATTGATGATTCACGCAAGA	1826
Db	1698	CTGGGGGCGACCAAGCCCTTTTGCCCACTTGAGCCAGCGGAGACAGCCCTGTGTCCACCTC	1757
QY	1827	CAACCGGGGACCCCAAGATGCCCTG--AACCTCGAGGATGAGGTGGA-TGATTTCTCTGAG	1883
Db	1758	CACCCCTCTCCGGAGAAGACCCCTGCTCTTCAGCACCCAGTGGAGCCCTGGATCGGAG	1817
QY	1884	CGGTGCCATCGATGCCCGCAGCATTGATCAGTGGGAAGGACCATGTGGCCGCGGTTTTT	1943
Db	1818	CCGTACCCCGCGGAGCTAGATGATGAATGCGACACCGGGGATGCCAAGTTCTTCCAGGT	1877
QY	1944	GCFTACCTTCCAGAGAGAGGATTTTGAGAAGAAGTACTCCCGGAAGTGGATCCCQCCTT	2003
Db	1878	CATTGASGAGCTCACTCGCAGAAACAGTGAAGCAGTCTGAAGGACTTCAACCCCACTGAC	1937
QY	2004	CGGAGCCTACGTTGCCTGTGGCTTCTTCGTTCTATCTGCTTCACTGCTTCACTCCAGCTTCT	2063
Db	1938	ACTGTACTTCAGAGAGAAGGATGSAGAAAGAGTACCGACTCTCGCAATCCCCGCCTT	1997
QY	2064	AATTTTCCCACTCCACCTGATGCTGGGATTTATGCCAGCATCTTCGTGCTGCTGCT	2123
Db	1998	CAAATACTATGAAGCCTGACCTTCCTGGTTTTCTCTCCAAC <sup>T</sup> TCATCATCCAGATGCT	2057
QY	2124	AATCACCGTGTGATCTGTGCTGTACTCTCTGTGGTTCTCTGTTCCTTAAGGCCCTGCA	2183
Db	2058	AGTGACAACAGGCCGCCAGCTCTGGCCATCAG---TATAGCATCACTTTTCCCTCTT	2114
QY	2184	ACCTCTGTCCCGCAGCATTTGCCGTCTACGGGCACATAGCACCCAGTTGGCATCTTTTC	2243
Db	2115	CTCTCTCATCTTTTGTCTGCTTCTCAGAGGACCTGATGAGGTGTGTCTGTAAGGCCCT	2174
QY	2244	CGTCTGCTGTGTTTACTTTCTGCOATTTGCCAATGTTCACTTCACTTAAOCACACCCCAT	2303
Db	2175	CAAGATGCTGCACATGGCTGCTGTCATGTCTGGCCTGGTGCCACACGACCGAGACTGAG	2234
QY	2304	ACGGAGCTGTGCAGCCCGATGCTGAATTTACACCTGCTGACATCACTGCTGCCACCT	2363
Db	2235	AATAGCCTTTGGGACCGCCACCATCTCTGTCTTTGCCATGGCCATTTACGAGCCTGTT	2294
QY	2364	GCAGCAGCTCAATTACTCTCTGGGCGCTGGATGCTCCCTCTGTGAGGGCACACTGCCAC	2423
Db	2295	CTTCTTCCCNACATCATCAGATGCCCTTTCACAGCTCCCAANTGTGTCTCCATGATTTC	2354
QY	2424	CTGAGCTTTCTGAGGTGTCCATCGGGAAACATGCTGCTGAGTCTCTTTGGCCAGCTCTGT	2483
Db	2355	CAACCTCTCTCTGGAGCTCCCTGGGTCTCTGCTCTCATAGTGTCCCATACTCCATGCA	2414

RESULT 11

RESULT II  
US-09-925-297-352

US-09-323-297-332  
; Sequence 352, Application US/09925297; sequence 332, Application  
; Patent No. US20020081659A1

QY	2484	CTTCTCGCACATCAGACGATCGGAGATTGGCCATGATCTTTGTCTTTGGGCTCATCTA	2543
Db	2415	CTGCTGCACGCTGGGGTTCTCTCCCTGCTCCCTCTTTCTGCAATGAGCTTCGAGCTGAA	2474
QY	2544	TTTGGTGCTCTTCTGCTGGGTCCCCAGCGCCCATCTTTTGACAACTATGACCTACTGCT	2603
Db	2475	GCTGCTGCTCTGCTGGCTGGCGCATCTTGCTCCCTCTTCTTCCCTGCATCCCATGC	2534
QY	2604	TGGCGTCCATGGCTTGGCTTCTTCCAAATGAGACCTTTTGATGGGCTGGACTGTCCAGCTGC	2663
Db	2535	CTGGCTCTCGGAATGCTCATGCTCGGCTCTATCTGGGCCCTTGGAGCTCCAGGCCGG	2594
QY	2664	AGGAGGTGGCCCTCAATATATGACCCTCTGATTCTTGCTGGTGTTTGGCTGGCGCT	2723
Db	2595	AGTGCTGAAGGAGCCCAACTGATGGTGCTATCTCCTTCTTCATCTTCTTCCACCT	2654
QY	2724	GTATCTGCATGCTCAGCAGGTGGAATCGACTGCCGCTTAAACTTCTCTGGAAGACTACA	2783
Db	2655	CCTTGTCTGCTCGCCAGAACTGATCTACTGCGCTGGACTTCCCTGTGGAAGAGAA	2714
QY	2784	GGCAACAGGGGAAAGAGAGATGAGAGAGCTACAGGCAATACACCGAGGCTGCTGCA	2843
Db	2715	GCTGAGCAGAGAGGAGGAGACAGAGACGATGGAGAACTTGACTCGGCTGCTCTTGA	2774
QY	2844	TAACTTCTGCCCAAGGAGCTGGCGGCCACCTTCTGGCCGGGAGCGCGCAATGATGA	2903
Db	2775	GACGTGCTCCCTGACACGCTGGCCCCCAGTTTCAATGGCCAGAACCGGGCAACGAGA	2834
QY	2904	ACTCTACTATCAGTCTGTGAGTGTGTGCTGTATTTTGGCTCCATTTGCCAACTTCTC	2963
Db	2835	TCCTACCAACAGTCTATGAATGCTTTGTGTCTCTTTCGCTCAGTCCCAGACTTCAA	2894
QY	2964	TGAGTTCTATGTCGAGCTGGAGCAACAATGAGGTTGCCGAGTGCCTGCGCTGCTCAA	3023
Db	2895	GGAGTTCTACTCTGAATCCAAACATCAATCATGAGGCTTAGAGTGTCTGAGGCTGCTCAA	2955
QY	3024	CGAGATCATCGCTGACTTTGATGAGATTATCAGCAGAGAGCGGTTCCGGCAGCTGGA	3084
Db	2955	TGAGATAATTGCTGATTTTGATGAGTGTCTTCCAGCCCAAGTTTCAGTGGGGTGGAGA	3014
QY	3084	GATCAGACGATTGTGAGCACTTACATGCTGCCTCAGGGCTGAACGCCAGCAC-----	3137
Db	3015	GATCAAGACCATCGGAGCACCTTACATGGCAGCACAGGCTTTAAATGGCACCTCTGGACA	3074
QY	3138	-----CTACGATCAGTGGGCGCTCCACATCACTGCTCCCTGGCTGACTAGCG	3188
Db	3075	GGATGCACAACAGGATGCTGAACGGAGCTGACGCCACCTTGGCATATGGTGGAAATTTGC	3134
QY	3186	CATGGCGCTCATGGCAGATGAACACATCAATGAGCACTCTTTCACAATTTCCAGAT	3245
Db	3135	CGTGGCCCTGGGTCTTAAGCTGGACGTCAATCAACAGCAATTCATTCAACACTTCGCGCT	3194
QY	3246	GAAGATTGGCTGAACATGGGCCAGTCGTGGCAGGTGTATCGGGGCTCGGAAGCCACA	3305
Db	3195	GCGAGTGGGTTTGAACCATGGACCCGTAGTAGCTGGAGTTATTGGGGCCCAAGAGCCGCA	3254
QY	3306	GTATGACATCTGGGGAACACAGTGAATGTCTTAGTCTATGGACAGCAGCGGGGTCCC	3365
Db	3255	ATATGACATTTGGGGCAACACAGTGAACGTGGCCAGCCGATGGAGAGTACAGSAGTCTCT	3314
QY	3366	CGACCGAATCCAGTGCACACGACCTGTACCGAGTTCTAGCTGCTCAAGGGCTACACGCT	3423
Db	3315	TGGCAAAATCCAAGTCACTGAGAGACAGCATGGGCCCTTACAGTCCCTGGGCTACACCTG	3374
QY	3426	GGAGTGTGAGGGGTGGTCAAGGTGAAGGGCAAGGGGGAGATGACACCTACTTCTCTCAA	3485
Db	3375	CTACAGCCGGGTGTCTCAAGGTGAAGGCAAGAGGCAAGGCACTGCTGCACCTACTTCTGAA	3434



GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA105  
; CURRENT APPLICATION NUMBER: US/09/925,297  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05989  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 928  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 352  
; LENGTH: 2601  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2520)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (2572)  
; OTHER INFORMATION: n equals a,t,g, or c  
; US-09-925-297-352

Query Match 11.2%; Score 395.8; DB 10; Length 2601;  
Best Local Similarity 51.1%; Pred. No. 4.5e-88;  
Matches 1301; Conservative 1; Mismatches 1143; Indels 100; Gaps 12;

Qy	927	AGCAGAGTGCTCAGCGCCAGGCTTTCAGGACCGCGAGTTACATCCAGGCCCGGCT	986
Db	34	AACAGCGCAAGCACCGAAGACTTCTCGAGCGCCCGCGCTGGAGGTGAAGAT	93
Qy	987	CCACCTCGAGCATGAGAAATCGGACGAGCGGCTGTGTCGGTATTGCCCCAGCA	1046
Db	94	GAACCTGGAAGCAGAGCCAGCCAGCAGGAGAACTCATGCTTCCATCTCGCCCCAGCA	153
Qy	1047	CGTTGCCATGAGATGAAGAAGACATCAACACA-----AAAAAAGAGACAT	1094
Db	154	CGTGGCTGACGAGATGCTGAAAGACATGAAGAAAGCAGAGCCAGAGACCGACGCA	213
Qy	1095	GTTCCACAAGATCTACATACAGAAAGATGACAATGTACAGCATCTGTTTGCAGACATGA	1154
Db	214	GTTCAACACCATGTACATGTACCGTACAGAGAACTGACATCTCTTTGCCGACATCGT	273
Qy	1155	GGGCTTACCAGCTGGCATCCAGTGCACCTGCGCAGAGCTGGTTCATGACCCCTGAATGA	1214
Db	274	GGGCTTTACCAGCTGTCTTCTGCTGCGAGTGCCCGCAGGAGCTTGTGAAGCTGTCAACGA	333
Qy	1215	GCTCTTTCCCGGTTTGACAAGCTGGCTGCGGAGAAATCACTGCTGAGGATCAAGATCTT	1274
Db	334	GCTCTTTGCCCGTTTGACAAGCTGGCAGCTTAAATACCACAGCTGCGGATTAAGATCTT	393
Qy	1275	GGGGACTGTTACTGTGTGTCAGGCTGCGGAGGCGCGGCGGACCATGCCACTG	1334
Db	394	GGGGACTGTTACTGTGTGTCAGGCTGCGGAGGCGCGGAGGACCATGCCACTG	453
Qy	1335	CTGTGTGAGATGGGGTGTGAGTGTGAGGCGCATCTGCTGTTGAGTGTGAGGTGACAGG	1394
Db	454	CTCCATCTCATGGGCTGGCCATGGTGGAGGCCATCTCGTATGTGCGGGAGAGACCAA	513
Qy	1395	TGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGCGCGTGCACCTGCGCGCTCTTGG	1454
Db	514	GACTGGGTGGACATGCGTGTGGGGTGCACACGGGCCCGCTGTGGGGGGCGCTTGGG	573
Qy	1455	CTTGGGAAATGGCATGTCGATGTGTGTCGAATGATGTGACCTGGCCACACATGGA	1514
Db	574	CCAGAAGCGCTGGAGTACGAGTGTGTCGACTGTGTCGACTGTGTCGACTGTGTCGACT	633
Qy	1515	AGCAGGAGCGGGCTGGCGCATCCACATCACTCGGGCAACACTGCACTGACCTGAACGG	1574
Db	634	GGCCGGCGGCATCCCTGGCGCGGTGCACATCTCCAGAGACCATGGACTCCCTGGAAGG	693

Qy	1575	GGACTACGAAGTGGAGCCAGCGCGTGTGTGCAAGCGCAACCGTACCTCAAGGAGCAGCA	1634
Db	694	GGAGTTTGTATGTGGAGCCAGCGATGGGGCAGCGCTGTGATTACCTAGAGAAGAGG	753
Qy	1635	CATTGAGACTTTCCTCATCTGGCGCC-AGCCAGAAACGGAAGAGAGAGAGGCGATGC	1693
Db	754	TATTGAAACCTACCTCATATTCCTTCAAGCCAGAGGTGAAGAAACACAGCCACCCAGAA	813
Qy	1694	TGGCAAGCTGACGCGACTCGGGCCAACTCCATGGAAGGCGTATGCCCGGATGGGTTTC	1753
Db	814	TGGCTCAAT-----GGCTCGGCCCTGCCAATGAGAGCACCAGCTTCTCAAGTCCAG	867
Qy	1754	CTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAAGGCGCTCCCGCCAGATGGGCAATGATG	1813
Db	868	CT-CCCCCTGCCCTCATTTGAGACCAAGGAGGCCAACGGAGTGCCCA-----CAGCAGTG	920
Qy	1814	ATTCCAGCAAAAGACACCGGGGCCAACCAAGATGCCCTGAACCTGTAGGATGAGGTGGATG	1873
Db	921	GGTCCACGTCGGAGAAGCCCGAGGAGCAGGATGCCAGCGCGGACACCCCTCATTCGCCCA	980
Qy	1874	AGTTCTCTGAGCCGTGCCATCGATGCCCGCAGCATTTGATCAGCTCGGGAAGACCATGTC	1933
Db	981	ACCCACGCCGAGGCTGCGCTGCAGGACCTGGCTGACCGAGTGGTGGATGCCCTCTCAAG	1040
Qy	1934	GCCGGTTTTTGTCTACC---TTCCAGAGAGAGGATTTTGAGAAGAAGTACTCCCGGAAGG	1990
Db	1041	ATGACGACGAGCTCAACGAGCTGCTCAACGAGGCGCTGCTTGAGCAGAGTGGCCGCCAAG	1100
Qy	1991	TGATCCCGGCTTCGGAGCGCTACGTTGCCCTGTGCGCTGTTGGTGTCTTGTCTTATCTGCT	2050
Db	1101	TAGTAAGAAGAGAGAAACACCTTCTCTTTGCCATGCGGTTTCATGGACCCGAGATGAAA	1160
Qy	2051	TCATCCAGCTTCTAATTTTCCACACTCCACCTCGATGCTTGGGATTTATGCCAGCATCT	2110
Db	1161	CCCGCTACTCGTGGAGAAGAGAGAGAGTGGGGCTGCTTCAGCTGCTCTCTGCTGCTG	1220
Qy	2111	TCCTGCT-----GCTGCTAATCACCGTGTGATCTGTGCTGTCTACTCTCTGTGTTCTC	2164
Db	1221	TCCTGCTGTGACGCGGCTGCTGAGATCTATCGACCCCTGGCTAATGACAACATATG	1280
Qy	2165	TGTTTCCCTAAGGCGCTGCAACGCTGTGTCGGCAGCATTTGTCGCTACGGSCACATAGCA	2224
Db	1281	TGACCTTCATGTTGGGGAGATCTGCTCTCATCTCATCTGACCATCTGCTCCTGGCTGCCA	1340
Qy	2225	CGCAGTGTGGCATCTTTTCGCTGCTGTTGTTTACTTTCGTCATTTGCCATTTGCCAACATGTCA	2284
Db	1341	TCCTTCCCGCGGCTTCTTCAAGAAAGTGTGGGCTTCTTCAACTTGGATTGACCGGACCC	1400
Qy	2285	CCTGTAACACACACCCCATACGGAGCTGTCAGCCCGGATGCTGAATTTAACAACCTGCTG	2344
Db	1401	GCTGGGCGAGAAACACCTGGGCCATGCTGCGCCATCTTCATCTGCTGATGATGCAATGTG	1460
Qy	2345	ACATCACTGCTGCGCACCTGCAGCAGCTCAATTTACTCTCTGGGCTGATGCTCCCCCTGT	2404
Db	1461	TGGACATGTCAGCTGCTCCAGTACTACAGGGACCCAGCAATGCAACGCGCAGGATGG	1520
Qy	2405	GTGAGGCGACCATCCACACTGTCAGCTTTCCTGAGGTGTCATCGGGAACATGCTGTGA	2464
Db	1521	AAACGGAGGCGAGCTGCTGGAGAAC---CCCAAGTATTACAACATATGTCGCCGCTGCTGT	1577
Qy	2465	GTCTCTTGGCCAGCTGTCTTCTTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCT	2524
Db	1578	CCCTCATCGCCACCATCATGCTGTGAGGTGTCAGCCACATGTTGAAGCTCAGCTCATGC	1637
Qy	2525	TTGCTTGGGCTCATCTATTTTGTGCTGCTTCTGCTGGTCCCGCCAGCCCGCATCTTTG	2584
Db	1638	TGCTGTCGCGAGGCGCGTGGCCACCATCAACCTCTATGCTGCGGCTCCCTCTTTGATG	1697
Qy	2585	ACAACTATGACTACTGCTTGGCTTCCATGGCTT-----GGCTTC	2624
Db	1698	AATACGACCAACAAGGTTTTCGGGAGCAGCACTTACCTATGTTGGCTTACGAGCAGATGC	1757
Qy	2625	TTCCAATGAGACCTTTTATGGGCTGGACTGTCCAGCTGTCAGGAGGAGGTTGGCCCTCAATA	2684



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Db 1758 AAGGATTCACACCTGGGCTCAATGGCACTGACAGGCTGC--CCCTGGTGCCTTCCAAAGTA 1815
Qy 2685 TATGACCCCTGTGATTCCTGCTGGTGTGGTCCGCTGCGCTGATCTGCATGCTCAGCAGGT 2744
Db 1816 CTCATGACGGTGATGGTGTTCCTCATGATGCTAGCTTCTACTACTTCTCCCGCCAGGT 1875
Qy 2745 GGAATCGACTCGCCGCCCTAAACTTCTCTGGAAACTACAGCAACAGGGGAAAGAGGA 2804
Db 1876 AGAAAACTGCGCAGGACACTTTTCTTCTGGAAGATTGAGTCCACGACACAGGAACG 1935
Qy 2805 GATGAGGAGCTACAGGCAATACACCCGAGGCTGCTGATACATTTCTGCCAAGGAGGT 2864
Db 1936 TGCTTATGAGATGGACGCTGGAAGGAGGCTTGGTCCACCAACATGTTGCTGAGCAGGT 1995
Qy 2865 GCGGCCCTCTCCCTGGCCCGGCGCAATCACTCACTACTACTACTACTAGTCTGTGA 2924
Db 1996 GCGAGCCCATTTCTCGGGGTCCAAGAAGAGATGAGAGCTGTATAGCCAGACATGA 2055
Qy 2925 GTGTGTGGCTGTATGTTGGCTCCCAATGCCAACTTCTCTGAGTTCTATGTGGAGCTGA 2984
Db 2056 TGAGATTGGAGTCATGTTGGCTCCCTGCCCAACTTCTGACTTCTACACAGAGGAGAG 2115
Qy 2985 GCGAACAATGAGGTGCGGAGTGGCTGCGGCTGCTCAACAGATCATCGCTGACTTTGA 3044
Db 2116 CATCAACAATGGTGTATGATGCTGCTGCTTCTCAATGAAATCATCTCRGATTTGA 2175
Qy 3045 TGAGATTATCAGCAGGAGGCGTTCGCGCAGCTGGAAGAGATCAAGAGATTGGTAGCAC 3104
Db 2176 CTCCTCTGGAACAATCCCAAGTTCGCGGTGATCACCAGATCAAAACCATTTGGCAGC 2235
Qy 3105 CTACATGGCTGCTCAGGGCTGAAGCC----- 3132
Db 2236 GTATATGCGGCTTCAGGAGTCACCCCGATGTCACACCAATGCTTTGCCAGCTCCAA 2295
Qy 3133 -----AGCACCTPAGATAGGTGGCGCTCCACATCACTGCGCTGGCTGACTAGC 3185
Db 2296 CAAGGAAGACAAAGTCCGAGAGAGAGCGCTGGCAGACCTGGCTGACCTGGCCGACTTCGC 2355
Qy 3186 CATCGGCTCTATGGAGCAGATGAAGCAGATCAATGAGCAGCTCTTCAACAATTTCCAGAT 3245
Db 2356 GCTGCCATGAGGATAGCTTCAACCAATCAACCAAGCTCTTCAATCACTTCACTGCT 2415
Qy 3246 GAAGATTGGGTGAACATGGGCCAGTCTGTCGAGGTCTCATCGGGGTCGGAAGCCACA 3305
Db 2416 GCGCATAGGCATGAACAAAGGCGGTTCGTGCTGGGTCTATCGGAGCCGGAACCCACA 2475
Qy 3306 GTATGACATCTGGGGACACAGTGAATGCTCTAGTCTGATGG-ACAGCAGGGGGTCC 3364
Db 2476 CTACGACATCTGGGCAATACAGTCAATGTAGCCAGAGGATGGNAGTCCACGCGGGTCA 2535
Qy 3365 CCGACCGAATCCAGGTGACCCAGGA 3389
Db 2536 TGGCAACATTCAGGTGAGAGGA 2560
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## RESULT 12

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US-09-750-240-1
; Sequence 1, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
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; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 314
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(314)
; OTHER INFORMATION: n = A,T,C or G
US-09-750-240-1
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Query Match 8.3%; Score 295.2; DB 10; Length 314;
Best Local Similarity 97.1%; Pred. No. 1.3e-63;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ATGTCATGTTAGTGGCTCCTGTCCTAAAGTGGATGAACGGAACACAGCCTGGGT 60
Db 1 ATGTCATGTTAGTGGCTCCTGTCCTAAAGTGGATGAACGGAACACAGCCTGGGT 60
Qy 61 GAACGCAATGGCAGACGCTTCGCGGCGCTGCGCACTCGGGCAGGTGGCTTCTGCAG 120
Db 61 GAACGCAATGGCAGACGCTTCGCGGCGCTGCGCACTCGGGCAGGTGGCTTCTGCAG 120
Qy 121 CCCGCTATATGAGCTGCTCCGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180
Db 121 CCCGCTATATGAGCTGCTCCGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180
Qy 181 CCTCGTCCCTCGCAGGATGACGCTTCATCCGGAGGGCGGCCAGGCAAGGCAAG 240
Db 181 CCTCGTCCCTCGCAGGATGACGCTTCATCCGGAGGGCGGCCAGGCAAGGCAAG 240
Qy 241 GAGCTGGGGCTCGCGGAGTGGCTTGGCTTCGAGGATACCGAGGTGACACGACAGG 300
Db 241 GAGCTGGGGCTCGCGGAGTGGCTTGGCTTCGAGGATACCGAGGTGACACGACAGG 300
Qy 301 GCGGGGACG 309
Db 301 GCGGGGACG 309
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## RESULT 13

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US-09-915-582-11
; Sequence 11, Application US/09915582
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723P1
; CURRENT APPLICATION NUMBER: US/09/915,582
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US01/01431
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/231,968
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1180
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1163)
; OTHER INFORMATION: n equals a.t,g, or c
; NAME/KEY: SITE
; LOCATION: (1164)
; OTHER INFORMATION: n equals a.t,g, or c
; US-09-915-582-11

Query Match      8.0%; Score 284.4; DB 10; Length 1180;
Best Local Similarity 59.8%; Pred. No. 1.1e-60;
Matches 505; Conservative 0; Mismatches 321; Indels 18; Gaps 1;

Qy 2660 CTGACGAGGAGGTGGCCCTCAAAATATATGACCCCTGTGATTCCTGCTGGTGGTGG 2719
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 189 CCGAGTGTCTGAAGGAGGCCAAATGATGGTGTCTCTCTCTCTCTCTCTCTCTCTCA 248

Qy 2720 CGCTGTATCTGCATCTCAGCAGGTGGAAATCGACTGCCGCCCTAAACTTCTCTGGAAC 2779
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 249 CCCTCCTGTCTGGCTGGCCAGCAATGATGTACTACTGCCGCCCTGGACTTCTGTGGAAGA 308

Qy 2780 TACAGCAACAGGGGAAAAAGAGGAGATGGAGGAGCTACAGGCATACAACCGGAGGCTGC 2839
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 309 AGAAGCTGAGCAGGAGGAGGAGAGACAGACGATGGAGAACTGACTCGGCTGCTCT 368

Qy 2840 TGCATACATTTCTGCCAAGAGAGCTGGCGGCCACTTCTGGCCCGGAGCGCCGAATG 2899
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 369 TGGAGAAGCTGCTCCCTGCACACGTGGCCGCCCGCCAGTTTCATTGGCCAGAACCGGCCAACG 428

Qy 2900 ATGAACCTTACTATCAGTCTGTGAGTGTGGCTGTATGTTTGGCTTCCATTTGCCAACT 2959
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 429 AGGATCTCTACACAGCTCTTAAATGCGTGTGTGCTCTTCCGCTTCAGTCCCACT 488

Qy 2960 TCTCTGAGTCTATGTGGAGCTGGAGGCAAAATAGAGGTGGCGAGTGCCTGGCGCTGC 3019
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Db 489 TCAGGAGTCTACTCTGAATCCAACATCAATCATGAGGGCTAGAGTGTCTGAGGCTGC 548

Qy 3020 TCACGAGATCATCTGCTGACTTTGATGATATATACGAGGAGGCGGTTCGGGAGCTGG 3079
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Db 549 TCAATGAGATAAATGCTGATTTGATGAGCTGCTCTCAAGCCCAAGTTTCTAGTGGGTGG 608

Qy 3080 AAAAGATCAAGACATTTGGTAGCACCTTACATGGCTGCTCAGGGCTGAACGCCAGCACCT 3139
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Db 609 AGAAGATCAAGACCATCGGAGCACCTTACATGGCAGCCACAGGCTTAAATGCCACCTCTG 668

Qy 3140 -----ACGATCAGTGGGCCGCTCCACATCACTGCCCTGCTGACT 3181
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 669 GACAGGATGCACAACAGGATGCTGAACGGAGCTGCAGCCACCTTGGCACATATGTTGGAAT 728

Qy 3182 ACGCCATGGCCTCATGGAGCAGATGAAGCACATCAATGAGCACTCTCTTCAACAATTTCC 3241
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 729 TTGCCGTGGCCCTGGGTCTAAGCTGGAACGCTCATCAACAGCATTCATTAACAACCTCC 788

Qy 3242 AGATGAAGATTTGGCTGAACATGGCCCGCAGTCGTCGAGGTGTCATCGGGCTCGGAAGC 3301
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 789 GCCTTGGAGTGGGTGAACCATGGACCGGTAGTGGAGTTATTGGGGCCAGAGAAGC 848

Qy 3302 CACAGTATGACATCTGGGGGAACACAGTGAATGTCTTAGTGTGATGACAGCACGGGG 3361
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Db 849 CGCAATGATGATTTGGGCAACACAGTGAACGTGGCCAGCCCGCATGGAGAGTACAGGAG 908

Qy 3362 TCCCGGACCGAATCCAGTGAACACGAGCAGTATACAGGTTTCTAGTGTGCCAAGGGCTACC 3421
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Db 909 TCCTTGGCAAAATCCAAGTACTGAGGAGACAGCATGGGCCCTACAGTCCCTGGGCTACA 968

Qy 3422 AGCTGGAGTGTCAAGGTGAAGGCAAGGGGAGATGACCACTTACTTCC 3481
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Db 969 CCTGCTACAGCCGGGTGTCTCAAGGTGAAGGCAAGGGGAGCTCTGCACTTACTTCC 1028

Qy 3482 TCAA 3485
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Db 1029 TGAA 1032
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RESULT 14
US-09-925-297-56
; Sequence 56, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (563)
; OTHER INFORMATION: n equals a.t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1115)
; OTHER INFORMATION: n equals a.t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1119)
; OTHER INFORMATION: n equals a.t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1135)
; OTHER INFORMATION: n equals a.t,g, or c
; US-09-925-297-56

Query Match      7.5%; Score 265.6; DB 10; Length 1140;
Best Local Similarity 59.8%; Pred. No. 5e-56;
Matches 491; Conservative 0; Mismatches 310; Indels 20; Gaps 2;

Qy 2669 GGGTGGCCCTCAATATATATGACCCCTGTGATTCCTGCTGGTGTGTCGCTGGCGTGTATC 2728
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Db 216 GGAAGACCTCAAGACCATGGCTCTCTCTCTCTCTCTATATATCTTACACACTGCTTG 275

Qy 2729 TGCATGCTCAGCAGGTGGAATCGACTGCCGCCCTAAACTTCTCTCTGGAACATACAGCAA 2788
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 276 TTCTGGCTAGACAGATGAATATTACTGTAGGTTAGACTTCTTATGGAAGAACAAATTCA 335

Qy 2789 CAGGGGAAAAGAGGAGATGGAGGAGCTACAGGCATACACCGGAGGCTGCTGCATAACA 2848
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 336 AAAAGAGCGGGAGGAGATAGAGACCATGGAGAACCTGAACCCGCTGCTGTGGAGAAGC 395

Qy 2849 TTCTGCCAACAGGAGCTGGCGGCCACTTCTTGGCCCGGAGCGCCCAATGATGAACCTCT 2908
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 396 TGCTTCCCGCAGCTGGCTGAGCAGCTTCTTGGCCAGAGGCTTGAAGATGAGGAGCTAT 455

Qy 2909 ACTATCAGTCTGTGAGTGTGTGCTTATGTTGCTTCAATTCGCAACTTCTCTGAGT 2968
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Db 456 ACCACCACTCTATGACTGCGTCTGCTCATGTTTGGCTCCATTCCTCGGATTTCAAGAAT 515

Qy 2969 TCTATGTGGAGCTGGAGGCAACAAATGAGGCTGCCGAGTGCCTGCGGCTGCTCAACAGA 3028
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Db 516 TTTATACAGAAATCCGACGTGAACAAAGGAGGCTTGGAAATGCCCTTCGGTTCCTGAACAGA 575

Qy 3029 TCATCGCTGACTTTTGTGATGATTTATCAGCGAGGAGCGGTTCCCGCAGCTGGAAGATCA 3088
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Db 576 TCATCGCTGACTTTTGTGATGATTTCTTTCCAGGCCAAATTCAGTGGAGTTGAAAGATTA 635

Qy 3089 AGACGATTTGGTAGCACCTTACATGCTGCCCTCAGGGCTGAACGCCAGCACCTTACGATCAG 3148
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Db 636 AGACCAATTTGGCAGCACATACATGCGCAGCAACAGGCTCTGAGCGCTGTGCCCCAGGAGC 695

Qy 3149 TGGGCGC-----CTCCACATCACTGCGCCTGGCTGACTACCCCATGC 3190
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Searched: 24791104 seqs, 12571243825 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3549	100.0	3549	18	US-09-472-667-5
2	3549	100.0	3549	29	US-09-750-240-5
3	3484.8	98.2	3552	18	US-09-472-667-10
4	3484.8	98.2	3552	29	US-09-750-240-10
5	3478.4	98.0	4942	42	US-10-201-000-1
6	3379.2	95.2	3582	29	US-09-750-240-12
7	3147	88.7	3706	68	US-60-248-592-183
8	3144.2	88.6	3356	68	US-60-245-228-549
9	2799.2	78.9	5826	80	US-60-360-207-5921
10	2751.2	77.5	4131	9	US-08-538-815-11
11	2693.8	75.9	5353	18	US-09-491-404-837
12	2693.8	75.9	5353	34	US-09-922-279-837
13	2693.8	75.9	5353	34	US-09-922-279A-837
14	1808.4	51.0	1812	18	US-09-472-667-3
15	1808.4	51.0	1812	29	US-09-750-240-3
16	1703.4	48.0	4523	41	US-10-175-158-1
17	1691.6	47.7	4356	3	US-07-899-068-1
18	1686.6	47.5	3969	3	US-07-751-460-1
19	1648.2	46.4	3924	9	US-08-538-815-9
20	1591.4	44.8	4349	80	US-60-360-207-19529
21	1441.8	40.6	4994	76	US-60-324-185-5707

c 22 1306.2 36.8 3489 25 US-09-652-915-9933  
23 1304.8 36.8 3230 68 US-60-245-228-547  
24 1304.8 36.8 3230 69 US-60-258-272-217  
25 1324.6 34.5 4676 65 US-60-213-360-1415  
26 962.4 27.1 3427 68 US-60-248-592-182  
27 886.8 25.0 1146 29 US-09-726-172-2380  
28 843 23.8 3137 66 US-60-223-545-2  
29 841.8 23.7 2554 40 US-10-104-047-1856  
c 30 822.6 23.2 18618 68 US-60-245-228-129  
c 31 822.6 23.2 36346 68 US-60-248-592-55  
32 737.2 20.8 3866 61 US-60-172-360-2113  
33 693.6 19.5 3621 71 US-60-278-232-1807  
34 595 16.8 3978 9 US-08-538-815-1  
35 586 16.5 837 1 PCT-US01-01359-23  
36 586 16.5 837 30 US-09-764-863-23  
37 586 16.5 837 37 US-09-989-442-23  
38 545 15.4 3066 18 US-09-471-275-5594  
39 545 15.4 3066 18 US-09-496-914A-5852  
40 545 15.4 3086 22 US-09-560-873A-5852  
41 545 15.4 3811 67 US-60-236-483-2  
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43 529.6 14.9 915 1 PCT-US01-01359-69  
44 529.6 14.9 915 30 US-09-764-863-69  
45 529.6 14.9 915 30 US-09-764-868-181

ALIGNMENTS

RESULT 1  
US-09-472-667-5  
; Sequence 5, Application US/09472667  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. Kirk  
; APPLICANT: Insel, Paul A.  
; APPLICANT: Ping, Pelpel  
; APPLICANT: Post, Steven R.  
; APPLICANT: Gao, Melhua  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
; FILE REFERENCE: 22002056722  
; CURRENT APPLICATION NUMBER: US/09/472,667  
; CURRENT FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: PCT/US99/02702  
; PRIOR FILING DATE: 1999-02-09  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 09/021,773  
; PRIOR FILING DATE: 1998-02-11  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: PCT/US97/15610  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/058,209  
; PRIOR FILING DATE: 1996-09-05  
; PRIOR APPLICATION NUMBER: PCT/US96/02631  
; PRIOR FILING DATE: 1996-02-27  
; PRIOR APPLICATION NUMBER: US 08/396,207  
; PRIOR FILING DATE: 1995-02-28  
; PRIOR APPLICATION NUMBER: US 08/485,472  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 3549  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-472-667-5

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 ATGTCATGGTTTATAGTGGCCCTCCCTGGTCCCTAAAGTGGATGAACGGAAACAGCGTGGGT 60  
  
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Db 61 GAACGCAATGGGAGAAAGCGTTCCGGCGCGCGTGGGCACTCGGGCAGGTGGCTTCTGTCAGC 120  
  
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Db 121 CCCCGCTATATAGTGGCTCCCGGATGACAGACCCAGCCCCACCCCTCGGGGGCCCC 180  
  
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Db 181 CTTGGTGGCCCTGGCAGGATGAGCCCTTCATCCGGAGGGGGGGCCCGCAGGAGGCAAG 240  
  
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Db 241 GAGCTGGGGCTGGGGGAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAAACACAGCG 300  
  
QY 301 GGGGGAGCGCTGAGGTGGCGCGCGCGAGCGGTGCCAGGAGTGGGGATCCTGTGGCGC 360  
Db 301 GGGGGAGCGCTGAGGTGGCGCGCGCGAGCGGTGCCAGGAGTGGGGATCCTGTGGCGC 360  
  
QY 361 CGTTTGGTGGAGTGTCCAGTGAAGCAGTTCGGTTCGGCCCAAGCTGGAGCGCCTGTAC 420  
Db 361 CGTTTGGTGGAGTGTTCAGTGAAGCAGTTCGGTTCGGCCCAAGCTGGAGCGCCTGTAC 420  
  
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Db 421 CAGCGGTACTTTTCCAGATGAACAGAGCAGCTGACGCTGCTGGTGGCGGTGCTGGTG 480  
  
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QY 541 GTGCGACTGTGGCCCTGTCGCCCGCCCTGTCGTGGGGCTCATGTTGGTGTGTAACCGG 600  
Db 541 GTGCGACTGTGGCCCTGTCGCCCGCCCTGTCGTGGGGCTCATGTTGGTGTGTAACCGG 600  
  
QY 601 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAAGTAACTGGTGGCATCCTGGCG 660  
Db 601 CATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAAGTAACTGGTGGCATCCTGGCG 660  
  
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Db 661 GCAGTGCAGGTTCGGGGCGGTTCGAGCAGACCCCGGCGAGCCCTCTGCGGGCGCTTGG 720  
  
QY 721 TGCCCTGTGTTCTTTGTATACATCGCATACACGCTCCTCCCATCCGATCGCGGCTGCC 780  
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Db 901 GTCATTAGCATCTGCACACACTATCAGCAGAGGTGCTCAGCGCCAGGCTTTTCAGGAG 960  
  
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Db 961 ACCCGCAGTTTACATCCAGGGCCCGCTCCACCTGCAGCATGAGAATCGGCAGGAGCGG 1020  
  
QY 1021 CTGCTGCTGTGGGTATTGGCCCCAGCAGCTTGCCATGGAGATGAAGAGACATCAACACA 1080



Qy	3241	CAGATGAAGATTGGCTGAACATGGGCCCAAGTCGTGGCAGGTGTCACTCGGGCTCGGAAG	3300
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Qy	3301	CCACAGTATGACATCTTGGGGGAACACAGTGAATGTCTTACTGTATGGACAGCACGGGG	3360
Db	3301	CCACAGTATGACATCTTGGGGGAACACAGTGAATGTCTTACTGTATGGACAGCACGGGG	3360
Qy	3361	GTCCCCGACCGAATCCAGGTGACCCAGGACCTGTGTACCAAGTTCCTAGCTGCCAAGGGCTAC	3420
Db	3361	GTCCCCGACCGAATCCAGGTGACCCAGGACCTGTGTACCAAGTTCCTAGCTGCCAAGGGCTAC	3420
Qy	3421	CAGCTGGAGTGTCTCAGGGGTGTGTCAAGTGTGAAGGCCAAGGGGAGATGACCACTACTTC	3480
Db	3421	CAGCTGGAGTGTCTCAGGGGTGTGTCAAGTGTGAAGGCCAAGGGGAGATGACCACTACTTC	3480
Qy	3481	CTCAATGGGGGCCCCAGCAGTGAACAGGSCCCAGCCACAAATTCAGCTGAAGGGACCAAG	3540
Db	3481	CTCAATGGGGGCCCCAGCAGTGAACAGGSCCCAGCCACAAATTCAGCTGAAGGGACCAAG	3540
Qy	3541	GTGGGCACT	3549
Db	3541	GTGGGCACT	3549

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RESULT 2
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; Sequence 5, Application US/09750240
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P. R.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3549
; TYPE: DNA
; ORGANISM: Homo sapiens
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Db	181		
Qy	241	GAGCTGGGGCTGGGGCAGTGGCCCTTGGGCTTCGAGGATACCGAGTGCACACGACGC	300
Db	241		
Qy	241	GAGCTGGGGCTGGGGCAGTGGCCCTTGGGCTTCGAGGATACCGAGTGCACACGACGC	300
Db	241		
Qy	301	GGCGGGACGGCTGAGTGGGGCCGACGCGGTGCCCAGGAGTGGCGATCTCTGTGGCGC	360
Db	301		
Qy	301	GGCGGGACGGCTGAGTGGGGCCGACGCGGTGCCCAGGAGTGGCGATCTCTGTGGCGC	360
Db	301		
Qy	361	CGTTTGGTGCAGTGTTCAGTCCGAAAGCAGTTCGCTTGGGCCAAGCTGGAGGCTGTAC	420
Db	361		
Qy	361	CGTTTGGTGCAGTGTTCAGTCCGAAAGCAGTTCGCTTGGGCCAAGCTGGAGGCTGTAC	420
Db	361		
Qy	421	CAGCGGTACTTTTTCCAGATGAACAGACAGCTGACGCTGCTGCTGCTGGGTGCTGGTG	480
Db	421		
Qy	421	CAGCGGTACTTTTTCCAGATGAACAGACAGCTGACGCTGCTGCTGCTGGGTGCTGGTG	480
Db	421		
Qy	481	CTGCTCAGCGGTGCTGTGGCTTTCCAAAGCCGACCGCCGCCCTCAGCCTGCCTAT	540
Db	481		
Qy	481	CTGCTCAGCGGTGCTGTGGCTTTCCAAAGCCGACCGCCGCCCTCAGCCTGCCTAT	540
Db	481		
Qy	541	GTGCACTGTGGCCGTGCGCCGGCCCTGTTCGTGGGGCTCATGGTGGTGTAAACGG	600
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Qy	601	CATAGCTTCCGCCAGAGACTCCATGTGGGTGGTGAAGTAACTGGCTGGGGCATCTGGCG	660
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Qy	601	CATAGCTTCCGCCAGAGACTCCATGTGGGTGGTGAAGTAACTGGCTGGGGCATCTGGCG	660
Db	601		
Qy	661	GCAGTGCAGTTCGGGGCGCTTTCGCAGCAGACCGCGGAGCCCTCTTCGGGGCTCTGG	720
Db	661		
Qy	661	GCAGTGCAGTTCGGGGCGCTTTCGCAGCAGACCGCGGAGCCCTCTTCGGGGCTCTGG	720
Db	661		
Qy	721	TGCCCTGTGTTCTTTGTATACATCGCATACAGCTCCTCCCATCCGATCGCGGCTGCC	780
Db	721		
Qy	721	TGCCCTGTGTTCTTTGTATACATCGCATACAGCTCCTCCCATCCGATCGCGGCTGCC	780
Db	721		
Qy	781	GTCTCAGCGGCTGGGCTCTCCACTTTGCATTTGATCTTGGCTGGCACTTAAACGT	840
Db	781		
Qy	781	GTCTCAGCGGCTGGGCTCTCCACTTTGCATTTGATCTTGGCTGGCACTTAAACGT	840
Db	781		
Qy	841	GGTGATGCCCTTCCTCTGGAAGCAGCTCGTGCCAATGTGCTGCTCTCGACACAAC	900
Db	841		
Qy	841	GGTGATGCCCTTCCTCTGGAAGCAGCTCGTGCCAATGTGCTGCTCTCGACACAAC	900
Db	841		
Qy	901	GTCAATTAGCATCTGCACACACTATCAGCAGAGTGTCTCAGCGCCAGGCTTTACGAG	960
Db	901		
Qy	901	GTCAATTAGCATCTGCACACACTATCAGCAGAGTGTCTCAGCGCCAGGCTTTACGAG	960
Db	901		
Qy	961	ACCGCGATTTACATCCAGCGCCGGCTCCACCTGCGACATGAGAATCGCAGCAGGCGG	1020
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Qy	961	ACCGCGATTTACATCCAGCGCCGGCTCCACCTGCGACATGAGAATCGCAGCAGGCGG	1020
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Qy	1021	CTGCTGCTGTCGTTATGCCCCAGCAGCTTGCCATGGAGATGAAAGAGACATCAACACA	1080
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Qy	1021	CTGCTGCTGTCGTTATGCCCCAGCAGCTTGCCATGGAGATGAAAGAGACATCAACACA	1080
Db	1021		
Qy	1081	AAAAAAGACATGTTCCACAGATCTACATACAGACCATGACAATGTCAGCATCCTG	1140
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Qy	1081	AAAAAAGACATGTTCCACAGATCTACATACAGACCATGACAATGTCAGCATCCTG	1140
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Qy	1141	TTTTCACACATTCAGGCGTTCCACGCTGGCATCCCACTGCACGTCCGACGAGCTGGTC	1200
Db	1141		
Qy	1141	TTTTCACACATTCAGGCGTTCCACGCTGGCATCCCACTGCACGTCCGACGAGCTGGTC	1200
Db	1141		
Qy	1201	ATGACCTGAATGAGCTCTTTTGCCCGGTTTGACAAAGCTGGCTGGGAGAACTACTGCGTG	1260
Db	1201		
Qy	1201	ATGACCTGAATGAGCTCTTTTGCCCGGTTTGACAAAGCTGGCTGGGAGAACTACTGCGTG	1260
Db	1201		



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Db	1261	AGATCAAGACTTTGGGGACCTGTGTTACTACTGTGTGCAGGGCTGCCGGAGGCCCGGGCC	1320
Qy	1321	GACCATTCCCACCTGCTGTGTGAGATGGGGTAGACATGATTGAGGCCATCTCGCTGGTA	1380
Db	1321	GACCATTCCCACCTGCTGTGTGAGATGGGGTAGACATGATTGAGGCCATCTCGCTGGTA	1380
Qy	1381	CGTGAAGTGACAGGTGTAATGTAACTGAGCCTGGGCATCCACAGCGGCGCGTGCAC	1440
Db	1381	CGTGAAGTGACAGGTGTAATGTAACTGAGCCTGGGCATCCACAGCGGSCGCTGCAC	1440
Qy	1441	TGGCGGTCCTTGGCTTGGCGAATTTGGCAGTTTCCATGTGTGGTCCAATGATGACCCGT	1500
Db	1441	TGGCGGTCCTTGGCTTGGCGAATTTGGCAGTTTCCATGTGTGGTCCAATGATGACCCGT	1500
Qy	1501	GCCAACCATGGAAGCAGGACCGCGCTGGCGCATCCACATCACTCGGGCAACA CTG	1560
Db	1501	GCCAACCATGGAAGCAGGACCGCGCTGGCGCATCCACATCACTCGGGCAACA CTG	1560
Qy	1561	CAGTACTTGAACGGGACCTACCAAGTTGAGCGCAGCGCTGTGGCAAAGCACAACGCGTAC	1620
Db	1561	CAGTACTTGAACGGGACCTACCAAGTTGAGCGCAGCGCTGTGGCAAAGCACAACGCGTAC	1620
Qy	1621	CTCAAGGACGACACATTTAGACTTTTCTCATCTCTGGCGCACCCAGAAAGAG	1680
Db	1621	CTCAAGGACGACACATTTAGACTTTTCTCATCTCTGGCGCACCCAGAAAGAG	1680
Qy	1681	GACAAAGGATGCTGSCCAAGCTGCAGCGGACTCGGGCCAACCTCCATGGAAGGCTGATG	1740
Db	1681	GAGAAGGATGCTGSCCAAGCTGCAGCGGACTCGGGCCAACCTCCATGGAAGGCTGATG	1740
Qy	1741	CCGCGATGGTTCCTGATCGTCCCTTCTCCGGACCAAGGACTCCAAGGCTTCCCGCAG	1800
Db	1741	CCGCGATGGTTCCTGATCGTCCCTTCTCCGGACCAAGGACTCCAAGGCTTCCCGCAG	1800
Qy	1801	ATGGGCAATGATGATTTCCAGCAAGAACACACCGGGGCACCCCAAGATGCCCTGAACCC TGAG	1860
Db	1801	ATGGGCAATGATGATTTCCAGCAAGAACACACCGGGGCACCCCAAGATGCCCTGAACCC TGAG	1860
Qy	1861	GATGAGTGGATGATCTCTGACGCGTCGCATCGATGCCGACGATGATCACTGATCGCGG	1920
Db	1861	GATGAGTGGATGATCTCTGACGCGTCGCATCGATGCCGACGATGATCACTGATCGCGG	1920
Qy	1921	AAGGACATGTGCGCGGTTTTTGCTCACTTCCAGAGAGAGATTTTGAGAAGAATAC	1980
Db	1921	AAGGACATGTGCGCGGTTTTTGCTCACTTCCAGAGAGAGATTTTGAGAAGAATAC	1980
Qy	1981	TCCCGAAGTGGATCCCGCTTCGGAGCCTACGTTGCCCTGTGCCCTGTGGTCTTCTGC	2040
Db	1981	TCCCGAAGTGGATCCCGCTTCGGAGCCTACGTTGCCCTGTGCCCTGTGGTCTTCTGC	2040
Qy	2041	TTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCCCTGATGCTGGGATTTAT	2100
Db	2041	TTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCCCTGATGCTGGGATTTAT	2100
Qy	2101	GCACGATCTTCTCTGCTGCTAATCACCGTGTGATCTGTGCTGTGTA TCTCTCTGTGGT	2160
Db	2101	GCACGATCTTCTCTGCTGCTAATCACCGTGTGATCTGTGCTGTGTA TCTCTCTGTGGT	2160
Qy	2161	TCCTGTTCCTTAAGCCCTGCAACGTCTGTCCCGCAGCATTTGCCGTCA CCGGCACAT	2220
Db	2161	TCCTGTTCCTTAAGCCCTGCAACGTCTGTCCCGCAGCATTTGCCGTCA CCGGCACAT	2220
Qy	2221	AGCACGCGAGTTGGCATCTTTTCGTCCTGCTTGTGTTACTTCTGCGCATTTGCCA AATG	2280
Db	2221	AGCACGCGAGTTGGCATCTTTTCGTCCTGCTTGTGTTACTTCTGCGCATTTGCCA AATG	2280
Qy	2281	TTCACTGTAAACACACCCCATACGGAGCTGTGCAGCCGGATGCTGAATTTAA CACT	2340
Db	2281	TTCACTGTAAACACACCCCATACGGAGCTGTGCAGCCGGATGCTGAATTTAA CACT	2340
Qy	2341	GCTGACATCACTGCCTGCCACCTGCAGAGCTCAATTTACTCTCTGGGCTCGATCTCC C	2400

[illegible]

Db 3421 CAGCTGAGTGTCTCAGAGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACCACTACTTTC 3480  
Qy 3481 CTCAATGGGGCCCCAGCAGTAAACAGGGGCCAGCCACAAATTTCAGCTGAAGGACCAAG 3540  
Db 3481 CTCAATGGGGCCCCAGCAGTAAACAGGGGCCAGCCACAAATTTCAGCTGAAGGACCAAG 3540  
Qy 3541 GTGGGCACT 3549  
Db 3541 GTGGGCACT 3549

RESULT 3

US-09-472-667-10  
; Sequence 10, Application US/09472667  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. Kirk  
; APPLICANT: Insel, Paul A.  
; APPLICANT: Ping, Peipel  
; APPLICANT: Post, Steven R.  
; APPLICANT: Gao, Methua  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART FAILURE  
; FILE REFERENCE: 220002056722  
; CURRENT APPLICATION NUMBER: US/09/472,667  
; CURRENT FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: PCT/US99/02702  
; PRIOR FILING DATE: 1999-02-09  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 09/021,773  
; PRIOR FILING DATE: 1998-02-11  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: PCT/US97/15610  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/058,209  
; PRIOR FILING DATE: 1996-09-05  
; PRIOR APPLICATION NUMBER: PCT/US96/02631  
; PRIOR FILING DATE: 1996-02-27  
; PRIOR APPLICATION NUMBER: US 08/396,207  
; PRIOR FILING DATE: 1995-02-28  
; PRIOR APPLICATION NUMBER: US 08/485,472  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 3552  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-472-667-10

Query Match 98.2%; Score 3484.8; DB 18; Length 3552;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 3517; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

Qy 1 ATGTCATGGTTTGTAGTGGCTTCTGGTCCCTAAAGTGGATGAACGGAACAGCCTGGGGT 60  
Db 1 ATGTCATGGTTTGTAGTGGCTTCTGGTCCCTAAAGTGGATGAACGGAACAGCCTGGGGT 60  
Qy 61 GAAGCAATGGCAGAAAGCGTTGCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120  
Db 61 GAAGCAATGGCAGAAAGCGTTGCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120  
Qy 121 CCGCGCTATATGAGTCCCTCCCGGGATGACAGCCACCCACCCCTGGGGCCCC 180  
Db 121 CCGCGCTATATGAGTCCCTCCCGGGATGACAGCCACCCACCCCTGGGGCCCC 180  
Qy 181 CCTCGGTGCCCTTGGCAGGATGAGCCCTTCATCCGAGGGCGCGCCAGGCAAG 240  
Db 181 CCTCGGTGCCCTTGGCAGGATGAGCCCTTCATCCGAGGGCGCGCCAGGCAAG 240

Db 181 CCTCGGTGCCCTTGGCAGGATGAGCCCTTCATCCGAGGGCGCGCCAGGCAAG 240  
Qy 241 GAGCTGGGGCTGGGGCAGTGGCCCTGGGCTTCAGAGATACCGAGGTGACAACACAGCG 300  
Db 241 GAGCTGGGGCTGGGGCAGTGGCCCTGGGCTTCAGAGATACCGAGGTGACAACACAGCG 300  
Qy 301 GGGGGAGCGCTGAGGTGGGCGCCGACGCGGTGCCAGGAGTGGGCGATCCTGTGCGCG 360  
Db 301 GGGGGAGCGCTGAGGTGGGCGCCGACGCGGTGCCAGGAGTGGGCGATCCTGTGCGCG 360  
Qy 361 CGTTTGGTGCAGGTGTTCCAGTGAAGCAGTTCGGTTCGGCCAGCTGGAGCGCCTGTAC 420  
Db 361 CGTCTGGTGCAGGTGTTCCAGTGAAGCAGTTCGGTTCGGCCAGCTGGAGCGCCTGTAC 420  
Qy 421 CAGCGTACTTTTTCCAGATGAACAGCAGCAGCTGACGCTGTGTGGCGGTGCTGGTG 480  
Db 421 CAGCGTACTTTTTCCAGATGAACAGCAGCAGCTGACGCTGTGTGGCGGTGCTGGTG 480  
Qy 481 CTGCTACAGCGGTGCTGGGCTTTCCAAAGCGCAGCCCGCCGCTCAGCCCTGCCTAT 540  
Db 481 CTGCTACAGCGGTGCTGGGCTTTCCAAAGCGCAGCCCGCCGCTCAGCCCTGCCTAT 540  
Qy 541 GTGCACTGTTGGCTGTGCGCGCCCTGTCTGGTGGGCTCATGTTGTTGTAACCGG 600  
Db 541 GTGCACTGTTGGCTGTGCGCGCCCTGTCTGGTGGGCTCATGTTGTTGTAACCGG 600  
Qy 601 CATAGCTTCGCCAGGACTCCATGTGGTGTGAGTAACGTGTGTGGCATCTCTGGCG 660  
Db 601 CATAGCTTCGCCAGGACTCCATGTGGTGTGAGTAACGTGTGTGGCATCTCTGGCG 660  
Qy 661 GCAGTGCAGGTGCGGGCGCTTTCGAGCAGACCCGCGCAGCCCTCTGGGGCTCTGG 720  
Db 661 GCAGTGCAGGTGCGGGCGCTTTCGAGCAGACCCGCGCAGCCCTCTGGGGCTCTGG 720  
Qy 721 TGCCCTGTGTTTGTATACATCGCATACAGCTCCTCCCATCCGATCGCGGTGCC 780  
Db 721 TGCCCTGTGTTTGTATACATCGCATACAGCTCCTCCCATCCGATCGCGGTGCC 780  
Qy 781 GTCTCAGCGGCTTGGGCTCTCCACCTTGATTTGATTTGGCCTTGCAACTTAACCGT 840  
Db 781 GTCTCAGCGGCTTGGGCTCTCCACCTTGATTTGATTTGGCCTTGCAACTTAACCGT 840  
Qy 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTTCTTCCCTGCAACA 900  
Db 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTTCTTCCCTGCAACA 900  
Qy 901 GTCAATTAGCATCTGCACACACTATCCAGCAGAGGTGCTCAGCGCCAGGCTTTTCAGGAG 960  
Db 901 GTCAATTAGCATCTGCACACACTATCCAGCAGAGGTGCTCAGCGCCAGGCTTTTCAGGAG 960  
Qy 961 ACCCGCAGTTTACATCCAGGCGCGGCTCCACCTGAGCATGAGAAATCGCAGAGGCGG 1020  
Db 961 ACCCGCAGTTTACATCCAGGCGCGGCTCCACCTGAGCATGAGAAATCGCAGAGGCGG 1020  
Qy 1021 CTGCTGCTGCTGTTATGCCCCCAGCAGTTGCCATGAGATGAAGAAAGACATCAACACA 1080  
Db 1021 CTGCTGCTGCTGTTATGCCCCCAGCAGTTGCCATGAGATGAAGAAAGACATCAACACA 1080  
Qy 1081 AAAAAAGAACAC --- ATGTTTCCACAAGATCTACATACAGAAAGATGACAAATGTCAGCATC 1137  
Db 1081 AAAAAAGAACATGATGTTCCACAAGATCTACATACAGAAAGATGACAAATGTCAGCATC 1140  
Qy 1138 CTGTTTGCAGACATGAGGCTTTCACAGCCTGGCAGTCCAGTGCACCTGCGCAGGAGCTG 1197  
Db 1141 CTGTTTGCAGACATGAGGCTTTCACAGCCTGGCAGTCCAGTGCACCTGCGCAGGAGCTG 1200  
Qy 1198 GTCATGACCTGATGAGCTTCTTGGCCGCTTTCAGAAAGCTGGCTGGGAGAAATCACTGC 1257  
Db 1201 GTCATGACCTGATGAGCTTCTTGGCCGCTTTCAGAAAGCTGGCTGGGAGAAATCACTGC 1260  
Qy 1258 CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGGAGGCCCG 1317  
Db 1261 CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGGAGGCCCG 1320

Qy	1318	GCGGACCACTGCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG	1317
Db	1321	GCCGACCACTGCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG	1380
Qy	1378	GTACGTGAGTGCACAGGTCTGAATGTAACTAGCAATGCCGTGGGCATCCACAGCGGCGCGTG	1437
Db	1381	GTACGTGAGTGCACAGGTCTGAATGTAACTAGCAATGCCGTGGGCATCCACAGCGGCGCGTG	1440
Qy	1438	CACCTCGGCGCTCCTTTGGCTTGCAGAAATGGCAGTTTCGATGTGTGGTCCCAATGATGTGACC	1497
Db	1441	CACCTCGGCGCTCCTTTGGCTTGCAGAAATGGCAGTTTCGATGTGTGGTCCCAATGATGTGACC	1500
Qy	1498	CTGGCCAAACCATATGGAAGCAGGAAGCCGGGCTGGCCGCATCCACATCATCTCGGGCAACA	1557
Db	1501	CTGGCCAAACCATATGGAAGCAGGAAGCCGGGCTGGCCGCATCCACATCATCTCGGGCAACA	1560
Qy	1558	CTGCACCTACTCTGAACCGGGSACTACGAAGCTGGAGCCAGGCCGTGTGTGCAAGCGCAACGCG	1617
Db	1561	CTGCACCTACTCTGAACCGGGSACTACGAAGCTGGAGCCAGGCCGTGTGTGCGGAGCGCAACGCG	1620
Qy	1618	TACCTCAAGGAGCAGCACATTTAGACATTTCTCATCTCTGGGCGCCAGCCAGAACGGAAA	1677
Db	1621	TACCTCAAGGAGCAGCACATTTAGACATTTCTCATCTCTGGGCGCCAGCCAGAACGGAAA	1680
Qy	1678	GAGGAAAGGCATGCTGGCCAAAGCTGCAGCGGACTCGGGCCCACTCCATGGAGGGCTG	1737
Db	1681	GAGGAAAGGCATGCTGGCCAAAGCTGCAGCGGACTCGGGCCCACTCCATGGAGGGCTG	1740
Qy	1738	ATGCCCGCATGGTTCCTGATCGTCGCTTCCTCCGGACCAAGGACTCCAAGGCCCTCCCGC	1797
Db	1741	ATGCCCGCTGGTTCCTGATCGTCGCTTCCTCCGGACCAAGGACTCCAAGGCCCTCCCGC	1800
Qy	1798	CAGATGGCAATGATGATTCCAGCAAGAACAACCCGGGSCACCCCAAGATGCCCTGAAGCCCT	1857
Db	1801	CAGATGGCAATGATGATTCCAGCAAGAACAACCCGGGSCACCCCAAGATGCCCTGAAGCCCT	1860
Qy	1858	GAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTTGATCAGCTG	1917
Db	1861	GAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTTGATCAGCTG	1920
Qy	1918	CGGAAGGACATGTGCGCGGTTTTGTCTCACTTCCAGAGAGAGGATTTTGAGAAGAAG	1977
Db	1921	CGGAAGGACATGTGCGCGGTTTTGTCTCACTTCCAGAGAGAGGATTTTGAGAAGAAG	1980
Qy	1978	TACTCCGGAAGTGGATCCCGGCTTCGGAGCCTACGTTGGCTGTGCCCTGTGGTCTTC	2037
Db	1981	TACTCCGGAAGTGGATCCCGGCTTCGGAGCCTACGTTGGCTGTGCCCTGTGGTCTTC	2040
Qy	2038	TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCCCTGATGCTTGGGATT	2097
Db	2041	TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCCCTGATGCTTGGGATC	2100
Qy	2098	TATGCCAGCATCTTCCTGCTGCTGAATACACCGTGTGATCTGTGCTGTGTACTCCTGT	2157
Db	2101	TATGCCAGCATCTTCCTGCTGCTGAATACACCGTGTGATCTGTGCTGTGTACTCCTGT	2160
Qy	2158	GGTTCTCTGTTCCCTAAGGCCCTGCAAGCTGTGTCCCGCAGCATTTGCCGCTCACGGGCA	2217
Db	2161	GGTTCTCTGTTCCCTAAGGCCCTGCAAGCTGTGTCCCGCAGCATTTGCCGCTCACGGGCA	2220
Qy	2218	CATAGCAGCGCACTTGGCATTTTTTCGCTCTGCTGTGTGTTTACTTCTGCCATTTGCCAAC	2277
Db	2221	CATAGCAGCGCACTTGGCATTTTTTCGCTCTGCTGTGTGTTTACTTCTGCCATTTGCCAAC	2280
Qy	2278	ATGTTTCACTGTAAACACACACCCCACTAGCGAGCTGTGACGCCCGGATGCTGAATTTAACTA	2337
Db	2281	ATGTTTCACTGTAAACACACACCCCACTAGCGAGCTGTGACGCCCGGATGCTGAATTTAACTA	2340
Qy	2338	CTTGCTGACATCACTGCTGCTGCCACCTGCAGCAGCTCAATTAATCTCTGCGGCTCGATGCT	2397
Db	2341	CTTGCTGACATCACTGCTGCTGCCACCTGCAGCAGCTCAATTAATCTCTGCGGCTCGATGCT	2400

Qy	2398	CCCTGTGTGAGGGCACCATGCCACCTGCGACGCTTTCTGTGAGTGTTCATCTCGGGAACATG	2451
Db	2401	CCCCGTGTGAGGGCACCATGGCCACCTGCGACGTTTCTGTGAGTACTTATCTCGGGAACATG	2460
Qy	2458	CTGCTGAGTCTCTTTGGCCAGCTGCTGCTTCTCTGCGACATCAGCAGCATCGGGAGTTGGCC	2517
Db	2461	CTGCTGAGTCTCTTTGGCGAGCTCTGTCTTCTGCGACATCAGCAGCATCGGGAAGTTGGCC	2520
Qy	2518	ATGATCTTTGTCTTTGGGGCTCATCTATTTTGTGTGCTTCTGTGCGTCCCGCCAGCCGCC	2577
Db	2521	ATGATCTTTGTCTTTGGGGCTCATCTATTTTGTGTGCTTCTGTGCGTCCCGCCAGCCACC	2580
Qy	2578	ATCTTTTGACAACATATGACCTACTGCTTGTGGCGTCCATGCTTGGCTTCTTCCAATGAGAAC	2637
Db	2581	ATCTTTTGACAACATATGACCTACTGCTTGTGGCGTCCATGCTTGGCTTCTTCCAATGAGAAC	2640
Qy	2638	TTTGTATGGGTGGACTGTCCAGCTCGAGGAGGGTGGCCCTCAATATATGACCCCTGTG	2697
Db	2641	TTTGTATGGGTGGACTGTCCAGCTCGAGGAGGGTGGCCCTCAAAATATATGACCCCTGTG	2700
Qy	2698	ATTCTGCTGGTGTTTGGCGTGGCGGTGTATCTGCGATGCTCAGCAGGTGGAAATCGACTGCC	2757
Db	2701	ATTCTGCTGGTGTTTGGCGTGGCGGTGTATCTGCGATGCTCAGCAGGTGGAGTCGACTGCC	2760
Qy	2758	CGCTTAACTTCTCTGTGAAACTACAGGCAACAGGGGAAAAAGAGGAGATGGAGGAGCTA	2817
Db	2761	CGCTTAGACTTCTCTGTGAACTACAGGCAACAGGGGAGAGGAGGAGATGGAGGAGCTA	2820
Qy	2818	CAGGCATACAACCGGAGGTGCTGCATACAATCTTGCCCCAAGGACGTGGGGGCCACTTC	2877
Db	2821	CAGGCATACAACCGGAGGTGCTGCATACAATCTTGCCCCAAGGACGTGGGGGCCACTTC	2880
Qy	2878	CTGGCCGGGAGGCGCGCAATGATGAACCTACTACTATCAGTCGTGTGAGTGTGGCGTGT	2937
Db	2881	CTGGCCGGGAGGCGCGCAATGATGAACCTACTACTATCAGTCGTGTGAGTGTGGCGTGT	2940
Qy	2938	ATGTTTGGCTTCCATTGCCAACTTCTCTGAGTTCTTATGTGGAGCTGGAGGCAACAATGAG	2997
Db	2941	ATGTTTGGCTTCCATTGCCAACTTCTCTGAGTTCTTATGTGGAGCTGGAGGCAACAATGAG	3000
Qy	2998	GGTGGCGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC	3057
Db	3001	GGTGTGAGTGTCCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC	3060
Qy	3058	GAGGAGCGTTCGCGCAGCTGGAAGAGATCAAGACGATTGGTAGCACATAGATGGCTGCC	3117
Db	3061	GAGGAGCGTTCGCGCAGCTGGAAGAGATCAAGACGATTGGTAGCACATAGATGGCTGCC	3120
Qy	3118	TCAGGGCTGAACCCGACGACCTACGATCAGGTTGGGCGCTCCACATCAGTGCCTGGCT	3177
Db	3121	TCAGGGCTGAACCCGACGACCTACGATCAGGTTGGGCGCTCCACATCAGTGCCTGGCT	3180
Qy	3178	GACTTACGCCATGGGGTCTATGGAGCAGATGAAGACACATCAATGAGCACTCCCTTCAACAAT	3237
Db	3181	GACTTACGCCATGGGGTCTATGGAGCAGATGAAGACACATCAATGAGCACTCCCTTCAACAAT	3240
Qy	3238	TTCCAGATGAAGATTGGGTGTAACATGGGCCAGTCGTGGCAGGTGTATCGGGGCTCGG	3297
Db	3241	TTCCAGATGAAGATTGGGTGTAACATGGGCCAGTCGTGGCAGGTGTATCGGGGCTCGG	3300
Qy	3298	AAGCCACGATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGCAGCAGCACG	3357
Db	3301	AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGCAGCAGCACG	3360
Qy	3358	GGGTTCGCCGACCGAAATCCAGGTGACCCAGGACCTGTACCGAGTTCTAGCTGCCAAGGGC	3417
Db	3361	GGGTTCGCCGACCGAAATCCAGGTGACCCAGGACCTGTACCGAGTTCTAGCTGCCAAGGGC	3420
Qy	3418	TACCAGCTGCACTGTCCGAGGGTGGTCAAGGTGAAGGGCAGGGGGGAGATGACCACTAC	3477
Db	3421	TACCAGCTGCACTGTCCGAGGGTGGTCAAGGTGAAGGGCAGGGGGGAGATGACCACTAC	3480
Qy	3478	TTCTCTAATGGGGGCCCGACGACTTAACAGGGCCCGCCAGCCACAAATTCAGCTGAAGGGACC	3537

Db 3481 TTCCTCAATGGGGCCCCAGCAGTTAAACAGGGCCCCAGCCACAAATTCAGCTGAAGGGACC 3540  
Qy 3538 AAGTGGGCACT 3549  
Db 3541 AAGTGGGCACT 3552  
RESULT 4  
US-09-750-240-10  
: Sequence 10. Application US/09750240  
: GENERAL INFORMATION:  
: APPLICANT: Hammon, H. K.  
: APPLICANT: Insel, P. A.  
: APPLICANT: Ping, P.  
: APPLICANT: Post, S. R.  
: APPLICANT: Gao, M.  
: TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
: TITLE OF INVENTION: FAILURE  
: FILE REFERENCE: 22002056723  
: CURRENT APPLICATION NUMBER: US/09/750,240  
: CURRENT FILING DATE: 2001-10-12  
: PRIOR APPLICATION NUMBER: US 09/472,667  
: PRIOR FILING DATE: 1999-12-27  
: PRIOR APPLICATION NUMBER: US 09/008,097  
: PRIOR FILING DATE: 1998-01-16  
: PRIOR APPLICATION NUMBER: US 08/924,757  
: PRIOR FILING DATE: 1997-09-05  
: PRIOR APPLICATION NUMBER: US 60/048,933  
: PRIOR FILING DATE: 1997-06-16  
: PRIOR APPLICATION NUMBER: US 08/708,661  
: PRIOR FILING DATE: 1996-09-05  
: NUMBER OF SEQ ID NOS: 13  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 10  
: LENGTH: 3552  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
US-09-750-240-10  
Query Match 98.2%; Score 3484.8; DB 29; Length 3552;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 3517; Conservative 0; Mismatches 32; Indels 3; Gaps 1;  
Qy 1 ATGTCATGTTTATGGCTCCTGGTCCCTAAAGTGGATGAACGAAACAGCCTGGGGT 60  
Db 1 ATGTCATGTTTATGGCTCCTGGTCCCTAAAGTGGATGAACGAAACAGCCTGGGGT 60  
Qy 61 GAACGCAATGGGCAGAGCGTTCCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCGCAAG 120  
Db 61 GAACGCAATGGGCAGAGCGTTCCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCGCAAG 120  
Qy 121 CCCGGCTATATAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGGCGGGCCCC 180  
Db 121 CCCGGCTATATAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTGGCGGGCCCC 180  
Qy 181 CCTCGGTGCCCTTGGCAGGATAGCCCTTCATCCGAGGGCGGCCCGCAGGCAAGGGCAAG 240  
Db 181 CCTCGGTGCCCTTGGCAGGATAGCCCTTCATCCGAGGGCGGCCCGCAGGCAAGGGCAAG 240  
Qy 241 GAGCTGGGGCTGGCGGCAGTGGCCCTTGGCTTCGAGATACCGAGTGCACACGACAGCG 300  
Db 241 GAGCTGGGGCTGGCGGCAGTGGCCCTTGGCTTCGAGATACCGAGTGCACACGACAGCG 300  
Qy 301 GCGGGAGCGGTGAGGTGGCGCGCGAGCGGTGCCAGGAGTGGCGCATCCTGCTGCGCG 360  
Db 301 GCGGGAGCGGTGAGGTGGCGCGCGAGCGGTGCCAGGAGTGGCGCATCCTGCTGCGCG 360  
Qy 361 CGTTTGTGCAAGTGTTCCTAGTGAAGCAGTTCGGTTTCGGCCAAAGCTGGAGCGCCCTGTAC 420  
Db 361 CGTCTGTGCAAGTGTTCCTAGTGAAGCAGTTCGGTTTCGGCCAAAGCTGGAGCGCCCTGTAC 420  
Qy 421 CAGCGGTACTTTTCCAGATGAACCAAGCAGCGCTGACGCTGCTGGTGGCGGTGCTGGTG 480

Db 421 CAGCGGTACTTTTCCAGATGAACCAAGCAGCGCTGACGCTGCTGATGGGGTCTGGTG 480  
Qy 481 CTGCTCACAGCGGTGCTGGCTTTCCAAAGCCGACCCCGCCCTCAGCCCTGCGCTAT 540  
Db 481 CTGCTCACAGCGGTGCTGGCTTTCCAAAGCCGACCCCGCCCTCAGCCCTGCGCTAT 540  
Qy 541 GTGCACTGTTGGCTGTGCCCGCCCTGTTCTGTGGGGCTCATGTTGTTGTAACCGG 600  
Db 541 GTGCACTGTTGGCTGTGCCCGCCCTGTTCTGTGGGGCTCATGTTGTTGTAACCGG 600  
Qy 601 CATAGCTTCCGCCAGGACTCCATGTGGTGGTGAAGTGAAGTGGTGGGATCCTGGCG 660  
Db 601 CATAGCTTCCGCCAGGACTCCATGTGGTGGTGAAGTGAAGTGGTGGGATCCTGGCG 660  
Qy 661 GCAGTGCAGGTTCGGGGCGCTTTCGGCAGACAGCCCGCAGCCCTCTGGGGCTCTGG 720  
Db 661 GCAGTGCAGGTTCGGGGCGCTTTCGGCAGACAGCCCGCAGCCCTCTGGGGCTCTGG 720  
Qy 721 TGCCCTGTGTTTGTATATACATCGCATACAGCTCTCCCATCCCATCCGATGCGGGTGC 780  
Db 721 TGCCCTGTGTTTGTATATACATCGCATACAGCTCTCCCATCCCATCCGATGCGGGTGC 780  
Qy 781 GTCTCAGCGGCTGGGCTCTCCACCTTGCAATTTGATCTTGGCTGGCAACTTAACCGT 840  
Db 781 GTCTCAGCGGCTGGGCTCTCCACCTTGCAATTTGATCTTGGCTGGCAACTTAACCGT 840  
Qy 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCAATGTCTGTGTTCTTCGACCAAC 900  
Db 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCAATGTCTGTGTTCTTCGACCAAC 900  
Qy 901 GTCATTAGCATCTGCACACTATCCAGCAGAGTGTCTCAGCGCCAGGCTTTCAGGAG 960  
Db 901 GTCATTAGCATCTGCACACTATCCAGCAGAGTGTCTCAGCGCCAGGCTTTCAGGAG 960  
Qy 961 ACCGCGAGTTACATCCAGGCGCCGCTCCACCTGCAGATCAGATCCGACGAGGACGG 1020  
Db 961 ACCGCGAGTTACATCCAGGCGCCGCTCCACCTGCAGATCAGATCCGACGAGGACGG 1020  
Qy 1021 CTGCTGCTGCTGGTATTTGCCCGCAGCAGCTTCCATGGAGATGAAGAAGACATCAACACA 1080  
Db 1021 CTGCTGCTGCTGGTATTTGCCCGCAGCAGCTTCCATGGAGATGAAGAAGACATCAACACA 1080  
Qy 1081 AAAAAGAACGAC --- ATGTTTCCACAAGATCTACATACAGAGCATGACATGTCAGCATC 1137  
Db 1081 AAAAAGAACGACATGATGTTTCCACAAGATCTACATACAGAGCATGACATGTCAGCATC 1140  
Qy 1138 CTGTTTTCAGACATTTAGGGCTTTCACCAGCTGCCAGTCCAGTCCAGTCCGAGGAGCTG 1197  
Db 1141 CTGTTTTCAGACATTTAGGGCTTTCACCAGCTGCCAGTCCAGTCCAGTCCGAGGAGCTG 1200  
Qy 1198 GTCATGACCTGAATGAGCTCTTTGCCCGGTTTACAAAGCTGGCTGGGAGAAATCACTGC 1257  
Db 1201 GTCATGACCTGAATGAGCTCTTTGCCCGGTTTACAAAGCTGGCTGGGAGAAATCACTGC 1260  
Qy 1258 CTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGAGGCGCGG 1317  
Db 1261 CTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGAGGCGCGG 1320  
Qy 1318 GCGGACCATCCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCGCTG 1377  
Db 1321 GCGGACCATCCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCGCTG 1380  
Qy 1378 GTAGCTGAGGTGACAGGTGTGAATGTGAACATGCGCTGGGCATGCCACAGCGGCGCGGTG 1437  
Db 1381 GTAGCTGAGGTGACAGGTGTGAATGTGAACATGCGCTGGGCATGCCACAGCGGCGCGGTG 1440  
Qy 1438 CACTGGGCTCCTTGGCTTGGGAAATGCAAGTTCGATGTGGTGTCCAAATGATGAC 1497  
Db 1441 CACTGGGCTCCTTGGCTTGGGAAATGCAAGTTCGATGTGGTGTCCAAATGATGAC 1500  
Qy 1498 CTGGCCAAACACATGGAAGCAGGAACCGGCTGGCGCATCCACATCACTCCGGCAACA 1557  
Db 1498 CTGGCCAAACACATGGAAGCAGGAACCGGCTGGCGCATCCACATCACTCCGGCAACA 1557

Db 1501 CTGGCCACACACATGGAGGCGAGGCGCGGCTGGCCGATCCACATCACTCGGGCAACA 1560  
Qy 1558 CTGCAGTACCTGAACGGGGACTACGAAGTGGAGCGAGCGCGTGTGGCAAGCGCAACGCG 1617  
Db 1561 CTGCAGTACCTGAACGGGGACTACGAAGTGGAGCGAGCGCGTGTGGCGAGCGCAACGCG 1620  
Qy 1618 TACCTCAAGGAGCAGCACAATTGAGACTTTCCTCATCTCTGGCGCGAGCAAGAAACGGA 1677  
Db 1621 TACCTCAAGGAGCAGCACAATTGAGACTTTCCTCATCTCTGGCGCGAGCAAGAAACGGA 1680  
Qy 1678 GAGGAGAAAGCATGCTGGCCAAAGCTGCAGGGGACTCGGGCCAACTCCATGGAAGGGCTG 1737  
Db 1681 GAGGAGAAAGCATGCTGGCCAAAGCTGCAGGGGACTCGGGCCAACTCCATGGAAGGGCTG 1740  
Qy 1738 ATGCCGCGATGGGTTCTGTGATGCTGCTTCTCCGGAGCAAGGAGCTTCAAGGCCCTTCGCG 1797  
Db 1741 ATGCCGCGCTGGTTCTGTGATGCTGCTTCTCCGGAGCAAGGACTCCAAGGCCCTTCGCG 1800  
Qy 1798 CAGATGGGCATGTGATGATTCAGCAAAAGACAACCGGGGCAACCAAGATGCCCTGAACCC 1857  
Db 1801 CAGATGGGCATGTGATGATTCAGCAAAAGACAACCGGGGCAACCAAGATGCCCTGAACCC 1860  
Qy 1858 GAGGATGAGGTGGATGAGTTCCTGAGCGGTGCCATCGATGCCCGCAGCATGATGATGATG 1917  
Db 1861 GAGGATGAGGTGGATGAGTTCCTGAGCGGTGCCATCGATGCCCGCAGCATGATGATGATG 1920  
Qy 1918 CGGAAGGACCATGTGGCGCGGTTTGTCTCACTTCCAGAGAGAGGATTTTGAAGAAG 1977  
Db 1921 CGGAAGGACCATGTGGCGCGGTTTGTCTCACTTCCAGAGAGAGGATTTTGAAGAAG 1980  
Qy 1978 TACTCCCGGAAGGTGGATGCCGCTGCGGAGCCCTACGTTGGCTGTGGCCCTGTGGCTCTTC 2037  
Db 1981 TACTCCCGGAAGGTGGATGCCGCTGCGGAGCCCTACGTTGGCTGTGGCCCTGTGGCTCTTC 2040  
Qy 2038 TGCTTCATCTGCTCATCCAGCTTCTAATTTCCACACTCCAGCCGTGATGCTTGGGAT 2097  
Db 2041 TGCTTCATCTGCTCATCCAGCTTCTAATTTCCACACTCCAGCCGTGATGCTTGGGAT 2100  
Qy 2098 TATGCCAGCATCTTCTGCTGCTGCTAATCACCGTGTGATGCTGTGCTGTACTCTCTGT 2157  
Db 2101 TATGCCAGCATCTTCTGCTGCTGCTAATCACCGTGTGATGCTGTGCTGTACTCTCTGT 2160  
Qy 2158 GGTTCCTGTTCCCTAAGGCCCTGCAAGCTGTCTCCCGCAGCATGTCGGCTCAGGGCA 2217  
Db 2161 GGTTCCTGTTCCCTAAGGCCCTGCAAGCTGTCTCCCGCAGCATGTCGGCTCAGGGCA 2220  
Qy 2218 CATAGCACCGAGTTGGCATCTTTCCGCTGCTGCTGTTTACTTCTGCTGCTGCTGCTGCT 2277  
Db 2221 CATAGCACCGAGTTGGCATCTTTCCGCTGCTGCTGTTTACTTCTGCTGCTGCTGCTG 2280  
Qy 2278 ATGTTACCTGTAAACACACCCCATACGGAGCTGTGAGCGCCCGATGCTGAATTTAA 2337  
Db 2281 ATGTTACCTGTAAACACACCCCATACGGAGCTGTGAGCGCCCGATGCTGAATTTAA 2340  
Qy 2338 CTGCTGACATCACTGCTGCCAGCTGAGCAGAGCTCAATTAATCTCTGCGGCTGGATGCT 2397  
Db 2341 CTGCTGACATCACTGCTGCCAGCTGAGCAGAGCTCAATTAATCTCTGCGGCTGGATGCT 2400  
Qy 2398 CCCCTGTGTAGGGCACCATGCCACCTGACGTTTCTCTGAGGTGTCCATCGGGAACATG 2457  
Db 2401 CCCCTGTGTAGGGCACCATGCCACCTGACGTTTCTCTGAGGTGTCCATCGGGAACATG 2460  
Qy 2458 CTGCTGAGTCTCTTGGCGAGCTGTCTCTCTGACATCAGCAGCATCGGGAAGTTGGCC 2517  
Db 2461 CTGCTGAGTCTCTTGGCGAGCTGTCTCTCTGACATCAGCAGCATCGGGAAGTTGGCC 2520  
Qy 2518 ATGATCTTTTGTCTTGGGCTCATCTATTGTGTGCTGCTTCTGCTGGGTCCCCAGCGCC 2577  
Db 2521 ATGATCTTTTGTCTTGGGCTCATCTATTGTGTGCTGCTTCTGCTGGGTCCCCAGCGCC 2580  
Qy 2578 ATCTTTGACAACTATGACCTACTGCTGGCGTCCATGCTTGGCTTCTTCCAAATGAGACC 2637  
Db 2581 ATCTTTGACAACTATGACCTACTGCTGGCGTCCATGCTTGGCTTCTTCCAAATGAGACC 2640

Qy 2638 TTTGATGGGCTGGACTGTCCAGCTGCAGGAGGGTGGCCCTCAAAATATATGACCCCTGTG 2697  
Db 2641 TTTGATGGGCTGGACTGTCCAGCTGCAGGAGGGTGGCCCTCAAAATATATGACCCCTGTG 2700  
Qy 2698 ATTCTGCTGGTGTGGCTGGCGCTGTATCTGATGCTAGCAGGTGGAATCGACTGCC 2757  
Db 2701 ATTCTGCTGGTGTGGCTGGCGCTGTATCTGATGCTAGCAGGTGGAATCGACTGCC 2760  
Qy 2758 CGCCTAACTTCCCTCTCGAAACTACAGCAACAGGGGAAAAGAGGAGATGAGAGGAGTA 2817  
Db 2761 CGCCTAGACTTCCCTCTCGAAACTACAGCAACAGGGGAAAAGAGGAGATGAGAGGAGTA 2820  
Qy 2818 CAGGCATACAAACCGAGGCTGCTGCATAAACAATTCCTGCCCAAGGACGCTGGCGGCCACTTC 2877  
Db 2821 CAGGCATACAAACCGAGGCTGCTGCATAAACAATTCCTGCCCAAGGACGCTGGCGGCCACTTC 2880  
Qy 2878 CTGCCCGGAGCGCGCGCAATGATGAACCTCTACTATCATGCTGTGAGTGTGGCTGTT 2937  
Db 2881 CTGCCCGGAGCGCGCGCAATGATGAACCTCTACTATCATGCTGTGAGTGTGGCTGTT 2940  
Qy 2938 ATGTTTGGCTCCATTGGCAACTTCTCTGAGTTCCTGAGTTCCTGAGGCTGGAGGCAACAATGAG 2997  
Db 2941 ATGTTTGGCTCCATTGGCAACTTCTCTGAGTTCCTGAGTTCCTGAGGCTGGAGGCAACAATGAG 3000  
Qy 2998 GGTGCCGAGTGCCTCGCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3057  
Db 3001 GGTGTCGAGTGCCTCGCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3060  
Qy 3058 GAGAGCGGTTCCGGCAGCTGGAAAAGATCAAGAGATTGGTAGCACCCTACATGCTGCC 3117  
Db 3061 GAGAGCGGTTCCGGCAGCTGGAAAAGATCAAGAGATTGGTAGCACCCTACATGCTGCC 3120  
Qy 3118 TCAGGCTGAACGCGCAGCACCTACGATCAGTGGGCGCTCCACATCAGTCCCTGGCT 3177  
Db 3121 TCAGGCTGAACGCGCAGCACCTACGATCAGTGGGCGCTCCACATCAGTCCCTGGCT 3180  
Qy 3178 GACTACGCCAATCGCGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3237  
Db 3181 GACTACGCCAATCGCGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAAT 3240  
Qy 3238 TTCCAGATGAAGATTGGCTGAACATGGCGCCAGTCTGGCAGGTGTCTATCGGGCTCGG 3297  
Db 3241 TTCCAGATGAAGATTGGCTGAACATGGCGCCAGTCTGGCAGGTGTCTATCGGGCTCGG 3300  
Qy 3298 AAGCACAGTATGACATCTGGGGAAACACAGTGAATGCTCTAGTCGTATGACAGCAGC 3357  
Db 3301 AAGCACAGTATGACATCTGGGGAAACACAGTGAATGCTCTAGTCGTATGACAGCAGC 3360  
Qy 3358 GGGTCCCGACCGAATCCAGGTGACCGACCGACCTGTACCAGTTCCTAGCTGCCAAGGC 3417  
Db 3361 GGGTCCCGACCGAATCCAGGTGACCGACCGACCTGTACCAGTTCCTAGCTGCCAAGGC 3420  
Qy 3418 TACAGCTGGAGTCTGAGGCGGTGCTCAAGGTGAAGGCAAGGGGAGATGACCACTTAC 3477  
Db 3421 TACAGCTGGAGTCTGAGGCGGTGCTCAAGGTGAAGGCAAGGGGAGATGACCACTTAC 3480  
Qy 3478 TTCCTCAATGGGGCCCCCAGCAGTTAAACAGGCCCCAGCCACAAATTCAGCTGAAGGGACC 3537  
Db 3481 TTCCTCAATGGGGCCCCCAGCAGTTAAACAGGCCCCAGCCACAAATTCAGCTGAAGGGACC 3540  
Qy 3538 AAGGTGGCACT 3549  
Db 3541 AAGGTGGCACT 3552

## RESULT 5

US-10-201-000-1

; Sequence 1, Application US/10201000

; GENERAL INFORMATION:

; APPLICANT: Tomlinson, James E.

; APPLICANT: COR Therapeutics, Inc.

; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYL

```
: TITLE OF INVENTION: CYCLASE
: FILE REFERENCE: 44481-5028-01-US
: CURRENT APPLICATION NUMBER: US/10/201.000
: CURRENT FILING DATE: 2002-07-24
: PRIOR APPLICATION NUMBER: US/09/474,076
: PRIOR FILING DATE: 1999-12-12
: PRIOR APPLICATION NUMBER: PCT/US98/13694
: PRIOR FILING DATE: 1998-07-01
: PRIOR APPLICATION NUMBER: 60/070,904
: PRIOR FILING DATE: 1997-07-01
: PRIOR APPLICATION NUMBER: 08/886,550
: PRIOR FILING DATE: 1997-07-01
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 4942
: TYPE: DNA
: ORGANISM: human type VI adenylyl cyclase
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (145)..(3648)
: US-10-201-000-1

Query Match      98.08; Score 3478.4; DB 42; Length 4942;
Best Local Similarity 98.94; Pred. No. 0;
Matches 3513; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

QY 1 ATGTCATGGTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGAAACAGCCTGGGGT 60
DB 145 ATGTCATGGTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGAAACAGCCTGGGGT 204

QY 61 GAACCAATGGGAGAGCGTTCCGGCGCGCTGGCACTCGGGCAGGTGCTTCTGCACG 120
DB 205 GAACCAATGGGAGAGCGTTCCGGCGCGCTGGCACTCGGGCAGGTGCTTCTGCACG 264

QY 121 CCCGCTATATAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCCCCCTGGGGCCCC 180
DB 265 CCCGCTATATAGCTGCCCTCCGGGATGCAGAGCCACCCAGCCCCCCTGGGGCCCC 324

QY 181 CCTCGGTGCCCTGGCAGGATGACGCCCTTATCCGGAGGGCGGCCAGGCAAGCAAG 240
DB 325 CCTCGGTGCCCTGGCAGGATGACGCCCTTATCCGGAGGGCGGCCAGGCAAGCAAG 384

QY 241 GAGTGGGGCTGGGGCAGTGGCCCTGGGCTTCAGAGATACCGAGGTGACAAACACAGCG 300
DB 385 GAGTGGGGCTGGGGCAGTGGCCCTGGGCTTCAGAGATACCGAGGTGACAAACACAGCG 444

QY 301 GCGGGAGCGCTGAGGTGGCGCGCAGCGGTGCCAGGAGTGGCGCATCTGCTGGCGC 360
DB 445 GCGGGAGCGCTGAGGTGGCGCGCAGCGGTGCCAGGAGTGGCGCATCTGCTGGCGC 504

QY 361 CGTTTGTGTCAGGTGTTCCAGTGAAGCAGTTCCTGTTTCGGCCAAAGCTGGAGCGCTGTAC 420
DB 505 CGTCTGTGTCAGGTGTTCCAGTGAAGCAGTTCCTGTTTCGGCCAAAGCTGGAGCACCTGTAC 564

QY 421 CAGCGGTACTTTTCCAGATGAACACAGAGAGCGCTGAGCTGCTGGTGGGGTGGTGGTG 480
DB 565 CAGCGGTACTTTTCCAGATGAACACAGAGAGCGCTGAGCTGCTGGTGGGGTGGTGGTG 624

QY 481 CTGCTCAGCGGTGCTGCTGGCTTTCACGCCACCCCGCCCTCAGCCTGCGCTAT 540
DB 625 CTGCTCAGCGGTGCTGCTGGCTTTCACGCCACCCCGCCCTCAGCCTGCGCTAT 684

QY 541 GTGCACTGTTGGCTGTGGCGCGCCCTGTTCTGTGGGGCTCATGGTGGTGTGTAACCGG 600
DB 685 GTGCACTGTTGGCTGTGGCGCGCCCTGTTCTGTGGGGCTCATGGTGGTGTGTAACCGG 744

QY 601 CATAGTCCGCCAGGACTCCATGTGGTGTGAGTAACTGAGTGTGGGATCCTGGCG 660
DB 745 CATAGTCCGCCAGGACTCCATGTGGTGTGAGTAACTGAGTGTGGGATCCTGGCG 804

QY 661 GCAGTGGAGTGGGGCTTTCGACAGACCCGCGAGCCCTCTGGGGCTCTGG 720
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DB 805 GCAGTGCAGGTGCGGGCGCTCTCGCAGCAGACCCGCGAGCCCCCTCTGGGGCCTCTGG 864
QY 721 TGGCCTGTGTTCTTTGTATATACATCGCATACAGCTCCTCCCATCCCATCCGCGCTGCC 780
DB 865 TGGCCTGTGTTCTTTGTATATACATCGCTCTACAGCTCCTCCCATCCCATCCGCGCTGCC 924
QY 781 GTCTCAGCGGCTTGGGCTCTCCACCTTGCATTTGATCTTGGCTGGCACTTAACCGT 840
DB 925 GTCTCAGCGGCTTGGGCTCTCCACCTTGCATTTGATCTTGGCTGGCACTTAACCGT 984
QY 841 GGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTCTTCTCTGACCAAC 900
DB 985 GGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTCTTCTCTGACCAAC 1044
QY 901 GTCAATTAGCATCTGCACACACTATCCAGCAGAGGTCTCAGCGCCAGGCTTTTCAGGAG 960
DB 1045 GTCAATTAGCATCTGCACACACTATCCAGCAGAGGTCTCAGCGCCAGGCTTTTCAGGAG 1104
QY 961 ACCGCGAGTTACATCCAGGCGCGCTCCACCTGCAGCATGAGAAATCGGAGCAGGAGCGG 1020
DB 1105 ACCGCGGTTTACATCCAGGCGCGCTCCACCTGCAGCATGAGAAATCGGAGCAGGAGCGG 1164
QY 1021 CTGCTGCTGTGGTATTGGCCAGCAGCTTGGCCATGGAGATGAAGAAGACATCAACACA 1080
DB 1165 CTGCTGCTGTGGTATTGGCCAGCAGCTTGGCCATGGAGATGAAGAAGACATCAACACA 1224
QY 1081 AAAAAAGAAC ---ATGTTCCACAAGATCTACATACAGAAAGCATGACATGTGCAGCATC 1137
DB 1225 AAAAAAGAACATGATGTTCCACAAGATCTACATACAGAAAGCATGACATGTGCAGCATC 1284
QY 1138 CTGTTTTCAGACATTTAGGGCTTTCACAGGCTGGCATCCAGTGCCATGCGCAGGAGCTG 1197
DB 1285 CTGTTTTCAGACATTTAGGGCTTTCACAGGCTGGCATCCCAAGTGCACCTGGCAGGAGCTG 1344
QY 1198 GTCAATGACCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAAATCACTGC 1257
DB 1345 GTCAATGACCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAAATCACTGC 1404
QY 1258 CTGAGGATCAAGATCTTTGGGGGACTGTTACTACTGTGTGTGTCAGGGCTGCCGAGGCCGG 1317
DB 1405 CTGAGGATCAAGATCTTTGGGGGACTGTTACTACTGTGTGTGTCAGGGCTGCCGAGGCCGG 1464
QY 1318 GCGGACCATGCCACTCCTGTGTGGAGATGGGGTACACATGATTGAGGCCATCTCCTGT 1377
DB 1465 GCGGACCATGCCACTCCTGTGTGGAGATGGGGTACACATGATTGAGGCCATCTCCTGT 1524
QY 1378 GTACGTGAGGTGACAGGTGTAATGTGAACATGCGCGTGGGCATCCACAGCGGCGCGTG 1437
DB 1525 GTACGTGAGGTGACAGGTGTAATGTGAACATGCGCGTGGGCATCCACAGCGGCGCGTG 1584
QY 1438 CACTGCGGCTCCTTGGCTTGGGAAATGGCAGTTCGATGTGGTCCAATGATGTGACC 1497
DB 1585 CACTGCGGCTCCTTGGCTTGGGAAATGGCAGTTCGATGTGGTCCAATGATGTGACC 1644
QY 1498 CTGCCCCAACCATGGAAGCAGGAAGCGGCTGCGCGCATCCACATCACTCGGGCAACA 1557
DB 1645 CTGCCCCAACCATGGAAGCAGGAAGCGGCTGCGCGCATCCACATCACTCGGGCAACA 1704
QY 1558 CTGCAGTACCTGAAACGGGGACTACGAAGTGAGCGCAGCGCTGGTGGCAAGCGCAAGCGG 1617
DB 1705 CTGCAGTACCTGAAACGGGGACTACGAAGTGAGCGCAGCGCTGGTGGCAAGCGCAAGCGG 1764
QY 1618 TACCTCAAGGAGCAGCAGATTTGAGACTTTCCTCATCTCTGGGCGCCAGCCAGAAACGAAA 1677
DB 1765 TACCTCAAGGAGCAGCAGATTTGAGACTTTCCTCATCTCTGGGCGCCAGCCAGAAACGAAA 1824
QY 1678 GAGGAGAAAGGCATGCTGGCCAAAGCTCGGGCCAACTCCATGGAAGGCTG 1737
DB 1825 GAGGAGAAAGGCATGCTGGCCAAAGCTCGGGCCAACTCCATGGAAGGCTG 1884
QY 1738 ATGCCGCGATGGGTTCCTGTGTCCTTCTCCCGGACCAAGGACTCAAGAGCCCTTCGCG 1797
DB 1885 ATGCCGCGATGGGTTCCTGTGTCCTTCTCCCGGACCAAGGACTCAAGAGCCCTTCGCG 1944
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QY 1798 CAGATGGCATGTGATGATTCCAGAAAGACACACCGGGGACCCCAAGATGCCCTGAACCCCT 1857  
DB 1945 CAGATGGCCATTGATGATTCAGCAAAACACAAACCGGGGACCCCAAGATGCCCTGAACCCCT 2004  
QY 1858 GAGGATGAGGTGAGTGTCTCTGAGCCGTCGCATCGATCGCCGAGCAGATTGATCAGCTG 1917  
DB 2005 GAGGATGAGGTGAGTGTCTCTGAGCCGTCGCATCGATCGCCGAGCAGATTGATCAGCTG 2064  
QY 1918 CGAAGGACCATGTGCGCGGTTTGTCTCACTTCCAGAGAGAGGATTTGAGAGAGAG 1977  
DB 2065 CGAAGGACCATGTGCGCGGTTTGTCTCACTTCCAGAGAGAGGATTTGAGAGAGAG 2124  
QY 1978 TACTCCCGAAGGTGGATCCCGGCTTCGAGAGCCTACGTTGGCTGTGCCCTGTGCTCTTC 2037  
DB 2125 TACTCCCGAAGGTGGATCCCGGCTTCGAGAGCCTACGTTGGCTGTGCCCTGTGCTCTTC 2184  
QY 2038 TGCCTCATCTGCTCATCCAGCTTCTAATTTTCCACACTCCAGCCTGATGCTTGGGATT 2097  
DB 2185 TGCCTCATCTGCTCATCCAGCTTCTAATTTTCCACACTCCAGCCTGATGCTTGGGATT 2244  
QY 2098 TATGCCAGCATCTTCTGCTGTCTAATACCGGTGCTGATCTGTGCTGTGCTTACTCTCTGT 2157  
DB 2245 TATGCCAGCATCTTCTGCTGTCTAATACCGGTGCTGATCTGTGCTGTGCTTACTCTCTGT 2304  
QY 2158 GGTTCCTCTGTTCCCTAAGGCCCTGCAACGCTGTGCCCGCAGCATTTGCTCGCTCACGGGCA 2217  
DB 2305 GGTTCCTCTGTTCCCTAAGGCCCTGCAACGCTGTGCCCGCAGCATTTGCTCGCTCACGGGCA 2364  
QY 2218 CATAGACCGGAGTTGGCATCTTTTCCGCTGCTGATCTGTGCTGTGCTTACTCTCTGT 2277  
DB 2365 CATAGACCGGAGTTGGCATCTTTTCCGCTGCTGATCTGTGCTGTGCTTACTCTCTGT 2424  
QY 2278 ATGTTCACTGTGAACACACACCCCATACGGAGCTGTGAGCCCGGATGCTGAATTTAACA 2337  
DB 2425 ATGTTCACTGTGAACACACACCCCATACGGAGCTGTGAGCCCGGATGCTGAATTTAACA 2484  
QY 2338 CTTGCTGACATCACTGCTGCCACCTGACGAGCTCAATTAATCTCTGCTGGGCTGGAGCT 2397  
DB 2485 CTTGCTGACATCACTGCTGCCACCTGACGAGCTCAATTAATTAATTAATTAATTAATTA 2544  
QY 2398 CCCCTGCTGAGGGACCATGCCACCTGCAGCTTTCCTGAGGTGCTCCATCGGGACATG 2457  
DB 2545 CCCCTGCTGAGGGACCATGCCACCTGCAGCTTTCCTGAGGTGCTCCATCGGGACATG 2604  
QY 2458 CTGCTGAGTCTTGGCCAGCTCTCTCTCTGTCACATCAGCAGCATCGGGAAGTTGGCC 2517  
DB 2605 CTGCTGAGTCTTGGCCAGCTCTCTCTCTGTCACATCAGCAGCATCGGGAAGTTGGCC 2664  
QY 2518 ATGATCTTTGCTTGGGCTCATCTATTTGCTGCTGCTGCTGGGTCGCCCGCCGCC 2577  
DB 2665 ATGATCTTTGCTTGGGCTCATCTATTTGCTGCTGCTGCTGGGTCGCCCGCCGCC 2724  
QY 2578 ATCTTTGACACTATGACTACTGCTTGGCTGCCATGCTTGGCTTCTTCCAAATGAGACC 2637  
DB 2725 ATCTTTGACACTATGACTACTGCTTGGCTGCCATGCTTGGCTTCTTCCAAATGAGACC 2784  
QY 2638 TTTGATGGCTGGACTTCCAGCTCAGGAGGGTGGCCCTCAAAATATATGACCCCTGTG 2697  
DB 2785 TTTGATGGCTGGACTTCCAGCTCAGGAGGGTGGCCCTCAAAATATATGACCCCTGTG 2844  
QY 2698 ATCTGCTGGTGTGCTGCTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2757  
DB 2845 ATCTGCTGGTGTGCTGCTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2904  
QY 2758 CGCCTAACTTCTCTGAAACTACAGGCAACAGGGGAAAAGAGAGAGATGAGAGCTA 2817  
DB 2905 CGCCTAGACTTCTCTGAAACTACAGGCAACAGGGGAAAAGAGAGATGAGAGCTA 2964  
QY 2818 CAGGCATACACCGGAGCTGCTGCTGATACATTTCTGCCCAAGAGCTGGCGCCCACTTC 2877  
DB 2965 CAGGCATACACCGGAGCTGCTGCTGATACATTTCTGCCCAAGAGCTGGCGCCCACTTC 3024

QY 2878 CTGGCCCGGAGCGCCGCAATCATGAATCTACTACTATCATCTAGTCTGCTGAGTGTGTGCTGTT 2937  
DB 3025 CTGGCCCGGAGCGCCGCAATCATGAATCTACTACTATCATCTGCTGAGTGTGTGCTGTT 3084  
QY 2938 ATGTTTGCTCTCATTTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAAATGAG 2997  
DB 3085 ATGTTTGCTCTCATTTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAAATGAG 3144  
QY 2998 GTGCGGAGTGTGCTGCGGCTGCTCAACGAGATCATCGCTGACTTTTGATGAGATTATCAGC 3057  
DB 3145 GTGCTGAGTGTGCTGCGGCTGCTCAACGAGATCATCGCTGACTTTTGATGAGATTATCAGC 3204  
QY 3058 GAGGAGCGGTTTCCGCGAGCTGGAAGATCAAGACGATTGTTAGCACCTTACATGCTGCC 3117  
DB 3205 GAGGAGCGGTTTCCGCGAGCTGGAAGATCAAGACGATTGTTAGCACCTTACATGCTGCC 3264  
QY 3118 TCAGGGCTGAAGCGGAGCAGCCTACGATCAGTGGGCGGCTCCACATCAGTGGCCCTGGCT 3177  
DB 3265 TCAGGGCTGAAGCGGAGCAGCCTACGATCAGTGGGCGGCTCCACATCAGTGGCCCTGGCT 3324  
QY 3178 GACTACGCGCATCGGCTCATGGAGCAGATGAAGCACATCAATGAGCAGCTCTCTCAACAT 3237  
DB 3325 GACTACGCGCATCGGCTCATGGAGCAGATGAAGCACATCAATGAGCAGCTCTCTCAACAT 3384  
QY 3238 TTCCAGATGAAGATTGGCTGAACATGGGCCAGTCGTGGCAGGTGTCATCGGGCTCGG 3297  
DB 3385 TTCCAGATGAAGATTGGCTGAACATGGGCCAGTCGTGGCAGGTGTCATCGGGCTCGG 3444  
QY 3298 AAGCCACAGTATGACATCTGGGGAAACACAGTGAATGCTCTAGTCTGATGACAGCAGC 3357  
DB 3445 AAGCCACAGTATGACATCTGGGGAAACACAGTGAATGCTCTAGTCTGATGACAGCAGC 3504  
QY 3358 GGGTCCCCGACCGCAATCCAGGTGACCGACCTGTACCAAGTTCTAGTCTGCCAAGGCG 3417  
DB 3505 GGGTCCCCGACCGCAATCCAGGTGACCGACCTGTACCAAGTTCTAGTCTGCCAAGGCG 3564  
QY 3418 TACCAGCTGGAGTGTGCGAGGGTGTCAAGGTGAAGGCAAGGGGAGAGTACCACCTAC 3477  
DB 3565 TACCAGCTGGAGTGTGCGAGGGTGTCAAGGTGAAGGCAAGGGGAGAGTACCACCTAC 3624  
QY 3478 TTCTCTCAATGGGGCCCCCAGCAGTTAACAGGGCCCCAGCCACAAATTCAGCTGAAGGACC 3537  
DB 3625 TTCTCTCAATGGGGCCCCCAGCAGTTAACAGGGCCCCAGCCACAAATTCAGCTGAAGGACC 3684  
QY 3538 AAGGTGGCACT 3549  
DB 3685 AAGGTGGCACT 3696

## RESULT 6

US-09-750-240-12

; Sequence 12, Application US/09750240

; GENERAL INFORMATION:

; APPLICANT: Hammon, H. K.

; APPLICANT: Insel, P. A.

; APPLICANT: Ping, P.

; APPLICANT: Post, S. R.

; APPLICANT: Gao, M.

; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART

; FILE REFERENCE: FAILURE

; CURRENT APPLICATION NUMBER: US/09750,240

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: US 09/472,667

; PRIOR FILING DATE: 1999-12-27

; PRIOR APPLICATION NUMBER: US 09/008,097

; PRIOR FILING DATE: 1998-01-16

; PRIOR APPLICATION NUMBER: US 08/924,757

; PRIOR FILING DATE: 1997-09-05

; PRIOR APPLICATION NUMBER: US 60/048,933

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: US 08/708,661

; PRIOR FILING DATE: 1996-09-05





[illegible]





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Db	842	GATGAAGAGACATCAACACAAAAAGAGACATGATTTCCACAGATCTACATACA	901
Qy	1116	GAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTCAGGGCTTCACAGCCTGGCATC	1175
Db	902	GAAGCATGACAATGTCAGCATCCTGTTTGCAGACATTCAGGGCTTCACAGCCTGGCATC	961
Qy	1176	CCAGTGCACTGCCAGAGACTGGTCATGACCCTGAATGAGCTCTTGCCTGGTTGACAA	1235
Db	962	CCAGTGCACTGCCAGAGACTGGTCATGACCCTGAATGAGCTCTTGCCTGGTTGACAA	1021
Qy	1236	GCTGGCTGCGGAGAACTACTGGCTGAGGATCAAGATCTTGGGGACATCTTACTACTGTG	1295
Db	1022	GCTGGCTGCGGAGAACTACTGGCTGAGGATCAAGATCTTGGGGACATCTTACTACTGTG	1081
Qy	1296	GTCAGGGCTGCCGAGAGCCCGGGCCGACCATGCCACATGCTGTGTGGAGATGGGGGTAGA	1355
Db	1082	GTCAGGGCTGCCGAGAGCCCGGGCCGACCATGCCACATGCTGTGTGGAGATGGGGGTAGA	1141
Qy	1356	CATGATTAGSCCATCTCCGCTGGTAGGTGACAGTGTGAATGTGAACATGCGCGT	1415
Db	1142	CATGATTAGSCCATCTCCGCTGGTAGGTGACAGTGTGAATGTGAACATGCGCGT	1201
Qy	1416	GGGCATCCACAGCGGGCGCTGCACATGCGGGCTCCTTGGCTTGGGAAATGGCAATTCGA	1475
Db	1202	GGGCATCCACAGCGGGCGCTGCACATGCGGGCTCCTTGGCTTGGGAAATGGCAATTCGA	1261
Qy	1476	TGTGTGTCCAATGATGTGACCTTGCCCAACCAACATGAAAGCAGGAAGCCGGGTGCGCG	1535
Db	1262	TGTGTGTCCAATGATGTGACCTTGCCCAACCAACATGAAAGCAGGAAGCCGGGTGCGCG	1321
Qy	1536	CATCCACATCACTCGGCAACACTGCAGTACCTGAACGGGACATACGAAGTGAGACCCAGG	1595
Db	1322	CATCCACATCACTCGGCAACACTGCAGTACCTGAACGGGACATACGAAGTGAGACCCAGG	1381
Qy	1596	CCGTGTGGCAAGCGAAGCGCTACCTCAAGGAGCAGACATTTGAGACTTTCCCTCATCCT	1655
Db	1382	CCGTGTGGCGAGCGAACCGCTACCTCAAGGAGCAGACATTTGAGACTTTCCCTCATCCT	1441
Qy	1656	GGGGCCAGCCAGAAAGAGAGAGAAAGGCAATGCTGGCCAAAGCTGCAGCGGATCG	1715
Db	1442	GGGGCCAGCCAGAAAGAGAGAGAAAGGCCATGCTGGCCAAAGCTGCAGCGGATCG	1501
Qy	1716	GGCCAACTCCATGAAGGCTGATGCGCGATGGGTTCTGATCGTGCCTTCTCCCGGAC	1775
Db	1502	GGCCAACTCCATGAAGGCTGATGCGCGCTGGGTTCTGATCGTGCCTTCTCCCGGAC	1561
Qy	1776	CAAGGACTCCAAGCGCTTCGGCCAGATGGGCATTGATGATTCACGAAAGACAACCGGG	1835
Db	1562	CAAGGACTCCAAGCGCTTCGGCCAGATGGGCATTGATGATTCACGAAAGACAACCGGG	1621
Qy	1836	CACCCAAGATGCCCTGAACCTTGAGATGAGTGGATGAGTTCCTGAGCGGTGCCATCGA	1895
Db	1622	CACCCAAGATGCCCTGAACCTTGAGATGAGTGGATGAGTTCCTGAGCGGTGCCATCGA	1681
Qy	1896	TGCCCCGAGCATTTGATCAGCTGGGAGAGCCATGTGGCGCGGTTTTTGTCACTTCCA	1955
Db	1682	TGCCCCGAGCATTTGATCAGCTGGGAGAGCCATGTGGCGCGGTTTTTGTCACTTCCA	1741
Qy	1956	GAGAGAGATTTTGAGAAAGTACTCCCGGAAGTGGATCCCGCTTCGGAGCCTACGT	2015
Db	1742	GAGAGAGATTTTGAGAAAGTACTCCCGGAAGTGGATCCCGCTTCGGAGCCTACGT	1801
Qy	2016	TGCGTGTGCCCTTGTGCTTCTGCTTCACTGCTTCACTCCAGCTTCTAAATTTTCCACA	2075
Db	1802	TGCGTGTGCCCTTGTGCTTCTGCTTCACTGCTTCACTCCAGCTTCTCACTTCCACA	1861
Qy	2076	CTCACCCCTGATGCTTGGGATTTATGCCAGCAATCTTCTGCTGCTGCTAATCACCGTGT	2135
Db	1862	CTCACCCCTGATGCTTGGGATTTATGCCAGCAATCTTCTGCTGCTGCTAATCACCGTGT	1921

Qy	2136	GATCTGTGCTGTACTCTCTCTGTGGTTCTCTGTTCCTCTAAGGCCCTGCAACGCTCTGTCCGG	2199
Db	1922	GATCTGTGCTGTACTCTCTGTGGTTCTCTGTTCCTCTAAGGCCCTGCAACGCTCTGTCCGG	1981
Qy	2196	CAGCATTTGCCGCTCAGCGGCACATAGCACGCGAGTTGGCATCTTTTCCGTCCTGCTTGT	2255
Db	1982	CAGCATTTGCCGCTCAGCGGCACATAGCACGCGAGTTGGCATCTTTTCCGTCCTGCTTGT	2041
Qy	2256	GTTTACTTCTGCCATTGCCAACAATGTTCACTCTTAACACACACCCCATACGAGAGCTGTGC	2315
Db	2042	GTTTACTTCTGCCATTGCCAACAATGTTCACTCTTAACACACACCCCATACGAGAGCTGTGC	2101
Qy	2316	AGCCCGGATGCTGAATTTAAACACTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAA	2375
Db	2102	AGCCCGGATGCTGAATTTAAACACTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAA	2161
Qy	2376	TTACTCTCTGGGCTGGATGCTCCCTCTGTGTGAGGCGACCATGCCACCTCAGACTTTCC	2435
Db	2162	TTACTCTCTGGGCTGGATGCTCCCTCTGTGTGAGGCGACCATGCCACCTCAGACTTTCC	2221
Qy	2436	TGAGGTGTCCATCGGGAACATGCTGCTGAGTCTCTTTGGCCAGCTCTGCTTCCTGCGACAT	2495
Db	2222	TGAGTACTTTCATCGGGAACATGCTGCTGAGTCTCTTTGGCCAGCTCTGCTTCCTGCGACAT	2281
Qy	2496	CAGCAGCATCGGGAAGTTGGCCATGATCTTTGCTCTTTGGGGCTCATCTAATTTGGTGTGCT	2555
Db	2282	CAGCAGCATCGGGAAGTTGGCCATGATCTTTGCTCTTTGGGGCTCATCTAATTTGGTGTGCT	2341
Qy	2556	TCTGCTGGTGTCCCCAGCGCCCATCTTTGACAACATAGACTTACTGCTTTGGCGTCCATGCG	2615
Db	2342	TCTGCTGGTGTCCCCAGCGCCCATCTTTGACAACATAGACTTACTGCTTTGGCGTCCATGCG	2401
Qy	2616	CTTGCGCTCTTCCAATAGAGACCTTTTGATGGGCTGGACTGTCCAGCTGCAGGAGGGTGGC	2675
Db	2402	CTTGCGCTCTTCCAATAGAGACCTTTTGATGGGCTGGACTGTCCAGCTGCAGGAGGGTGGC	2461
Qy	2676	CCTCAAAATATAGACCCCTGTGATTCGTCTGTGTGTTTGGCTTGGCGCTGTATCTGCATGCG	2735
Db	2462	CCTCAAAATATAGACCCCTGTGATTCGTCTGTGTGTTTGGCTTGGCGCTGTATCTGCATGCG	2521
Qy	2736	TCACGAGTGGATCGACTGCGCGCTAACTTCCTCTGGAAACTACAGGCAACACAGGGGA	2795
Db	2522	TCACGAGTGGATCGACTGCGCGCTAGACTTCTCTCTGGAAACTACAGGCAACACAGGGGA	2581
Qy	2796	AAAAGAGGATGGAGAGCTACAGGCATACAACCGAGGCTGCTGCATAACATCTTGCC	2855
Db	2582	GAAGGAGGATGGAGAGCTACAGGCATACAACCGAGGCTGCTGCATAACATCTTGCC	2641
Qy	2856	CAAGGAGCTGGCGGCCACTTCTTGCCCGGAGCGCGCGCAATGATGAACCTCTACTATCA	2915
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Qy	2916	GTCGTGTGAGTGTGTGGCTGTATGTTTGGCTTCCATTCGCAACTTCTCTGAGTTCTATGT	2975
Db	2702	GTCGTGTGAGTGTGTGGCTGTATGTTTGGCTTCCATTCGCAACTTCTCTGAGTTCTATGT	2761
Qy	2976	GGAGCTGGAGGCAACAATGAGGGTGCAGAGTCCCTGCGGCTGCTCAACGAGATCATCGC	3035
Db	2762	GGAGCTGGAGGCAACAATGAGGGTGCAGAGTCCCTGCGGCTGCTCAACGAGATCATCGC	2821
Qy	3036	TGACTTTTGATGA-----	3047
Db	2822	TGACTTTTGATGAGGTACTTTTCCAGTTGGCTGGTGGCGAGAGTGGGGGTACTTGG	2881
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Qy	3090	GACGATTTGAGCACCTACATGCTGCCTCAGGGCTGAACGCCAGCACCTACGATCAAGT	3149
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TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLVL  
TITLE OF INVENTION: CYCLASE AND USES THEREFOR  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/538,815  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: UTSD:450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4131 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-538-815-11

Query Match 77.5%; Score 2751.2; DB 9; Length 4131;  
Best Local Similarity 86.7%; Pred. No. 0;  
Matches 3080; Conservative 0; Mismatches 463; Indels 11; Gaps 4;

Qy 1 ATGTCATGTTAGTGGCTCCTGCTAAAGTGGATGAACGAAACAGCCCTGGGGT 60  
Db 56 ATGTCATGTTAGCGGCTCCTGGTCCCAAGTGGATGAACGAAACAGCCCTGGGG 115  
Qy 61 GAACGCAATGGCAGAACGCTTCGCGCGCTGSCACTCGGGCAGGTGCTTGCACG 120  
Db 116 GAACGCAATGGCAGAACGCTTCGCGCGCTGSCACTCGGGCAGGTGCTTGCACG 172  
Qy 121 CCCCGCTATATAGTGGCTCCGGATGCAGAGCCACCCAGCCACCCCTGCGGGCCC 180  
Db 173 CCCCGCTACATAGTGGCTCCAAAGTGTGGAGCCACCCAGCCACCCCTGCGAGCTCG 232  
Qy 181 CCTGGTCCCCCTGGCAGGATGAGCCCTTATCCGGAGGGCGCCAGGCAAGGGCAAG 240  
Db 233 ACTGGTGGCTGGCAGGATGAGCCCTTATCCAGAGGGCTGGCGGGAGGGGGTGTG 292  
Qy 241 CAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACACAGCG 300  
Db 293 GAGCTGGGGCTGCGGTGAGTGGCTTGGGTTTATGACACTGAGGTG---ACCACCG 349  
Qy 301 GCGGGAGCGGTGAGGTGGCGCCGACGCGGTGCCAGAGGTGGCGGATCTGCTGGCGC 360  
Db 350 ATGGGACAGCTGAAGTGGCACCAGACACATCGCTCGAAGCGGTCCCTGCTGGCGAC 409  
Qy 361 CGTTGGTGGCAGGTGTTCCAGTCGAGCAGTTCGTTTCGGCCAGCTGGAGCGCTGTAC 420  
Db 410 CGGTAGCGAGGTGTTCCAGTCTAAGCAGGTTCGCGTCCGCCAGCTGAGCGCTGTAC 469  
Qy 421 CAGCGGTACTTTTCCAGATGAACACAGCAGCCTGACGCTGCTGGTGGCGGTGCTGTG 480  
Db 470 CAGCGGTACTTCTCCAGATGAACACAGCAGCCTGACGCTGCTCATGGCGGTGCTGTG 529

Qy 481 CTGCTCACAGCGGTGCTGCTGGCTTTTCCAGCCGACCCGCCGCCCTCAGCCCTGCTAT 540  
Db 530 CTCCTCATGGCTGTACTGTTGACCTTCCACGCGCGCTGCCCTCAGCGCTGCTTAT 589  
Qy 541 GTGGCACTGTTGGCTGTGCGCGCGCGCTGTTCTGGGGCTCATGGTGTGTAAACGG 600  
Db 590 GTGGCCCTGCTGACCTGCTGCCCTCGCTCTTTTGGGTACTCATGGTGTGTAAACGA 649  
Qy 601 CATAGCTTCCGCCAGGACTCCATGTGGTGGTGAAGTAACTGGTGTCTGGGCTCGCG 660  
Db 650 CATAGCTTCCGCCAGGACTCCATGTGGTGGTGAAGTAACTGGTGTCTGGGCTCAT 709  
Qy 661 GCAGTGCAGGTGCGGGGCGCTTTCGAGCAGACCGCGCAGCCCTCTGCGGGCTCTGG 720  
Db 710 GCGCTGCAAGTGGGGGTGCGCTTGGCAGCAACCCAGCAGCCCTCAGCAGCGCTTGG 769  
Qy 721 TGCCTGTGTTCTTGTATACATGCATACAGCTCTCCGCCATCCGCATCGGCGCTGCC 780  
Db 770 TGCCTGTGTTCTTGTATACATGCATACAGCTCTCCGCCATTCGATCGGAGCGCC 829  
Qy 781 GTCCTCAGCGGCTTGGCTCTCCACCTTGCATTGTGCTTGGCTGGCACTTAAACGT 840  
Db 830 GTGCTCAGTGGCTGGCTTTCACCTGCTTGTGCTTGGCTGGCACTTCAACAAT 889  
Qy 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTCTCTCTGCACCAAC 900  
Db 890 GGTGACCCCTTCTTGGGAAGCAGCTCGGTGCTTAACTGCTGCTCTCTGTGCAACA 949  
Qy 901 GTCATTAGCATCTGCACACACTATCCAGCAGAGGTGCTCAGCGCCAGCGCTTTCAGAG 960  
Db 950 GCCATCGGTGCTGCAGCAGCTACCCCGCTGAAGTGTCTCAGCGCAAGCGCTTTCAGAG 1009  
Qy 961 ACCGCGAGTTACATCCAGCGCGCTCCACCTGCAGCATGAGAAATGCGCAGCAGGCGG 1020  
Db 1010 ACCGCTGTTACATCCAGCGCGCTGCACCTGCAGCATGAGAAATGCGCAGGAAACG 1069  
Qy 1021 CTGCTGCTGTCGGTATTCGCCCGCAGCAGCTTGCATGAGAGTGAAGAAGACATCAACA 1080  
Db 1070 CTGCTGCTGTCGGTGTTCGCCCGCAGCATGTTGCCATGGAATGAAGAAGATCAACA 1129  
Qy 1081 AAAAAAGAGAC---ATGTTCCACAAGATCTACATACAGAGCATGACAATGTCAAGCATC 1137  
Db 1130 AAAAAAGAGACATGATGTTCCACAAGATTTACATCCAGAAGCATGACAATGTCAAGCATC 1189  
Qy 1138 CTGTTTGCAGACATGAGGGCTTCCACGCTGGCATCCAGTGCACCTGCGCAGGAGCTG 1197  
Db 1190 CTGTTTGCAGACATGAGGGCTTCCACGAGCTGGCTCCAGTGCACCTGCGCAGGAACTG 1249  
Qy 1198 GTCATGACCTGATGAGCTCTTTGCCCGGTGTCAGAGTGGCTGCGGAGAACTACATGC 1257  
Db 1250 GTCATGACCTGATGAGCTCTTTGCCCGGTGTCAGAGTGGCTGCGGAGAACTACATGC 1309  
Qy 1258 CTGAGGATCAAGATCTTGGGGGACTGTTACTGTTGTCAGGGCTCCCGAGGCGCGG 1317  
Db 1310 CTGAGGATCAAGATCTTAGGAGACTGTTACTGTTGTCGGGGCTCCCGAGGCGCGG 1369  
Qy 1318 GCCGACCATGCCCCACTGCTGTGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG 1377  
Db 1370 GCAGACCATGCCACTGCTGTGGAGATGGGGGTAGACATGATGAGGCCATCTCGCTG 1429  
Qy 1378 GTAGCTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGAGTCCACAGCGGGCGCTG 1437  
Db 1430 GTGGCTGAGGTGAAGGGTGTAAATGTGAACATGCGCGTGGGATCCACAGCGGGCGTGA 1489  
Qy 1438 CACTGCGCGCTCTTGGCTTGGGAAATGGCAGTTCGATGTTGTTGTTCAATGATGTGACC 1497  
Db 1490 CACTGCGGTGCTTGGCTTGGGAAATGGCAGTTCGATGTTGTTGTTCAATGATGTGACC 1549  
Qy 1498 CTGCGCAACACATGGAAGCAGGAGCGGGCTGCCGCATCCACATCACTCGGCAACA 1557  
Db 1550 CTGCGCAACACATGGAAGCAGGAGCGGGCTGCCGCATCCACATCACTCGGCGCA 1609  
Qy 1558 CTGAGTACCTGAACGGGGACTACAGTGGAGCGAGCGGTGTTGGCAAGCGCAACGCG 1617

Db 1610 CTGACGATACCTGAAACGGGGACTATTGAGGTGAGACCGCCGTGGCGTGGAGCGCAACGGCG 1669  
Qy 1618 TACCTCAAGGAGCAGCAGCATTTGAGACTTTCTCATCTATCTGGCGCCAGCAGCAAGACGAAA 1677  
Db 1670 TACCTCAAGGAGCAGCAGCATTTGAGACTTTCTCATCTATCTAGGAGCCAGCAGCAAGACGAAA 1729  
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Db 1730 GAGGAGAAAGCATGCTGGTCAAGCTCAGCGGACGCGGCAACTCCATGGAAGGACTG 1789  
Qy 1738 ATGCCCGGATGGGTTCCTGATCTGCTGCTTCTCCCGGACCAAGGACTCCAGGCCCTTCGCG 1797  
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Qy 1798 CAGATGGGCACTGATGATTTCCAGCAAAAGACAAACCGGGGACCCCAAGATGCCCTGAACCCCT 1857  
Db 1850 CAGATGGGCACTGATGATTTCCAGCAAAAGACAAACCGGGGACCCCAAGATGCTCTGAACCCCT 1909  
Qy 1858 GAGGATGAGTGGATGATGCTGAGCCGTTGCCATGATGCCCGCAGCATTTGATCAGCTG 1917  
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Qy 1918 CGGAGGACCATGTCGCCCGGTTTTGCTCACCTTCAGAGAGAGATTTTGAGAAAG 1977  
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Qy 1978 TACTCCCGGAGGTGGATTCGCCCGTTCCGAGCCCTACGTTGCTGTCGCTGTCGCTGCTTC 2037  
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Qy 2038 TGCTTATCTGCTTCATCCAGCTTCTAATTTTCCACATCCACCCCTGATGCTTGGGATT 2097  
Db 2090 TGCTTATCTGCTTCATCCAGCTTCTGATTTCCACATCCACCCCTGATGCTTGGGATT 2149  
Qy 2098 TATCCAGCATCTTCTGCTGCTGCTTATCAGCGTGTGATGCTGCTGCTGCTGCTGCTGCTGCT 2157  
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Db 2450 CCGTCTGAGGAGCAGCATGCGCCACCTACGAGCTTTCCTGAGGTGCTGCTGAGGAGCATG 2509  
Qy 2458 CTGCTGAGTCTCTTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2517  
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Qy 2518 ATGATCTTTGCTTGGGCTCATATTTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2577  
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Qy 3238 TCCAGATGAAGATTTGGCTGAACTGGGCCAGCTGCTGCGCAGGTGCTGCTGCTGCTGCTGCT 3297  
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Db 3410 GGGTCCCGCAGCAGTCCAGGTGACCCAGCAGCTGTACAGGTCTTCTGCTGCTGCTGCTGCT 3469  
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Db 3470 TACAGCTGAGTGTGCGAGGGTGGTCAAGGTGAAGGCAAGGGGAGATGACACCTAC 3529  
Qy 3478 TTCTCAATGGGCGCCAGCAGTGAACAGGGGCGCA--GCCACAATTTAGCTGAAGGGA 3535  
Db 3530 TTCTCAATGGGCGCCAGCAGTGAACAGGGGCGCA--GCCACAATTTAGCTGAAGGGA 3589  
Qy 3536 CCAAGGTGGGCACT 3549  
Db 3590 CCAAGGTGGGCACT 3603

RESULT 11  
US-09-491-404-837  
; Sequence 837, Application US/09491404  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Yuanhua T.  
; APPLICANT: Tillinghast, John  
; APPLICANT: Sinku, Ankura  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: Novel Contigs Obtained



; TITLE OF INVENTION: From Various Libraries

; FILE REFERENCE: 785

; CURRENT APPLICATION NUMBER: US/09/491.404

; CURRENT FILING DATE: 2000-01-27

; NUMBER OF SEQ ID NOS: 3796

; SOFTWARE: pc\_sp\_genes version 1.0

; SEQ ID NO 837

; LENGTH: 5353

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: sig\_peptide

; LOCATION: (1669)...(1804)

; OTHER INFORMATION: this location contains the signal peptide sequence,

; OTHER INFORMATION: MLGIYASIFLLLLITVLICAVYSCGSLFPKALQRLSRIVSRRAH, Run with SignalP

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (3)...(2946)

; OTHER INFORMATION: similar to gi2887419 in the genepept database release 114,

; OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters

US-09-491-404-837

Query Match 75.98; Score 2693.8; DB 18; Length 5353;  
Best Local Similarity 93.18; Pred. No. 0;  
Matches 2935; Conservative 1; Mismatches 33; Indels 182; Gaps 4;

Qy 422 AGCGGTACTTTTCCAGATGAACAGAGCAGCCTGACGCTGCTGGTGGCGGTGCTGGTGC 481

Db 1 AGCGGTACTTCTCCAGATGAACAGAGCAGCCTGACGCTGCTGATGGCGGTGCTGGTGC 60

Qy 482 TGCTCACAGCGGTGCTGCTGGCTTTCCAAAGCCGACCCGCCCTCAGCCTGCCTATG 541

Db 61 TGCTCACAGCGGTGCTGCTGGCTTTCCACGCCGACCCGCCCTCAGCCTGCCTATG 120

Qy 542 TGGCACTTGGCTGTGCCCGCCCTGTTGCTGGGCTCATGGTGTGTAAACCGC 601

Db 121 TGGCACTTGGCTGTGCCCGCCCTGTTGCTGGGCTCATGGTGTGTAAACCGC 180

Qy 602 ATAGCTTCGGCAGGACTCCATGTGGGTGGTAACTGCTGCTGGGCATCCTTGGCGG 661

Db 181 ATAGCTTCGGCAGGACTCCATGTGGGTGGTAACTGCTGCTGGGCATCCTTGGCGG 240

Qy 662 CAGTGCAGGTGGGGCGCTTTCCGAGCAGACCCGCGAGCCCTCTCGGGGCTCTGGT 721

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Db 361 TCCTCAGCGGCTGGGCTCTCCACCTTGCACTTTGATCTTGGCTTGGCACTTAACCGTG 420

Qy 842 GTGATGCCCTTCCCT-TGGAAGCAGCTCGGTGCCAATGTGCTGTCTTCCCTTGCAACAC 900

Db 421 GTGATGCCCTTCCCTTTGGAGCAGCTCGGTSCCAATGTGCTGTCTTCCCTTGCAACAC 480

Qy 901 GTCATTAGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCGCCAGCCCTTTCAGAG 960

Db 481 GTCATTAGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCGCCAGCCCTTTCAGAG 540

Qy 961 ACCCGCAGTTACATCCAGCGCGGCTCCACCTTGCACTGAGCATGAGAACTGGCAGGAGCGG 1020

Db 541 ACCCGCGTTACATCCAGCGCGGCTCCACCTTGCACTGAGCATGAGAACTGGCAGGAGCGG 600

Qy 1021 CTGCTGCTGTGGTATTGCCCGCAGCAGCTTGCCATGGAGATGAAGAAGACATCAACACA 1080

Db 601 CTGCTGCTGTGGTATTGCCCGCAGCAGCTTGCCATGGAGATGAAGAAGACATCAACACA 660

Qy 1081 AAAAAAGAGAC---ATGTTCCAGAGATCTACATACAGAGCATGACAATGTACGATC 1137

Db 661 AAAAAAGAGACATGATGTTCACAAAGATCTACATACAGAGCATGACAATGTACGATC 720

Qy 1138 CTGTTTGCAGACATTGAGGCTTCCACAGCCTGGCATCCCACTGCACCTGCAGGAGCTG 1197

Db 721 CTGTTTGCAGACATTGAGGCTTCCACAGCCTGGCATCCCACTGCACCTGCAGGAGCTG 780

Qy 1198 GTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGGTGCGGAGAACTACATGC 1257

Db 781 GTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGGTGCGGAGAACTACATGC 840

Qy 1258 CTGAGGATCAAGATCTTGGGGAGCTGTACTACTGTGTGTCAGGGCTCCCGAGGCCCGG 1317

Db 841 CTGAGGATCAAGATCTTGGGGAGCTGTACTACTGTGTGTCAGGGCTCCCGAGGCCCGG 900

Qy 1318 GCCACCATGCCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTTCGCTG 1377

Db 901 GCCACCATGCCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTTCGCTG 960

Qy 1378 GTAGCTGAGGTGACAGGTGTGAATGTGAACATGGCGGTGGGATCCACAGCGGGGCGCTG 1437

Db 961 GTAGCTGAGGTGACAGGTGTGAATGTGAACATGGCGGTGGGATCCACAGCGGGGCGCTG 1020

Qy 1438 CACTGCGGCTCCTTGGCTTGGGAAATGCGAGTTCGATGTGTGTCCTCAATGATGTGACC 1497

Db 1021 CACTGCGGCTCCTTGGCTTGGGAAATGCGAGTTCGATGTGTGTCCTCAATGATGTGACC 1080

Qy 1498 CTGGCCAAACCATGGAAGAGAGCGGCTGGCCGCATCCACATCACTCGGGCAACA 1557

Db 1081 CTGGCCAAACCATGGAAGAGAGCGGCTGGCCGCATCCACATCACTCGGGCAACA 1140

Qy 1558 CTGCACTACCTGAACGGGACTACGAATGGAGCGAGCCGTGGTGGCAAGCGCAACCG 1617

Db 1141 CTGCACTACCTGAACGGGACTACGAATGGAGCGAGCCGTGGTGGCAAGCGCAACCG 1200

Qy 1618 TACCTCAAGAGAGCAGCATTTGAGACTTTCCTCATCTCTGGGCGCCAGCAGAAACGGAA 1677

Db 1201 TACCTCAAGAGAGCAGCATTTGAGACTTTCCTCATCTCTGGGCGCCAGCAGAAACGGAA 1260

Qy 1678 GAGGAGAAAGCATGCTGGCCAAAGCTGCAGCGGACTCGGGGCCAATCCATGAGAGGGCTG 1737

Db 1261 GAGGAGAAAGCATGCTGGCCAAAGCTGCAGCGGACTCGGGGCCAATCCATGAGAGGGCTG 1320

Qy 1738 ATGCGCGATGGGTCTCTGATGCTGCTCTCCGGAGCAAGGACTCCAAAGGCTTCCG 1797

Db 1321 ATGCGCGCTGGGTCTCTGATGCTGCTCTCCGGAGCAAGGACTCCAAAGGCTTCCG 1380

Qy 1798 CAGATGGCATTTGATGATTCCAGCAAGCAACACCGGGGCCACCAAGATGCCCTGAACCT 1857

Db 1381 CAGATGGCATTTGATGATTCCAGCAAGCAACACCGGGGCCACCAAGATGCCCTGAACCT 1440

Qy 1858 GAGGATGAGGTGGATGAGTTCTGAGCGGTGCCATTCGATGCCCGCAGCATTTGATCAGCTG 1917

Db 1441 GAGGATGAGGTGGATGAGTTCTGAGCGGTGCCATTCGATGCCCGCAGCATTTGATCAGCTG 1500

Qy 1918 CGAAGAGACATGTGCGCGGCTTTTGTCTACCTTCCAGAGAGGAGATTTCAGAGAGAG 1977

Db 1501 CGAAGAGACATGTGCGCGGCTTTTGTCTACCTTCCAGAGAGGAGATTTCAGAGAGAG 1560

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Db 1561 TACTCCGGAAGGTGGATCCCGGCTTCGAGAGCTACGTTGCTGTGCGCTGTGTCCTTC 1620

Qy 2038 TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCTGATGCTTGGGAT 2097

Db 1621 TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCTGATGCTTGGGATC 1680

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Qy 2158 GGTTCCTGTTCCCTTAAGCGCTGCAAGCTGTGTCGCCAGCATTTCCGCTCACGGCA 2217

Db 1741 GGTTCCTGTTCCCTTAAGCGCTGCAAGCTGTGTCGCCAGCATTTCCGCTCACGGCA 1800

Qy	2218	CATAGCACCCAGCTTGGCATCTTTTCCGTCCTGCTGTGTGTTTACTTCTGCGCATTTGCCAAC	2277
Db	1801	CATAGCACCCAGCTTGGCATCTTTTCCGTCCTGCTGTGTGTTTACTTCTGCGCATTTGCCAAC	1860
Qy	2278	ATGTTTCACTGTAAACACACCCCCCATACGGAGCTGTGCAGCCCGATCTGAAITTAACA	2337
Db	1861	ATGTATC-----	1866
Qy	2338	CCTGCTGACATCAGTGCCTGCCACCTGCAGCAGCTCAATTA	2397
Db	1867	-----	1866
Qy	2398	CCCTGTGTGAGGCGCACCATATGCCACCTGCAGCTTTC	2457
Db	1867	-----	1881
Qy	2458	CTGCTGAGTCTCTTTGGCCAGCTGCTCTTCCTGCACATCAGCAGCATCGGAGTTGGCC	2517
Db	1882	CTGCTGAGTCTCTTTGGCCAGCTGCTCTTCCTGCACATCAGCAGCATCGGAGTTGGCC	1941
Qy	2518	ATGATCTTTGCTTTGGGGCTCATCTATTTTGGTGTGCTTCTGCTGGTCCGCCACCGCC	2577
Db	1942	ATGATCTTTGCTTTGGGGCTCATCTATTTTGGTGTGCTTCTGCTGGTCCGCCACCGCC	2001
Qy	2578	ATCTTTGACAACATATGACCTACTGCTTGGCGTCCATGCTTGGCTTCTTCCAATGAGACC	2637
Db	2002	ATCTTTTGACAACATATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC	2061
Qy	2638	TTTGATGGCTGACACTGTCCAGCTGCAGGGAGGTTGGCCCTCAAAATATATGACCCCTGTG	2697
Db	2062	TTTGATGGCTGACACTGTCCAGCTGCAGGGAGGTTGGCCCTCAAAATATATGACCCCTGTG	2121
Qy	2698	ATTCTGCTGCTGTTTGGCTGGCGTGTATCTGCATGCTCAGCAGGTGGAAATCGACTGCC	2757
Db	2122	ATTCTGCTGCTGTTTGGCTGGCGTGTATCTGCATGCTCAGCAGGTGGAGTGCAGTGGCC	2181
Qy	2758	CGCTAAACTTCTCTGGAACTACAGGCAACAGGGGAAAAGAGAGATGGAGGAGCTA	2817
Db	2182	CGCTTAGACTTCTCTGGAACTACAGGCAACAGGGGAGAAGGAGAGATGGAGGAGCTA	2241
Qy	2818	CAGGCATACAAACCGAGGCTGCTGCATACATTCGCCCAGGAGACGTGGCGGCCCACTTC	2877
Db	2242	CAGGCATACAAACCGAGGCTGCTGCATACATTCGCCCAGGAGACGTGGCGGCCCACTTC	2301
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Db	2302	CTGGCCCGGAGCGCCGCAATGATGAACCTCTACTATCAGTCTGCTGAGTGTGTGGCTGTT	2361
Qy	2938	ATGTTTGCCTCCATTTGCCAACTTCTCTGAGTTCATATGTGAGCTGGAGGCAAAATGAG	2997
Db	2362	ATGTTTGCCTCCATTTGCCAACTTCTCTGAGTTCATATGTGAGCTGGAGGCAAAATGAG	2421
Qy	2998	GGTGCCGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATG	3046
Db	2422	GGTGCCGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGACTTTGATGAGTCTCCTTG	2481
Qy	3047	-----AGATTATCAGCGAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGG	3098
Db	2482	TGTTGTTACATTTATCAGCGAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGG	2541
Qy	3099	TAGCACTACATGGCTGCCTCAGGGCTGAACGCCAGCACCTACGATCAGGTGGGCGGCTC	3158
Db	2542	TAGCACTACATGGCTGCCTCAGGGCTGAACGCCAGCACCTACGATCAGGTGGGCGGCTC	2601
Qy	3159	CCACATCAGTGCCTTGCTGACTACGCCATGCGGGCTCATGGAGCAGATGAAGCAATCAA	3218
Db	2602	CCACATCAGTGCCTTGCTGACTACGCCATGCGGGCTCATGGAGCAGATGAAGCAATCAA	2661
Qy	3219	TGACACTCTCTCAACAAATTTCCAGATGAAGATTGGGCTGAACATGGGCCACGTCGTGGC	3278
Db	2662	TGACACTCTCTCAACAAATTTCCAGATGAAGATTGGGCTGAACATGGGCCACGTCGTGGC	2721
Qy	3279	AGGTGTCTATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGGAAACACAGTGAATGTCTC	3338

RESULT 12

US-09-922-279-837

: Sequence 837, Application US/09922279

: GENERAL INFORMATION:

; APPLICANT: Tang, Yuanhua T.

APPLICANT: Tillinghast, Joanna I.

APPLICANT: sinku Ankur

APPLICANT: Lijun Chenabua

APPLICANT: LIU, Chenghua

APPLICANT: Dermanac, Radoje T.  
TITLE OF INVENTION: Novel Centric Obtained

; TITLE OF INVENTION: Novel Contigs Obtained From Various Ribonuclease Inhibitors

FILE REFERENCE	TITLE OF INVENTION
708	

FILE REFERENCE: 785

;; CURRENT APPLICATION NUMBER: US/00-02

; CURRENT FILING DATE: 2001-08-03

;; PRIOR APPLICATION NUMBER: 09/

; PRIOR FILING DATE: 2001-01

; NUMBER OF SEQ ID NOS: 3796

; SOFTWARE: pt\_

; SEQ ID NO 837

; LENGTH: 5353

; TYPE: DNA

; ORGANISM:

; FEATURE:

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; NAME/KEY: sig_peptide
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; LOCATION: (1669)..(1804)
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; OTHER INFORMATION: this location contains the signal peptide sequence,

; OTHER INFORMATION: MLG

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; NAME/KEY: misc_feature
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; LOCATION: (3)...(2946)

OTHER INFORMATION: similar to gi2887419 in the genepept datab

OTHER INFORMATION

Query Match	75 q%.	Score	2693	8.	DB	34.	Length	5353.
-------------	--------	-------	------	----	----	-----	--------	-------

Query Match Best Local Similarity 93.18: Pred No 0: score 2693.8, 75.98;

Best Local Similarity 93.18; Pred. No. 0;  
Matches 2025; Conservative 1; Mismatches 33; Indels 182; Cans 4.

OV 422 AGCGGTACTTTTCCAGATGAACACAGAGCCTGACCGCTGCTGGTGGCGGTGCTGGTGC 481

[illegible]

QY 482 TGCTCACAGCGGTGCTGCTGGCTTTCAGCCGCCCGCCGCTATG 541

Db 61 TGC<sup>T</sup>CACAGCGTGCTGCTGGCT<sup>T</sup>TCCACGCCGACCCGCCCGCCCTATG 120

121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 111

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Db 241 CAGTCAGGTCGGGGCGCTTCGCGAGCAGACCCGCGCAGCCCTCTCGGSCCTCTCGT 300  
QY 722 GCCCTGTCTTTGTATACATCGCATACAGCTCTCCCATCCGCGATCGGGCTGCGG 781  
Db 301 GCCCTGTCTTTGTATACATCGCATACAGCTCTCCCATCCGCGATCGGGCTGCGG 360  
QY 782 TCCTCAGCGGCTGGGCTCTCCACCTTGTCATTTGCTGCTGGCCTGGCAACTTAACCGTG 841  
Db 361 TCCTCAGCGGCTGGGCTCTCCACCTTGTCATTTGCTGCTGGCCTGGCAACTTAACCGTG 420  
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Db 541 ACCCGCGGTTACATCCAGCGCGGCTCCACCTGCGAGCATGAGAATCGGCAGCAGAGCGG 600  
QY 1021 CTGCTGCTGTCGGTATGCCCCAGCAGCGTGGCCATGGAGATGAAAGAGACATCAACACA 1080  
Db 601 CTGCTGCTGTCGGTATGCCCCAGCAGCGTGGCCATGGAGATGAAAGAGACATCAACACA 660  
QY 1081 AAAAAAGAGAC- --ATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAAGATC 1137  
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QY 1138 CTGTTTTCAGACATTTGAGGGCTTACCAGCGCTGGCATCCAGTGCACTGCGCAGGAGCTG 1197  
Db 721 CTGTTTTCAGACATTTGAGGGCTTACCAGCGCTGGCATCCAGTGCACTGCGCAGGAGCTG 780  
QY 1198 GTCATGACCTGAATGAGTCTTTGCCCGGTTTGACAGCTGGCTGGCGAGAGATCACTGCG 1257  
Db 781 GTCATGACCTGAATGAGTCTTTGCCCGGTTTGACAGCTGGCTGGCGAGAGATCACTGCG 840  
QY 1258 CTGAGGATCAAGATCTGGGGGACCTTACTACTGTGTCAGGGCTGCCGAGGCGCGG 1317  
Db 841 CTGAGGATCAAGATCTGGGGGACCTTACTACTGTGTCAGGGCTGCCGAGGCGCGG 900  
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Db 901 GCCGACCATGCCACTGTGTGGAGATGGGGGTAGACATGATGAGGCCATCTCGCTG 960  
QY 1378 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCCGTGGGCATCCACAGCGGGCGGCTG 1437  
Db 961 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCCGTGGGCATCCACAGCGGGCGGCTG 1020  
QY 1438 CACTCGCGGCTCTTGGCTTGGGAAATGGCAATGTCGATGTGTGTCCTCAATCATGTGACC 1497  
Db 1021 CACTCGCGGCTCTTGGCTTGGGAAATGGCAATGTCGATGTGTGTCCTCAATCATGTGACC 1080  
QY 1498 CTGGCCAAACCATGGAAGCAGGAGCGGGCTGGCGCATCCACATCACTCGGGCAACA 1557  
Db 1081 CTGGCCAAACCATGGAAGCAGGAGCGGGCTGGCGCATCCACATCACTCGGGCAACA 1140  
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QY 1678 GAGGAAAGGACATGCTGGCCAAAGTGCAGCGGACTTCGGGCCAACTTCCATGGAAGGGCTG 1737  
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Db 1681 TATGCCAGCATCTTCTGCTGCTATATCACCCTGCTGATGCTGCTGCTGCTGCTGCTGCT 1740  
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Db 1882 CTGCTGAGTCTTTGGCCAGCTCTGCTCTTCCATGACATCAGCAGCATCGGGAAGTTGGCC 1941  
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QY 2638 TTTGATGGGCTGGACTGTCACCTGAGGGGTTGGGCTTCAAAATATATGACCCCTGCTG 2697  
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QY 2698 ATCTGCTGCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2757  
Db 2122 ATCTGCTGCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2181  
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Db 2182 CGCCTAGACTTCTCTGGAACATACAGGCAACAGGGGAAAAAGAGAGATGAGGAGCTA 2241  
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Db 2902 GGGGAGATGACCACTTACTTCTCAATGGGGGCCCGCAGCATTAACAGGGGCCAGGCCAC 2961
Qy 3519 AAATTGAGTCAAGGGACCAAGGTGGCACT 3549
Db 2962 AAATTGAGTCAAGGGACCAAGGTGGCACT 2992
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RESULT 13
US-09-922-279A-837
; Sequence 837, Application US/09922279A
; GENERAL INFORMATION:
; APPLICANT: Tang, Yuanhua T.
; APPLICANT: Tillinghast, John
; APPLICANT: Sinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 785
; CURRENT APPLICATION NUMBER: US/09/922,279A
; PRIOR FILING DATE: 2001-08-03
; PRIOR FILING DATE: 2000-01-25
; SOFTWARE: pt_sp_genes Version 1.0
; SEQ ID NO 837
; LENGTH: 5353
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1669)...(1804)
; OTHER INFORMATION: this location contains the signal peptide sequence,
; OTHER INFORMATION: MGIYASIFLLLLITVLICAVYSCGSLFPKALQLRSIRVSRHAH, Run with Signal
; NAME/KEY: misc_feature
; LOCATION: (3)...(2946)
; OTHER INFORMATION: similar to gi2887419 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
US-09-922-279A-837
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Query Match 75.9%; Score 2693.8; DB 34; Length 5353;
Best Local Similarity 93.1%; Pred. No. 0;
Matches 2935; Conservative 1; Mismatches 33; Indels 182; Gaps 4;
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Db 1 AGCGGTACTTTTCCAGATGAACCCAGAGCCTGAGCTGCTGCTGGCGGTGCTGGTGC 60
Qy 482 TGCTCACAGCGGTGCTGCTGGCTTTTCCAAAGCCGACCCGCCGCCCTCAGCCTGCCTATG 541
Db 61 TGCTCACAGCGGTGCTGCTGGCTTTTCCAGCGCCGACCCGCCGCCCTCAGCCTGCCTATG 120
Qy 542 TGGCACTGTTGGCTGTGGCGCCGCCCTGTTCGTGGGGCTCATGGTGTGTAAACCGGC 601
Db 121 TGGCACTGTTGGCTGTGGCGCCGCCCTGTTCGTGGGGCTCATGGTGTGTAAACCGGC 180
Qy 602 ATAGCTTCGCGCAGGACTTCCATGTGGTGTGTAGTAACTTGGCTGTGGCATCTCTGGCGG 661
Db 181 ATAGCTTCGCGCAGGACTTCCATGTGGTGTGTAGTAACTTGGCTGTGGCATCTCTGGCGG 240
Qy 662 CAGTGCAGGTGCGGGGCGCTTTCGACAGACCGCCGACGCCCTCTCGGGGCTCTGCTG 721
Db 241 CAGTGCAGGTGCGGGGCGCTTTCGACAGACCGCCGACGCCCTCTCGGGGCTCTGCTG 300
Qy 722 GCCCTGTGTTTGTATACATCCGCTACAGCTCTCTCCCATCCGATCGGAGCTGCGG 781
Db 301 GCCCTGTGTTTGTATACATCCGCTACAGCTCTCTCCCATCCGATCGGAGCTGCGG 360
Qy 782 TCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATTTGGCTTGGCACTTAAACCGTG 841
Db 361 TCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATTTGGCTTGGCACTTAAACCGTG 420
Qy 842 GTGATGCTTCTCTC-TGGAAGCAGCTCGGTGCCAATGTGCTGTCTTCTCTGACCAAC 900
Db 421 GTGATGCTTCTCTC-TGGAAGCAGCTCGGTGCCAATGTGCTGTCTTCTCTGACCAAC 480
Qy 901 GTCATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 960
Db 481 GTCATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 540
Qy 961 ACCGCGAGTTACATCCAGCGCCGCTCCACCTGCAGCATGAGAATCGGCAGCAGGAGCGG 1020
Db 541 ACCGCGAGTTACATCCAGCGCCGCTCCACCTGCAGCATGAGAATCGGCAGCAGGAGCGG 600
Qy 1021 CTGCTGCTGTGGTATTGCCCGAGCAGCTTGGCCATGGAGATGAAAGAAGACATCAACACA 1080
Db 601 CTGCTGCTGTGGTATTGCCCGAGCAGCTTGGCCATGGAGATGAAAGAAGACATCAACACA 660
Qy 1081 AAAAAAAGAAC---ATGTTCCACAAGATCTACATACAGAAGCATGACAATGTGAGCATC 1137
Db 661 AAAAAAAGAACATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTGAGCATC 720
Qy 1138 CTGTTTGCAGACATTGAGGGCTTCCAGCAGCTGCGATCCCACTGCCAGGAGGCTG 1197
Db 721 CTGTTTGCAGACATTGAGGGCTTCCAGCAGCTGCGATCCCACTGCCAGGAGGCTG 780
Qy 1198 GTCATGACCTGAAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGGGAGAATCACTGC 1257
Db 781 GTCATGACCTGAAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGGGAGAATCACTGC 840
Qy 1258 CTGAGGATCAAGATCTTGGGGGAGCTGTACTACTGTGTCTGAGGCTGCCGGAGGCCGG 1317
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Db 841 CTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTCTCAGGGCTGCCGGAGCCCGG 900  
QY 1318 GCCGACCATGCCACTGCTGTGTGAGATGGGGTAGACATGATTGAGGCCATCTCGCTG 1377  
Db 901 GCCGACCATGCCACTGCTGTGTGAGATGGGGTAGACATGATTGAGGCCATCTCGCTG 960  
QY 1378 GPACGTAGGTCACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGCGCGCTG 1437  
Db 961 GTACGTAGGTCACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGCGCGCTG 1020  
QY 1438 CACTCGCGGCTCTTGGCTTGGGAAATGGCAGTTGCGATGTGTGTCGAATGTGACC 1497  
Db 1021 CACTCGCGGCTCTTGGCTTGGGAAATGGCAGTTGCGATGTGTGTCGAATGTGACC 1080  
QY 1498 CTGGCAACACATGGAAGCAGGAGCGGGCTGGCCGATCCACATCACTCGGCAACA 1557  
Db 1081 CTGGCAACACATGGAAGCAGGAGCGGGCTGGCCGATCCACATCACTCGGCAACA 1140  
QY 1558 CTGCACTACCTGAACGGGGACTACGAAGTGGAGCGCGGTGGTGGCAAGCGCAACGCG 1617  
Db 1141 CTGCACTACCTGAACGGGGACTACGAAGTGGAGCGCGGTGGTGGCAAGCGCAACGCG 1200  
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QY 1678 GAGGAGAAAGGATGCTGGCCAACTGACGCGACTCGGGCCAACTCCATGGAAGGGCTG 1737  
Db 1261 GAGGAGAAAGGATGCTGGCCAACTGACGCGACTCGGGCCAACTCCATGGAAGGGCTG 1320  
QY 1738 ATGCCGCGATGGTTCCTGATGCTGCTTCCCGGACCAAGGACTCCAAAGGCTTCGCG 1797  
Db 1321 ATGCCGCGATGGTTCCTGATGCTGCTTCCCGGACCAAGGACTCCAAAGGCTTCGCG 1380  
QY 1798 CAGATGGCATGTGATGATTCAGCAAAAGACACCGGGCCAGCCAGATGCCCTGAACCT 1857  
Db 1381 CAGATGGCATGTGATGATTCAGCAAAAGACACCGGGCCAGCCAGATGCCCTGAACCT 1440  
QY 1858 GAGGATGAGGTGATGATGATTCAGCGCGTGCATCGATCGCCGAGGATGATGATGATG 1917  
Db 1441 GAGGATGAGGTGATGATGATTCAGCGCGTGCATCGATCGCCGAGGATGATGATGATG 1500  
QY 1918 CGGAAGGACCATGTGGCGGGTTTGTGCTACCTTCCAGAGAGAGATTTGAGAAGAG 1977  
Db 1501 CGGAAGGACCATGTGGCGGGTTTGTGCTACCTTCCAGAGAGAGATTTGAGAAGAG 1560  
QY 1978 TACTCCGGAAGTGTATCCCGCTTCGAGCGCTACGTTGCGCTGTCCTGCTCTC 2037  
Db 1561 TACTCCGGAAGTGTATCCCGCTTCGAGCGCTACGTTGCGCTGTCCTGCTCTC 1620  
QY 2038 TGCTTCATCTGCTCATCCAGCTTCTAATTTTCCACACTCCACCGCTGATGCTTGGGAT 2097  
Db 1621 TGCTTCATCTGCTCATCCAGCTTCTAATTTTCCACACTCCACCGCTGATGCTTGGGAT 1680  
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QY 2158 GGTTCCTGTTCCCTAAGGCCCTGCAACGCTGTGTCGCGAGCATGTCGCTTCACGGGA 2217  
Db 1741 GGTTCCTGTTCCCTAAGGCCCTGCAACGCTGTGTCGCGAGCATGTCGCTTCACGGGA 1800  
QY 2218 CATACACCGCATGTGGCATCTTTCCGCTCTGCTGTGTTTACTTCTGCCATTTGCCAAC 2277  
Db 1801 CATACACCGCATGTGGCATCTTTCCGCTCTGCTGTGTTTACTTCTGCCATTTGCCAAC 1860  
QY 2278 ATGTTCACTGTAAACACACCCCATACGGAGCTGTGACGCCGATGCTGAATTAACA 2337  
Db 1861 ATGTAC----- 1866  
QY 2338 CTGCTGACATCACTGCTGCCCTGCAACCTGACGAGCTCAATTTACTCTCTGGGCTGATGCT 2397  
Db 1867 ----- 1866

QY 2398 CCCCTGTGTGAGGGCACCATGCCACCTGCAGCTTTCCTGAGGTGTCCATCGGAACATG 2457  
Db 1867 -----TTTCATCGGACATG 1881  
QY 2458 CTGCTGAGTCTCTTGGCCAGCTCTCTCTTCCTGACATCAGCAGCATCGGAAGTTGGCC 2517  
Db 1882 CTGCTGAGTCTCTTGGCCAGCTCTCTCTTCCTGACATCAGCAGCATCGGAAGTTGGCC 1941  
QY 2518 ATGATCTTGTCTTGGGCTCATCTATTTGGTGTCTCTCTCTGCTGGTCCCGCCGCGC 2577  
Db 1942 ATGATCTTGTCTTGGGCTCATCTATTTGGTGTCTCTCTCTGCTGGTCCCGCCGCGC 2001  
QY 2578 ATCTTTGACAACTATGACCTACTGCTTGGCTGCCATGGCTTCTTCCAAATGAGACC 2637  
Db 2002 ATCTTTGACAACTATGACCTACTGCTTGGCTGCCATGGCTTCTTCCAAATGAGACC 2061  
QY 2638 TTTGATGGCTGGACTGTCAGCTGACGAGAGGGTGGCCCTCAAAATATATGACCCCTGTG 2697  
Db 2062 TTTGATGGCTGGACTGTCAGCTGACGAGAGGGTGGCCCTCAAAATATATGACCCCTGTG 2121  
QY 2698 ATCTGCTGGTGTGGCTGGCTGCTGATCTGCAATGCTCAGCAGGTGGAATCGACTGCC 2757  
Db 2122 ATCTGCTGGTGTGGCTGGCTGCTGATCTGCAATGCTCAGCAGGTGGAATCGACTGCC 2181  
QY 2758 CGCCTAAACTTCTCTGGAACACTACAGGCAACAGGGGAAAAAGAGAGAGAGAGCTA 2817  
Db 2182 CGCCTAGACTTCTCTGGAACACTACAGGCAACAGGGGAGAGAGAGAGAGCTA 2241  
QY 2818 CAGGATCAACCGGAGGCTGCTGATTAACATTCCTGCCCCAAGAGGTGGCGGCCACTTC 2877  
Db 2242 CAGGATCAACCGGAGGCTGCTGATTAACATTCCTGCCCCAAGAGGTGGCGGCCACTTC 2301  
QY 2878 CTGGCCCGGAGCGCGCAATGATGAATCTACTATCAGTCTGTGAGTGTGCTGTGTT 2937  
Db 2302 CTGGCCCGGAGCGCGCAATGATGAATCTACTATCAGTCTGTGAGTGTGCTGTGTT 2361  
QY 2938 ATGTTTGGCTTCCATTCGCAACTTCTCTGAGTTCTATGTGAGCTGGAGGCAACATGAG 2997  
Db 2362 ATGTTTGGCTTCCATTCGCAACTTCTCTGAGTTCTATGTGAGCTGGAGGCAACATGAG 2421  
QY 2998 GGTGCGGAGTGGCTGGGCTGCTCAACGAGATCATCGTACTGCTTTGATGAGTCTCCTTG 3046  
Db 2422 GGTGCGGAGTGGCTGGGCTGCTCAACGAGATCATCGTACTGCTTTGATGAGTCTCCTTG 2481  
QY 3047 -----AGATTATCAGCAGGAGCGGTTCCGCGAGCTGGAAAGATCAACAGCATTCG 3098  
Db 2482 TGTGTTTTCAGATTATCAGCGAGGAGCGGTTCCGCGAGCTGGAAAGATCAACAGCATTCG 2541  
QY 3099 TAGCACCTACATGGCTGCTCAGGGCTGAACGCCAGCAGCTACGATCAGGTGGCGGCTC 3158  
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QY 3159 CCACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3218  
Db 2602 CCACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2661  
QY 3219 TGAGCAGCTCTTCAACAATTTCCAGATGAAGATTTGGGCTGGAACATGGGGCCAGTCTGTCG 3278  
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QY 3279 AGGTGTATCGGGGTTCGGAAGCCACAGTATGACATCTTGGGGGAAACACAGTGAATGTCTC 3338  
Db 2722 AGGTGTATCGGGGTTCGGAAGCCACAGTATGACATCTTGGGGGAAACACAGTGAATGTCTC 2781  
QY 3339 TACTGTATGAGACAGCAGCGGGGTCCCCACCGAATCCAGGTGACCCAGGACCTGTACCA 3398  
Db 2782 TACTGTATGAGACAGCAGCGGGGTCCCCACCGAATCCAGGTGACCCAGGACCTGTACCA 2841  
QY 3399 GGTTCCTAGCTGCCAAGGGCTACAGCTGAGTGTGTCGAGGGTGGTCAAGGTGAAGGGCAA 3458  
Db 2842 GGTTCCTAGCTGCCAAGGGCTACAGCTGAGTGTGTCGAGGGTGGTCAAGGTGAAGGGCAA 2901

QY 3459 GGGGAGATGACCACTTCTCTCAATGGGGCCCGACAGTTTAAACAGGGCCCGACGCCAC 3518  
Db 2902 GGGGAGATGACCACTTCTCTCAATGGGGCCCGACAGTTTAAACAGGGCCCGACGCCAC 2961  
QY 3519 AAATTCAGCTGAAGGACCAAGGTGGCACT 3549  
Db 2962 AAATTCAGCTGAAGGACCAAGGTGGCACT 2992

RESULT 14  
US-09-472-667-3  
: Sequence 3, Application US/09472667  
: GENERAL INFORMATION:  
: APPLICANT: Hammond, H. Kirk  
: APPLICANT: Insel, Paul A.  
: APPLICANT: Ping, Peipei  
: APPLICANT: Post, Steven R.  
: APPLICANT: Gao, Meihua  
: TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
: FILE REFERENCE: 22002056722  
: CURRENT APPLICATION NUMBER: US/09/472,667  
: CURRENT FILING DATE: 1999-12-27  
: PRIOR APPLICATION NUMBER: PCT/US99/02702  
: PRIOR FILING DATE: 1999-02-09  
: PRIOR APPLICATION NUMBER: US 09/008,097  
: PRIOR FILING DATE: 1998-01-16  
: PRIOR APPLICATION NUMBER: US 09/021,773  
: PRIOR FILING DATE: 1998-02-11  
: PRIOR APPLICATION NUMBER: US 08/924,757  
: PRIOR FILING DATE: 1997-09-05  
: PRIOR APPLICATION NUMBER: PCT/US97/15610  
: PRIOR FILING DATE: 1997-09-05  
: PRIOR APPLICATION NUMBER: US 08/708,661  
: PRIOR FILING DATE: 1996-09-05  
: PRIOR APPLICATION NUMBER: US 60/048,933  
: PRIOR FILING DATE: 1997-06-16  
: PRIOR APPLICATION NUMBER: 60/058,209  
: PRIOR FILING DATE: 1996-09-05  
: PRIOR APPLICATION NUMBER: PCT/US96/02631  
: PRIOR FILING DATE: 1996-02-27  
: PRIOR APPLICATION NUMBER: US 08/396,207  
: PRIOR FILING DATE: 1995-02-28  
: PRIOR APPLICATION NUMBER: US 08/485,472  
: PRIOR FILING DATE: 1995-06-07  
: NUMBER OF SEQ ID NOS: 11  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 3  
: LENGTH: 1812  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
US-09-472-667-3

Query Match 51.0%; Score 1808.4; DB 18; Length 1812;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 636 TAACCTGGTGTGGGCATCTCGGCGCAGTGCAGTCCGGGGCGCTTTTCGCAGCAGACCC 695  
Db 3 TAACCTGGTGTGGGCATCTCGGCGCAGTGCAGTCCGGGGCGCTTTTCGCAGCAGACCC 62  
QY 696 GCGCAGCCCTCTCGGGGCGCTCTGGTGCCTGTGTTCTTTGTATACATCGCATACAGCT 755  
Db 63 GCGCAGCCCTCTCGGGCGCTCTGGTGCCTGTGTTCTTTGTATACATCGCATACAGCT 122  
QY 756 CCTCCCCATCGCATCGGGGCTGCGCTTCCTCAGCGGGCTGGGCTCTCCACCTTGCATTT 815  
Db 123 CCTCCCCATCGCATCGGGGCTGCGCTTCCTCAGCGGGCTGGGCTCTCCACCTTGCATTT 182  
QY 816 GATCTTGGCTTGGCAACTTAACCTGTGTGATGCTTCTCTGGAAGCAGCTCGGTGCGAA 875  
Db 183 GATCTTGGCTTGGCAACTTAACCTGTGTGATGCTTCTCTGGAAGCAGCTCGGTGCGAA 242

QY 876 TGTGCTCTGTCTCTGTCACCAACGCTATTAGCATCTGCACACACTATATCCAGCAGAGT 935  
Db 243 TGTGCTCTGTCTCTGTCACCAACGCTATTAGCATCTGCACACACTATATCCAGCAGAGT 302  
QY 936 GTCTCAGCGCCAGCCCTTTTCAGGAGACCCGAGTTACATCCAGGCCGGCTTCACCTGCA 995  
Db 303 GTCTCAGCGCCAGCCCTTTTCAGGAGACCCGAGTTACATCCAGGCCGGCTTCACCTGCA 362  
QY 996 GCATGAGAATCGCAGCAGGCGGCTGCTGCTGCGGTATTCGCCAGCAGCTTGGCAT 1055  
Db 363 GCATGAGAATCGCAGCAGGCGGCTGCTGCTGCGGTATTCGCCAGCAGCTTGGCAT 422  
QY 1056 GGAGATGAAAGAGACATCAACACAAAAGAGAGACATGTTCCACAAAGATCTACATACA 1115  
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QY 1116 GAAGCATGACAATGTGAGCATCTGTTTTCAGAGACATTTGAGGGCTTCACGACCTGGCATC 1175  
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QY 1176 CCAGTGCACCTGCCAGGAGCTGGTTCATGACCTGAATGAGCTCTTCCCGGGTTTGACA 1235  
Db 543 CCAGTGCACCTGCCAGGAGCTGGTTCATGACCTGAATGAGCTCTTCCCGGGTTTGACA 602  
QY 1236 GCTGGCTGCGGAGAAATCACTGCTGAGGATCAAGATCTTGGGGACTGTTACTACTGT 1295  
Db 603 GCTGGCTGCGGAGAAATCACTGCTGAGGATCAAGATCTTGGGGACTGTTACTACTGT 662  
QY 1296 GTCAGGGCTGCCGAGGCCCGGGCCGACCATGCCACTGCTGTGTGGAGATGGGGGTAGA 1355  
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QY 1356 CATGATTGAGGCCATCTCGCTGGTGTGAGGTGACAGGTGCTGAATGTGAACATGCGCGT 1415  
Db 723 CATGATTGAGGCCATCTCGCTGGTGTGAGGTGACAGGTGCTGAATGTGAACATGCGCGT 782  
QY 1416 GGGCATCCAGCGGGCGCGTGCACCTGCGGCGCTCTTGGCTTGGGAAATGGCAGTTGCA 1475  
Db 783 GGGCATCCAGCGGGCGCGTGCACCTGCGGCGCTCTTGGCTTGGGAAATGGCAGTTGCA 842  
QY 1476 TGTGTGTGTCGAATGATGTGACCTTGGCCAAACCATGGAAGAGAGAGCCGGCTGGCCG 1535  
Db 843 TGTGTGTGTCGAATGATGTGACCTTGGCCAAACCATGGAAGAGAGAGCCGGCTGGCCG 902  
QY 1536 CATCCACATCACTCGGCAACACTGCACTGAGTACCTGAACGGGGACTTACGAAGTGGAGCCAG 1595  
Db 903 CATCCACATCACTCGGCAACACTGCACTGAGTACCTGAACGGGGACTTACGAAGTGGAGCCAG 962  
QY 1596 CCGTGTGGCAAGCGCAACCGCTACCTCAAGGAGCAGCACAATTGAGACTTTCTCATCCT 1655  
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QY 1656 GGGCGCCAGCAGAAACGGAAGAGAGAAAGCATGCTGGCCAAAGCTGCAGCGGACTCG 1715  
Db 1023 GGGCGCCAGCAGAAACGGAAGAGAGAAAGCATGCTGGCCAAAGCTGCAGCGGACTCG 1082  
QY 1716 GGGCAACTCCATGGAAGGCTGATGCGCGATGGTTCCTGATGCTGCTTCTCCCGGAC 1775  
Db 1083 GGGCAACTCCATGGAAGGCTGATGCGCGATGGTTCCTGATGCTGCTTCTCCCGGAC 1142  
QY 1776 CAAGGACTCCAAAGCCCTTCGCGCAGATGGGCAATTGATGATTCAGCAAAAGAACCCGGG 1835  
Db 1143 CAAGGACTCCAAAGCCCTTCGCGCAGATGGGCAATTGATGATTCAGCAAAAGAACCCGGG 1202  
QY 1836 CACCCAGATGCTGCAACCTTGAGGATGAGGTGAGTCTCTGAGCGCTGCCATCGA 1895  
Db 1203 CACCCAGATGCTGCAACCTTGAGGATGAGGTGAGTCTCTGAGCGCTGCCATCGA 1262  
QY 1896 TGCCCGCAGCATTTGATCAGCTGCGGAAGGACCATGTGCGCGGTTTGTCTCACTTTCCA 1955  
Db 1263 TGCCCGCAGCATTTGATCAGCTGCGGAAGGACCATGTGCGCGGTTTGTCTCACTTTCCA 1322  
QY 1956 GAGAGAGGATTTTGAAGAAGTACTCCCGGAAGGTGGATCCCGCGCTTCGGAGCCTACGT 2015





Db	1083	GGCCAAC	TCCATGGAAGGCGCTGATGCGCGGATGGGTTCCTGATCGTGCCTTCTCCCGGAC	11142
Qy	1776	CAAGGACTCA	AAGGCGCTTCCGCGAGATGGCATTTGATGATTTCCAGCAAAAGACAACCGGG	1835
Db	1143	CAAGGACTCA	AAGGCGCTTCCGCGAGATGGCATTTGATGATTTCCAGCAAAAGACAACCGGG	1202
Qy	1836	CACCAAGATGCC	CTGAACCCCTGAGGATGAGGTGATGAGTTCCTGAGCGGTGCCATCGA	1895
Db	1203	CACCAAGATGCC	CTGAACCCCTGAGGATGAGGTGATGAGTTCCTGAGCGGTGCCATCGA	1262
Qy	1896	TGCCCGCAGCA	TGTAGCTCGGAAGACCATGTGCGCGGTTTTTGTCTACCTTTCCA	1955
Db	1263	TGCCCGCAGCA	TGTAGCTCGGAAGACCATGTGCGCGGTTTTTGTCTACCTTTCCA	1322
Qy	1956	GAGAGGAGATTT	GAGAAAGTACTCCCGNAGGTGATCCCGGCTTCGGAGGCTACGT	2015
Db	1323	GAGAGGAGATTT	GAGAAAGTACTCCCGNAGGTGATCCCGGCTTCGGAGGCTACGT	1382
Qy	2016	TGCTGTGCCCT	TGTTGGTCTTCTGCTTTCATCTGCTTCATCCAGGTTCTTAATTTTCCCACA	2075
Db	1383	TGCTGTGCCCT	TGTTGGTCTTCTGCTTTCATCTGCTTCATCCAGGTTCTTAATTTTCCCACA	1442
Qy	2076	CTCCACCCGTAG	CTTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTAATCACCCTGCT	2135
Db	1443	CTCCACCCGTAG	CTTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTAATCACCCTGCT	1502
Qy	2136	GATCTGTGCTGT	GTACTCCTGTGGTTCTCTGTTCCTAAGGCCCTCGAAAGTCTGTGCCG	2195
Db	1503	GATCTGTGCTGT	GTACTCCTGTGGTTCTCTGTTCCTAAGGCCCTCGAAAGTCTGTGCCG	1562
Qy	2196	CAGCATTTGCCG	TCTACGGGACATAGCACCGCAGTTGGGATCTTTTCCGCTCGCTGTGT	2255
Db	1563	CAGCATTTGCCG	TCTACGGGACATAGCACCGCAGTTGGGATCTTTTCCGCTCGCTGTGT	1622
Qy	2256	GTTTACTTCTG	CATGCCAACATGTTCACTGTAAACACACCCCCATACGGAGCTGTGC	2315
Db	1623	GTTTACTTCTG	CATGCCAACATGTTCACTGTAAACACACCCCCATACGGAGCTGTGC	1682
Qy	2316	AGCCCGGATGCT	GTGAATTTAAACACTGCTGACATCACTGCTTGGCACTTTTCCGCTCGCTGTGT	2375
Db	1683	AGCCCGGATGCT	GTGAATTTAAACACTGCTGACATCACTGCTTGGCACTTTTCCGCTCGCTGTGT	1742
Qy	2376	TTACTCTCTG	GGGCTGGATGCTCCCTGTGTGAGGGCACCATGCCACCTTGCAGCTTTTC	2435
Db	1743	TTACTCTCTG	GGGCTGGATGCTCCCTGTGTGAGGGCACCATGCCACCTTGCAGCTTTTC	1802
Qy	2436	TGAGGTGTCC	2445	
Db	1803	TGAGGTGTTC	1812	

Search completed: February 23, 2003, 07:32:26  
Job time : 7037.57 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 22:29:24 ; Search time 604.737 Seconds  
(without alignments)  
9128.329 Million cell updates/sec

Title: US-09-750-240-5  
Perfect score: 3549  
Sequence: 1 atgtcatggttttagtgccct.....aaggaccagggtgggcact 3549

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2850587 seqs, 777717511 residues

Total number of hits satisfying chosen parameters: 5701174

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2799.2	78.9	5826	6	US-10-144-771-5921
2	1591.4	44.8	4349	6	US-10-144-771-19529
3	1060.2	29.9	1386	1	PCT-US02-36759-83
4	505.2	14.2	3518	6	US-10-121-911A-2
5	473.4	13.3	6196	1	PCT-US02-34621-1
6	473.4	13.3	6196	6	US-10-282-942-1
7	459	12.9	4008	7	US-60-436-643-3039
8	452.4	12.7	2731	6	US-10-305-720-1344
9	432.4	12.2	5124	6	US-10-144-771-18424
10	428	12.1	3357	6	US-10-338-044-2053
11	425.2	12.0	4633	6	US-10-144-771-16338
12	410.8	11.6	3458	6	US-10-144-771-3825
13	397.4	11.2	3820	6	US-10-144-771-855
14	362.8	10.2	3756	6	US-09-724-676-11592
15	362.8	10.2	3756	6	US-09-724-676A-11592
16	346	9.7	2253	6	US-10-144-771-16113
17	339	9.6	2949	5	US-09-724-676-11593
18	339	9.6	2949	5	US-09-724-676A-11593
19	338.2	9.5	4079	6	US-10-305-720-1412
20	338.2	9.5	5370	5	US-09-724-676-11576
21	338.2	9.5	5370	5	US-09-724-676A-11576
22	338.2	9.5	5680	5	US-09-724-676-11577
23	338.2	9.5	5680	5	US-09-724-676A-11577
24	320.6	9.0	3158	6	US-10-144-771-14946
25	308.6	8.7	1661	6	US-10-144-771-15361
26	284.4	8.0	1180	6	US-10-277-802-11
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					Sequence 19529, A
					Sequence 83, Appl
					Sequence 2, Appl
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					Sequence 1, Appl
					Sequence 3039, Ap
					Sequence 1344, Ap
					Sequence 18424, A
					Sequence 2053, Ap
					Sequence 16338, A
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					Sequence 855, App
					Sequence 11592, A
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					Sequence 14946, A
					Sequence 15361, A
					Sequence 11, Appl

RESULT 1  
US-10-144-771-5921  
; Sequence 5921, Application US/10144771  
; GENERAL INFORMATION:  
; APPLICANT: VENTNER, J. Craig  
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF  
; FILE REFERENCE: CLO01321  
; CURRENT APPLICATION NUMBER: US/10/144.771  
; CURRENT FILING DATE: 2002-05-15  
; NUMBER OF SEQ ID NOS: 47235  
; SEQ ID NO 5921  
; LENGTH: 5826  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-144-771-5921

Query Match 78.9%; Score 2799.2; DB 6; Length 5826;  
Best Local Similarity 87.5%; Pred. No. 0;  
Matches 3110; Conservative 0; Mismatches 433; Indels 11; Gaps 4;

Qy	1	ATGTCATGTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAACACAGCTGGGGT	60
Db	96	ATGTCATGTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAACACAGCTGGGGG	155
Qy	61	GAACGCAATGGGACAGACGGTTTCGGCGCGCGTGGCACTCGGGCAGGTGCTTCTGCAG	120
Db	156	GAACGCAATGGGACAGACGG---CCACGCCACGCGAATCGAGCCAGTGGCTTCTGC	212
Qy	121	CCCCCTATATGAGTGGCTCGGGATGCAGAGCCACCCGCCACCCCTCGCGGGCCCC	180
Db	213	CCTCCTACATGAGTGGCTCAAGATGGGAGCCACCCGCCACCCCTCTGCAGCTCAC	272
Qy	181	CCTCGGTCCCTTGGCAGGATGACCCCTTCATCCGGAGGGCGGCCAGGCAAGGCAAG	240
Db	273	ACTCGGTCCCTTGGCAGGATGACCCCTTCATCAGAGGGCGGGCGCGGAGGGGTGTG	332
Qy	241	GAGCTGGGGTGGCGGCGAGTGGCCCTTGGGCTTCGAGGATACCGAGGTGACACACAGG	300
Db	333	GAGCTGGGGTGGCGGCGAGTGGCCCTTGGGCTTTCAGACACTGAGGTGACACACAGG	392
Qy	301	GGCGGAGCGGTGAGTGGCGCGCGCGGTGGCCAGGAGTGGCGGATCTCTGCTGGCGC	360
Db	393	GGC---ACAGCTGAAGTGGCACCGGATACATCGCTCGAGAGCGGTCCCTGCTGGCAC	449
Qy	361	CGTTTGGTGCAGTGTTCAGTCAAGAGTTCCTCGTTCGGCCAAAGTGGAGCGCTGTAC	420
Db	450	CGCTTGTGCAGTGTTCAGTCAAGAGTTCCTCGTTCGGCCAAAGTGGAGCGGTGTAC	509
Qy	421	CAGCGGTACTTTTCCAGATGAACACGAGACGCTGACGCTGCTGCTGGCGGTGCTGGTG	480

Sequence 588, App  
Sequence 11582, A  
Sequence 11582, A  
Sequence 11583, A  
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Sequence 11586, A  
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Sequence 11587, A  
Sequence 11587, A  
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Sequence 11581, A  
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Sequence 23772, A  
Sequence 11594, A  
Sequence 11594, A  
Sequence 11595, A  
Sequence 11595, A  
Sequence 11584, A

Db 510 CACGGTACTTCTCCAGATGAACACAGGAGCCTCAGCTGCTCATGGCGGTGCTGGTG 569  
Qy 481 CTGCTCAGCGGTGCTGGGCTTTCCAAAGCGCCACCCCGCCCTCAGCCTGCGCTAT 540  
Db 570 CTGCTCATGGGTGACTGTTGACTTTCCAGCTGCGGCTGCCAGCCTCAGCCTGCTTAC 629  
Qy 541 GTGSCACTGTTGGGCTGTGCGCGCCCTGTCTGTTGCGGGCTCATGTTGTTGTAACCGG 600  
Db 630 GTGSCCTGTGACCTGTGCTCTGCTCTTTTGTGTACTCATGTTGTTGTTAACCAG 689  
Qy 601 CATAGCTTCGCCAGGACTCCATGTGGGTGGTGAATGAACGTGGTGTGGGATCCTGGCG 660  
Db 690 CACAGCTTCGCCAGGACTCCATGTGGGTGGTGAATGAACGTGGTGTGGGATCCTAGCA 749  
Qy 661 GCAGTGAAGTTCGGGGGCTTTCCGACGACAGCCCGGCGAGCCCTCTGCGGGCTCTGG 720  
Db 750 GCGGTGAAGTTCGGGGGCTTCGCGAGCCCAATCCACAGAGCCCTCGGGGGCTTTGG 809  
Qy 721 TGCCCTGTGTTGTTATACATGCGATACAGGCTCTCTCCCATCGCATGCGGGGTGCC 780  
Db 810 TGCCCGGTGTTCTGCTTACATCACCTACACTCTTCTCCCATTCGATCGAGCGCA 869  
Qy 781 GTCTCAGCGGCTGGGCTCTCACCTTCATTTGATTTGGCTCGCAACTTAACCGT 840  
Db 870 GTACTCAGCGGCTGGGCTCTTACTCTGATTTGATTTGGCTCGGAGCTCAACAGC 929  
Qy 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTTCTCTGACCAAC 900  
Db 930 AGCGACCCCTTCTTGAAGCAGCTCGGTGCTAAGCTGGTCTTCTCTGACCAAT 989  
Qy 901 GTCATTAGCATTCGACACACTATCCAGCAGAGTGTCTCAGCGCCAGGCTTTTCAGGAG 960  
Db 990 GCCATCGGTGTGCACACACTACCTCTGCTGAAGTGTCTCAGCGCCAAAGCTTTTCAGGAG 1049  
Qy 961 ACCGCGATTTACATCCAGGCGCGCTCCACCTGCAGCATGAGATCGGAGCAGGACCG 1020  
Db 1050 ACCGAGGTTACATCCAGGCGGCTGCACCTGCAGCATGAGAACCTGCAGGAGACGG 1109  
Qy 1021 CTGCTGCTGCTGTTATGCCCCAGCAGCTTGCATGAGATGAAGAAGACATCAACACA 1080  
Db 1110 CTGCTGCTATCGGTGTGCCCCAGCAGCTTGCCATGAGATGAAGAAGACATCAACACA 1169  
Qy 1081 AAAAAAGAAC--ATGTTCCACAGATCTACATACAGAGCATGACATGTCAGATC 1137  
Db 1170 AAAAAAGAGACATGATGTTTCCATGAATCTACATCCAGAGCATGATATGTCAGATC 1229  
Qy 1138 CTGTTTCAGACATTTGAGGCTTCAACAGCTGGCATCCAGTGCAGTGGCGAGGAGCTG 1197  
Db 1230 CTGTTTCGGACATTTGAGGCTTCAACAGCTGGCTCCAGTGCATGTCAGGAACTG 1289  
Qy 1198 GTCATGACCTGAATGAGCTCTTTGCCCGTTTGACAAAGCTGGCTGCGGAGATFCACTGC 1257  
Db 1290 GTCATGACCTGAATGAGCTCTTTGCCCGTTTGACAAAGCTGGCTGCGGAGATFCACTGT 1349  
Qy 1258 CTGAGGATCAAGATCTTGGGGGACTGTTACTGCTGCTGTCAGGCTGCGGAGGCGCGG 1317  
Db 1350 CTGAGGATCAAGATCTTAGGAGCTGTTACTGCTGCTGTCAGGCTGCGGAGGCGCGG 1409  
Qy 1318 GCCGACCATGCCACTGCTGTGTGGAGATGGGGTAGACATGATTTAGGCGCATCTCGCTG 1377  
Db 1410 GCAGATCACGCCACTGCTGTGTGGAGATGGGGTAGACATGATTCGAAGCCATCTCGCTG 1469  
Qy 1378 GTAGGTGAGGTGACAGGTGTAATGTAACATGCGCTGGGCATTCACAGCGGCGCGTG 1437  
Db 1470 GTGCGTGAGGTAAACAGGTGAACGTGAACATGCGTGGGCATCCACAGCGGAGCTG 1529  
Qy 1438 CACTGCGGCTCTTGGCTTCGGAATGACGTTCCATGTGGTCCATGATGTAC 1497  
Db 1530 CATTTGGGCTGCTTGGCTTACGGAATGCAATGCTGCTGGTCAAAACGATGTAC 1589  
Qy 1498 CTGCGCAACACATGGAAGCAGGAAGCGGCTGGCGCATCCACATCACTTCGCGGCAACA 1557

Db 1590 CTGGCTAACACATGAGAGCGGGGGCGCGCATCCACATCACTTCGGGCTACA 1649  
Qy 1558 CTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGGCGGTGGTGAAGCGCAACGCG 1617  
Db 1650 CTGCAGTACTTGAACGGGGACTATGAGTGGAGCCAGGCGGTGGTGAAGCGCAATGCG 1709  
Qy 1618 TACCTCAAGGAGCAGACATTTGAGACTTTCTCATCTGCGGCGCCAGCCAGAAACGAAA 1677  
Db 1710 TACCTCAAGGAGCAGTGCATTTGAGACCTTCTCATATTTGGCGCGACCAAAACGAAA 1769  
Qy 1678 GAGGAGAAAGGATGCTGGGCCAAGCTCAGGGACTCGGGCCCACTCATGGAAGGCTG 1737  
Db 1770 GAGGAGAAAGGATGCTGGGCCAAGCTTTCAGCGGACAGGGGCCAACTCATGGAAGGACTG 1829  
Qy 1738 ATGCCGCGATGGGTTCCTGATGCTGCTTCTCCCGGACCAAGACTCTCAAGGCTTCGCG 1797  
Db 1830 ATGCCGCGCTGGGTTCCTGACCGTGCCTTCTCCCGGACCAAGACTCTAAGGCATTCGCG 1889  
Qy 1798 CAGATGGGCATTTGATGATTTCCAGCAAGAACACCGGGGACCCCAAGATGCCCTGAACCCCT 1857  
Db 1890 CAGATGGGCATTTGATGATTTTCAGCAAGAACACCGGGGTGCCAAGATGCTCTGAACCCCT 1949  
Qy 1858 GAGGATGAGTGGATGAGTTCCTGAGCGGTGCCATGATGCCGACAGCTTGATAGCTG 1917  
Db 1950 GAGATGAGTGGATGAGTTCCTGGGCGGAGCCATCATGCCCCGAGCATCGACCACTG 2009  
Qy 1918 CGAAGGACCATGTGCGCGCGGTTTTTGTCTCACCTTCCAGAGAGAGGATTTTGAGAAGAAG 1977  
Db 2010 CGTAAGGACCATGTGCGCGCGGTTCTCTGCTCACCTTCCAGAGAGAGGATTTTGAGAAGAAG 2069  
Qy 1978 TACTCCGGAAGTGGATCCCGGCTTCGGAGCCTACGTTGCCTGTGCCCTGTGGCTTTC 2037  
Db 2070 TATTCAGGGAAGTAGATCTCCTCGCTTCGGAGCCTACGCTGCTGCGCTCTGCTGCTGCT 2129  
Qy 2038 TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCTGATGCTTGGGAT 2097  
Db 2130 TGCTTCATCTGCTTTCATCCAGCTTCTGTTGCCATCTCCACCTGATGCTGCGGAT 2189  
Qy 2098 TATGCCAGCATCTCTGCTGCTAATCAACGCTGCTGATGCTGCTGCTGCTGCTGCTGCT 2157  
Db 2190 TATGCCGCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2249  
Qy 2158 GGTCTCTGTTCCCTAAGGCGCTGCAAGCTGCTGCCGAGCATTTGCCCTCAGGCA 2217  
Db 2250 GGTCTCTGTTTCCCGCAAGGCGCTGCAAGCCTGCTGCCGCAATATTTGCCCTCAGGCTG 2309  
Qy 2218 CATAGCACCGAGTGGCATCTTTTCCGCTGCTGCTGTTTACTTCTGCTGCTGCTGCTGCTGCT 2277  
Db 2310 CACAGCACCGGCTGGAACTTCTCGGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2369  
Qy 2278 ATGTTACCTGTAAACACACCCCATAGGAGCTGTGCCGCGGATGCTGAATTTAAACA 2337  
Db 2370 ATGTTTACCTGTAAACACACCCCATAGGAGCTGTGCCGCGGATGCTGAATTTAAACA 2429  
Qy 2338 CTTGCTGACATCACTGCTGCCACTGTCAGCAGCTCAATTAATCTCTGCGGCTGCTGCTGCT 2397  
Db 2430 CCAGCGGATGTCAGCGCTGCCACTACACAGCTCAATTAATCTCTGCGGACTGCTGCTGCT 2489  
Qy 2398 CCGCTGTGTGAGGCGCACTGCTGCCACTGTCAGCTTTTCTGAGGTGCTCCATCGGGAACATG 2457  
Db 2490 CCGCTGTGTGAGGCGCACTGCTGCCACTGTCAGCTTTTCTGAGTACTTCTGCTGCGGAACGCTG 2549  
Qy 2458 CTGCTGAGTCTTTCGGGCGCTGCTGCTTCTGCAATCAGCAGCATCGGGAAGTTCGCC 2517  
Db 2550 CTGCTGAGTCTTTCAGCGAGCTGCTGCTTCTACACATCAGCAGCATCGGGAAGTTCGCC 2609  
Qy 2518 ATGATCTTCTTTCGGGCTCATCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2577  
Db 2610 ATGACCTTCTTTCGGGCTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2669  
Qy 2578 ATCTTTGACAACTATGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2637  
Db 2670 ATCTTTGACAACTATGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2729

Qy	2638	TTTGTATGGGCTGGACTCTCCACCTCGCAGGAGGGTGCCCTCAAAATATATGACACCCCTGTG	2697
Db	2730	TTTGTATGGGCTGGACTGCCACGCTCTGGGAGGGTAGCGCTCAAAATATATGACCCCGCTG	2789
Qy	2698	ATTCTGCTGCTGTTTCGCTGGCGTGTATCTGCATGCTCAGCAGGTGGAAATCGACTGCC	2757
Db	2790	ATTCTGCTGCTGTTTCGCCCTGGCAGCTGTATCTGCATGCACAAAGGTGGAATCGACTGCC	2849
Qy	2758	CGCCTAAACTTCTCTGGAACATACAGGCAACAGGGGAAAAGAGGAGATGGAGAGACTA	2817
Db	2850	CGCCTGGACTTCTCTGTGGAAGTTACAGGCAACAGGGGAGAAGGAGGAGATGGAGAGACTA	2909
Qy	2818	CAGGCATACAACCGGAGGCTGTCATACATCTTCGCCCAAGGACGTGGCGGCCCACTTC	2877
Db	2910	CAGGCATACAACCGAGGTGCTGCATACATCTTCCCAAGGACGTGGCGGCCCACTTC	2969
Qy	2878	CTGGCCCGGAGGCGCGCAATCACTACTATCAGTCTGTAGTGTGTGGCTGTT	2937
Db	2970	CTGGCCCGGAGCGCCGCAACGATGAGTGTACTACCAAGTCTGTGAATGTGTGGCTGTC	3029
Qy	2938	ATGTTTGCCCTCCATGTCCTAACTCTCTGAGTCTCTATGTGGAGCTGGAGGCAAAACATGAG	2997
Db	3030	ATGTTTGCCCTCCATGTCCTAACTCTCTGAGTGTCTACGTGGAGCTCGAGGCAAAACAGCAG	3089
Qy	2998	GGTCCGAGTGGCTGGCGTCTGCTCAACGAGATCATCGCTGACTTTGTATGAGATTATCAGC	3057
Db	3090	GGCGTGGAGTGGCTGGCGTCTCAATGAGATCATCGCAGACTTTGACGAGATCATCAGT	3149
Qy	3058	GAGGAGGGTTCGGGAGCTGGAAAGATCAAGACGATTTGGTAGCACTACATGGCTGCC	3117
Db	3150	GAGGAGAGATTCGGGAGTTCGGAGAGATCAAGACCATCGGTAGCACCTACATGCGCGCC	3209
Qy	3118	TCAGGGCTGAACGCCAGCACCTACGATCAGGTGGCGCGCTCCACATCAGTGCCTCGCT	3177
Db	3210	TCGTGGGCTAAATGCCAGCACCTATGACCAGTTCGGCCGCTCACACATCACGGCGCTGGCT	3269
Qy	3178	GACTAGCCATGGGCTCATGAGCAGATGAAGCACATCAATGAGCACTCTCTCAACAAT	3237
Db	3270	GACTATGCCATGGGCTCATGAGCAGATGAAGCACATCAATGAGCACTCTCTTCAACAAT	3329
Qy	3238	TTCCAGATGAAGATTGGGCTGAACATGGCCCGCAGTCGTGGCAGGTGTATCGGGGCTCGG	3297
Db	3330	TTCCAGATGAAGATCGGGTGAACATGGGTCCGGTGTAGCAGGCGTCATTTGGGCGCCGA	3389
Qy	3298	AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACG	3357
Db	3390	AAGCCACAGTATGACATCTGGGGAATACCGTGAATGTTTCCAGTCGTATGGACAGCACT	3449
Qy	3358	GGGGTCCCGACCGAATCCAGGTGACACGGGACCTGTACCAAGTTCTAGCTGCCAAGGGC	3417
Db	3450	GGAGTTCTCTGACCGAATACAGGTGACTACGGACCTTATACCAAGTTCTAGCTGCCAAGGGC	3509
Qy	3418	TACCAGCTGGAGTTCGAGGGTGTCTAAGGTGAAGGCAAGGGGAGATGACCACTAC	3477
Db	3510	TACCAGCTGGAGTTCGAGGGTGTCTAAGGTGAAGGAAAAGGGGAGATGACCACTAC	3569
Qy	3478	TTCTCTAATGGGGGCCCGCAGCACTTAAACAGGGCCCGAGC--CACAAATTCAGCTCAAGGGA	3535
Db	3570	TTCTCTAAGGGGGCCCGCAGCACTTAGCAGATGCGAGCAAGCTGAGATTACACCAAGGGA	3629
Qy	3536	CCAAGTGGGCACT	3549
Db	3630	CCAAGTGGGCATT	3643

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RESULT 2
US-10-144-771-19529
; Sequence 19529, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321

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: CURRENT APPLICATION NUMBER: US/10/144,771
:
: CURRENT FILING DATE: 2002-05-15
:
: NUMBER OF SEQ ID NOS: 47235
:
: SEQ ID NO 19529
:
: LENGTH: 4349
:
: TYPE: DNA
:
: ORGANISM: HUMAN
:
: FEATURE:
:
: NAME/KEY: misc_feature
:
: LOCATION: (1)...(4349)
:
: OTHER INFORMATION: n = A,T,C or G
:
: US-10-144-771-19529

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Query Match	44.83;	Score 1591.4;	DB 6;	Length 4349;
Best Local Similarity	70.7%;	Pred. No. 0;		
Matches 222;	Conservative 0;	Mismatches 871;	Indels 48;	Gaps 6;
Qy 345	CGCATCTCTGCTGGCGCGCTTTGGTGCAGGTCTTCCAGTGAAGCAGTTCCTGTCGGGCAA	404		
Db 123	GGGCGCTGCTGCCTGGCCTTGCTGCAGATATTCGGCTCTAAGAAGTTCGCGTCGGACAA	182		
Qy 405	GCTGAGGCGCTGTACACAGCGGTACTTTTTCAGATGAACACAGACAGCCTGACGCTGCT	464		
Db 183	ACTGAGCGCTGTACACAGCGCTACTTCTTCGGCTGAACACAGACAGCTCTCACATGCT	242		
Qy 465	GGTGGCGGTGCTGTGCTGTCTACAGCGGTGCTGCTGGCTTTTCAAGCGCACCGGCCG	524		
Db 243	CATGGCCGTGCTGTGCTGTGTGCGCTGGTCATGCTGGCTTTTCCACGGCGCGGCCCCC	302		
Qy 525	CCCTACAGCTGCCATGTGGCACTGTGGCGCTGTGGCGCGCCCTGTTCGTGGGGCTCAT	584		
Db 303	GCTCATAGACCTACCTTGGCGGTGTGGCAGCTGCTGTGGCGGTGATCTTATCATGGC	362		
Qy 585	GGTGGTGTAAACGGCATAGCTTCCGCCAGSAGCTTCCATGTGGGTGGTGAAGTGAAGTGCT	644		
Db 363	CGTGTCTGCAACCGTGCAGCGTTTCCACCAGACCAATGGCGCTGGCGCTGCTATGCGCT	422		
Qy 645	GCTGGGCATCTGGCGGAGTGCAGGTGGGGGCGCTTTCGACAGACACCGCGCAGGCC	704		
Db 423	CATTGCAAGTGTGTGGCGGTCCAGTAGTGGGCGTGTGTGTCACAGCCACGACGAGGC	482		
Qy 705	CTCTGCGGCGCTGCTGGTCCCTGTCTCTTTGTATATACATCGATCGATCGCTTCCCCAT	764		
Db 483	CTCGAGGGCATCTGTGTGGACCGTGTCTTCTCATCTATACCATCTACACCTTGTGCTGT	542		
Qy 765	CCGATGCGGGCTGCCGTCTCAGCGGCTGGGCGCTCTCCACCTTGCATTGTGCTTGGC	824		
Db 543	CGCATGAGGCTGCGGTGCTCAGCGGGTGTCTTCTGTGCGCTCTCCACTTGGCCATCTC	602		
Qy 825	CTGGCACTTAAACGTGGTGATGCTTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGT	884		
Db 603	TCTGCACACCAACTCCCAGSAGCAGTGTCTCTGTAACAGCAGTGTCTCTCAATGTCTCAT	662		
Qy 885	GTTCCTCTGCACCAAGCTCATAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCG	944		
Db 663	CTTCTCTGCACCAACATTTGGGTGTGTGCATCTACTACCCAGCTGAGTCTCCAGAG	722		
Qy 945	CCAGGCGTTTCAGGAGACCCGAGTTACATCCAGGCGGCTCCACCTTGCAGCATGAGAA	1004		
Db 723	ACAGGCGTTCCAGGAGACCCGGAGTGTATCCAGGCTCGGCTCATTTCCAGCGGGAGAA	782		
Qy 1005	TCGGCAGCAGGCGGCTGCTGTGCGTATTGGCCCGCAGCAGCTTGCCATGGAGATGAA	1064		
Db 783	CCAGCAACAGAGGCGTCTCTGTCTGTCTTCTTCCCGGTCATGTGGCCATGGAGATGAA	842		
Qy 1065	AGAAGCATCAACACAAAAAAGA ---CATGTCTCCACAAGATCTACATACAGAGCA	1121		
Db 843	AGCAGACATCAACGCCAAGCAGGAGGATATGATGTTCACAAGATCTACATCCAGAGCA	902		
Qy 1122	TGACAATGTACATCTCTGTTTTCAGACATTTGAGGGCTTACCAGCCTGGCATCCCACTG	1181		
Db 903	TGACAATGTAGCATCTCTGTTTGTGACATCGAGGGTTTACCAGCCTGGCTTCCCACTG	962		

Qy 1182 CACTGCGCAGAGAGTGTCATGACCCCTGAATGAGCTCTTTGCCGGTGTGACAAAGCTGGC 1241  
Db 963 TACTGCCCAAGAACTGGTGCATGACCCCTCAATGAGCTCTTGCCCGCTTTGACAAGTTGGC 1022  
Qy 1242 TGGGAGAAATCACATGCCCTGAGGATCAAGATCTTGGGGAGCTTTACTACTGTGTGTGAGG 1301  
Db 1023 TGGGAGAAATCACATGTTTACGGATTAAGATCTCTGGGGATGTTTACTACTGCGTCTCGGG 1082  
Qy 1302 GCTCCGAGGCGCGCGCCGACCATGCCACTGCTGTGTGGAGATGGGGTAGACATGAT 1361  
Db 1083 GCTGCCCTGAAGCCAGAGCGGCACCATGCCACTGCTGTGGAGATGGGAATGACATGAT 1142  
Qy 1362 TGAGGCCATCTCGCTGTGATGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCAT 1421  
Db 1143 CGAGGCCATCTCGTTGGTCCGGAGGTGACAGGGGTGAACCTGAACATGCGCGTGGGAAT 1202  
Qy 1422 CCACAGGGGCGCTGCACCTCGCGCTCTTGGCTTCGGGAAATGGCAGTTTCGATGTGTG 1481  
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Qy 1482 GTCCAATGATGTACCTTGGCCAAACACATGGAAGCAGGAAGCGCGCTGCCCGCATCCA 1541  
Db 1263 GTCTAAGATGTCACTCTGGCCAAACACATGGAAGCTGTGGCAAGGGCGGCCCATCCA 1322  
Qy 1542 CATCACTCGGGCAACATCTGCAGTACCTGAACGGGGAATGACAGTGAAGCGAGCGCCGTGG 1601  
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Qy 1602 TGGCAAGCGAAGCGGTACCTCAAGGAGCAGCAGATTTGAGACATTTCTCATCTCGGGCGC 1661  
Db 1383 TGGCGATCGCAGTGCCTTACCTCAAGGAGCAGCAGATTTGAGACATTTCTCATCTTGAAGCTG 1442  
Qy 1662 CAGCGAAGAAAGGAGGAAAGGAGTGCCTGGCCAAAGTGCAGGCGGAGTCTCGGGCCAA 1721  
Db 1443 TACCAGAAGCGGAAAGAGAGAGGCGCATGATCGCCAAAGATGAACCGCCAGAGAACCAA 1502  
Qy 1722 CTCCATGGAAGGGCTGATGCCCGATGGGTTCTTGATGCTGGCTTCCTT-----C 1769  
Db 1503 CTCCATGGAAGAACTCCGCTCACTGGGAGCGCGCGCCCTTCTACAACTTTGGG 1562  
Qy 1770 CCGGACCAAGGACTTCAAGGCTTTCGCCAGATGGGCAATTTGATTTCCAGCAAGACAA 1829  
Db 1563 CGCAACAGGTGTCAAGAGAGATGAAGAGATGCTTGCCTATGCTTGCCCTGGTTTC 1622  
Qy 1830 CCGGGGACCCAGATGCCCTGAACCTGAGGATGAGGTGATGATGCTTCTGAGCCGTGC 1889  
Db 1623 CAGGAATGCCAGGAAAGTGGAAACCCAGAGGATGAAGTGGACGAGTTTCTGGGTGCGGC 1682  
Qy 1890 CATCGATGCCGAGCATTTGATCAGCTGCGGAAGGACCATCTGCGCGGTTTTGTCTCAC 1949  
Db 1683 CATCGATGCCAGGAGCATTCGACAGACTGCGCATCTGAACAGTCCGCAAGTTCTCTGAC 1742  
Qy 1950 CTTCCAGAGAGGATTTTGAAGAAGTACTCCCGGAAGTGGATCCCGCTTTCGGAGC 2009  
Db 1743 CTTCAGGAGCCGACTTAGAAGAAGTACTCCAAGCAGGTGGATGACCGATTTGGTGC 1802  
Qy 2010 CTAGGTTGCCCTGTGCTGTGTTGCTTCTGCTTCATCTGCTTCATCCAGCTTCTTAATTT 2069  
Db 1803 CTATGTGGCTGCGCCCTGCTTGTGTTTCTTCTCATCTGCTTTGTCAGATCAACATTTG 1862  
Qy 2070 CCCACATCCACCTGATGCTTGGATTTATGCCAGCATCTTCTGCTGCTGTGCTAATCAC 2129  
Db 1863 GCGCCATCTTCTTATGCTGAGTTTCTACCTGTGCTGTGCTGCTGCTTGGT 1922  
Qy 2130 CGTGCTGATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2189  
Db 1923 GGTGTTGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1961  
Qy 2190 GTCCCGCAGCATGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2249  
Db 1962 CTCAGGAAGATAGTGGGATCCAAAGAGAACAGCAGCCTGCTGCGGGGTATTTACCATCAC 2021  
Qy 2250 GCTTGTGTTTACTTCTGCCATTGCCACATGTTCACTGTAACCAACACCCCATACGAG 2309

Db 2022 CCTGGTCTTCTCGGCTTTTGTCAACATGTTTCATGTGCAACTCTAAGAACCTTGGTGG 2081  
Qy 2310 CTGTGACCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCCCTGCCACCTGACGCA 2369  
Db 2082 CTGCGTGGCAGAGAGACAAACATCAAGGTGAACAGGTCAACGCATGTGATGTGATGGA 2141  
Qy 2370 GC-----TCAAATACATCTCTGGGCTTGGATGTCTCCCTGTGTGAGGGCCACCATGCCAC 2423  
Db 2142 GTCGGCTTCAACTACAGCTTGGCGACGAGCAGGGCTTCTGTGGCAAGCCCAACCCAA 2201  
Qy 2424 CTGAGCTTTCTGAGGTGCTCATCGGGAACATGCTGCTGAGTCTTGTGGCCAGCTCTGT 2483  
Db 2202 CTGCAACTTCCAGAGTACTTCACTACAGGTGCTGCTCAGCCTGTGCGCTGCTCGCT 2261  
Qy 2484 CTTCTCCACATCAGCAGCATCGGAAGTTGGCCATCATCTTGTCTTGGGGCTCATCTA 2543  
Db 2262 GTTCTCCAGATCAGCTGCAATTTGAAAGCTGGTGTCTCATGCTGGCCATTTGAGTTTCACTA 2321  
Qy 2544 TTTGGTCTGCTTCTGCTGGGTCCCCCAGCGCCCATTTTGAACAATATGACCTACTGCT 2603  
Db 2322 T---GTGCTCATCGTGGAGGTGCCCGCGTCACTCTTCGACAACGCTGACCTTCTGGT 2378  
Qy 2604 TGGGCTCCATGGCTTGGCTTCTTCCAAATGAGACCTTTGATGGGCTGGACHTGTCAGCTGC 2663  
Db 2379 CACGCGCAATGCCATAG---ACTTCAGCAACAGCGGACCTCCCAAGTGGCTTGAGCATGC 2435  
Qy 2664 AGGAGGCTGGCCCTCAATATATGACCTGTGATTTCTGCTGCTTGTGGCTTGGCGCT 2723  
Db 2436 ACCAAGTGGCGTGAAGTGGTGACGCCCATCATCTCTGCTTCTGCTGCTGCTGCT 2495  
Qy 2724 GTATCTGCATCTCAGCAGGTGGAATGACTGCGCGCTAAACTTCTCTGGAACATACA 2783  
Db 2496 GTATCTGCATGCCAGCAGGTGGAGTCCACTGCTGCGCTTGACTTCTCTGGAACATGCA 2555  
Qy 2784 GGCACAGGGGAAAGAGAGATGGAGAGCTACAGGCATACACAGCGAGGCTGCTGCA 2843  
Db 2556 GGCACAGAGAGAGAGAGATGGAGAGCTGCAAGGCTTACAATCGGCGCTTGTGCA 2615  
Qy 2844 TAACATTTCTGCCAAGGACGTGGCGCCACTTCTTGGCGGAGCGCGCAATGATGA 2903  
Db 2616 CAACATTTCTGCCAAGGACGTGGCTGCCACTTCTTGGCGGAGCGCAATGACGA 2675  
Qy 2904 ACTTACTATCAGTCTGCTGAGTGTGGCTGTGATGTTTGGCTCCATTTGCCAACTTCTC 2963  
Db 2676 GCTGTACTACCAATGCTGCGAGTGTGGCTGTGATGTTTGGCTTCCATTTGCCAACTTCTC 2735  
Qy 2964 TGAGTTCTATGTGAGCTGGAGCAAACTAGGGTGGCGAGTGGCTGCGCTGCTCAA 3023  
Db 2736 CGAATTTATGTAGAGTGAAGCCAACTAGAGGCGTGAAGGCTGCTGCTGCTGCTCAA 2795  
Qy 3024 CGAGATCATCGCTGACTTTGATGAGATTTATCAGCGAGAGCGGTTCCGCGAGCTGGA 3083  
Db 2796 TGAGATCATCGACATTCGATGAGATCATCAGTGAAGTGGTTTACAGGAGCTGGA 2855  
Qy 3084 GATCAAGCAGATTTGGTAGCCTTACATGGCTGAGGCTGAACCGCAGCCTACGA 3143  
Db 2856 GATCAAGCAGATTTGGTAGCCTTACATGGCTGAGGCTTCAACGACTCCACATGA 2915  
Qy 3144 TCAGTGGGCGCTGCCACATCACTGCGCTGAGTACGCGCATGCGCTGCTGCTGAGCA 3203  
Db 2916 CAAGGAGGCAAGACCCACATCAAGGCTTTTGAAGCTTTCGCTATGAAGCTGATGGA 2975  
Qy 3204 GATGAAGCAGATCAATGAGCCTCTTTCAACAATTTCCAGATGAAGATTTGGCTGA 3263  
Db 2976 AATGAAGTACATCAATGAGCCTCTTTCAACAATTTCCAGATGAAGATTTGGCTCA 3035  
Qy 3264 GGGCCAGTGTGGCAGGTGTGATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGAA 3323  
Db 3036 TGGACCTGTATGGCTGAGTTCATTTGGGGCTCGCAAGCCTCAGTATGACATCTGGGCA 3095  
Qy 3324 CACAGTCAATGCTCTAGTGTGATGGACAGCAGCGGGGTCCCGACCGAATCCAGTGC 3383

Db 3096 TACAGTGAATGGCCAGCCGATGACAGCACTGGGTGCTGACCGCATCCAGGTAC 3155  
Qy 3384 CACGACCTGTACCAAGTTCTAGCTGCCAAGGCTTACCAAGGCTGAGTGTGCGAGGGGTGGT 3443  
Db 3156 TACAGATATGTACCAAGTGTGCGGCCCAACACATACCAAGTGGAGTCCCGGGGTGTGGT 3215  
Qy 3444 CAAGTGAAGGCCAAGGGGA 3464  
Db 3216 CAAGGTCAAGGCCAAGGAAGA 3236

## RESULT 3

PCT-US02-36759-83

; Sequence 83, Application PC/TUS0236759

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: DUGGAN, Brendan M.

; APPLICANT: YANG, Junning

; APPLICANT: GIETZEN, Kimberly J.

; APPLICANT: LEE, Soo Yeun

; APPLICANT: TANG, Y. Tom

; APPLICANT: AZIMZAI, Yalda

; APPLICANT: WALIA, Narinder K.

; APPLICANT: WARREN, Bridget A.

; APPLICANT: BARROSO, Ines

; APPLICANT: BECHA, Shanya D.

; APPLICANT: YUE, Henry

; APPLICANT: LEHR-NASON, Patricia M.

; APPLICANT: THANGAVELU, Kavitha

; APPLICANT: LEE, Sally

; APPLICANT: EMERLING, Brooke M.

; APPLICANT: KABLE, Amy E.

; APPLICANT: KHARE, Reena

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: GANDHI, Aneena R.

; APPLICANT: TRAN, Uyen K.

; APPLICANT: RICHARDSON, Thomas W.

; APPLICANT: MARQUIS, Joseph P.

; APPLICANT: LAL, Preeti G.

; APPLICANT: FORSYTHE, Ian J.

; APPLICANT: LEE, Ernestine A.

; APPLICANT: SWARNAKAR, Anita

; APPLICANT: KALLICK, Deborah A.

; APPLICANT: GRIFFIN, Jennifer A.

; APPLICANT: ELLIOTT, Vicki S.

; APPLICANT: GORVAD, Ann E.

; APPLICANT: HAFALIA, April J.A.

; APPLICANT: ISON, Craig H.

; APPLICANT: JIN, Pei

; APPLICANT: JIANG, Xin

; APPLICANT: JACKSON, Alan

; APPLICANT: BHATIA, Umesh

; APPLICANT: BURRILL, John D.

; APPLICANT: BLAKE, Julie J.

; APPLICANT: HO, Ann

; APPLICANT: ZHENG, Wenjin

; APPLICANT: GAO, Jing

; TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS

; FILE REFERENCE: PF-1279 PCT

; CURRENT APPLICATION NUMBER: PCT/US02/36759

; CURRENT FILING DATE: 2002-11-13

; PRIOR APPLICATION NUMBER: US 60/333,097

; PRIOR FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: US 60/335,274

; PRIOR FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: US 60/340,542

; PRIOR FILING DATE: 2001-12-14

; PRIOR APPLICATION NUMBER: US 60/342,166

; PRIOR FILING DATE: 2001-12-18

; PRIOR APPLICATION NUMBER: US 60/347,580

; PRIOR FILING DATE: 2002-01-11

; PRIOR APPLICATION NUMBER: US 60/348,687

; PRIOR FILING DATE: 2002-01-14

; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: PERL Program  
; SEQ ID NO 83  
; LENGTH: 1386  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No: 7506194CB1  
PCT-US02-36759-83

## Query Match

29.9%; Score 1060.2; DB 1; Length 1386;

Best Local Similarity 97.5%; Pred. No. 1.5e-232;

Matches 1077; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 ATGTCATGGTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGGAAACACAGCTGGGGT 60  
Db 25 ATGTCATGGTTAGTGGCTCCTGGTCCCTAAAGTGGATGAACGGAAACACAGCTGGGGT 84  
Qy 61 GAACGCAATGGGCAGAACGGTTTCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120  
Db 85 GAACGCAATGGGCAGAACGGTTTCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 144  
Qy 121 CCCGCTATATGAGCTGCTCGGGATGCAGAGCCACCCAGCCCTCGGGGGCCC 180  
Db 145 CCCGCTATATGAGCTGCTCGGGATGCAGAGCCACCCAGCCCTCGGGGGCCC 204  
Qy 181 CTCTGGTCCCTCGGCGAGTACGCTTTCATCCGGAGGGCGGCCAGGCAAGGCAAG 240  
Db 205 CTCTGGTCCCTCGGCGAGTACGCTTTCATCCGGAGGGCGGCCAGGCAAGGCAAG 264  
Qy 241 GAGCTGGGGCTCGGGCAGTGGCCCTTGGGCTTCGAGGATACCGAGGTGACACACAGCG 300  
Db 265 GAGCTGGGGCTCGGGCAGTGGCCCTTGGGCTTCGAGGATACCGAGGTGACACACAGCG 324  
Qy 301 GCGGGACGCTGAGGTGGCGCCGACCGGTGCCAGAGTGGCGATCTCTGTGGCGC 360  
Db 325 GCGGGACGCTGAGGTGGCGCCGACCGGTGCCAGAGTGGCGATCTCTGTGGCGC 384  
Qy 361 GCTTGGTGCAGGTGTTCCAGTCCAGTCCAGTCCGTCGGGCAAGCTGAGGCGCTGTAC 420  
Db 385 GCTTGGTGCAGGTGTTCCAGTCCAGTCCGTCGGGCAAGCTGAGGCGCTGTAC 444  
Qy 421 CAGCGGTACTTTTCCAGTCAACAGACAGACCTGACGCTGCTGGTGGCGGTGCTGTG 480  
Db 445 CAGCGGTACTTTTCCAGTCAACAGACAGACCTGACGCTGCTGATGCGGTGCTGTG 504  
Qy 481 CTGCTCACAGCGGTGCTGCTGGCTTTCCAGCCGACCCGCCGCCCTCAGCCTGCCTAT 540  
Db 505 CTGCTCACAGCGGTGCTGCTGGCTTTCCAGCCGACCCGCCGCCCTCAGCCTGCCTAT 564  
Qy 541 GTGGCACTGTTGGCTGTGGCGCCGCTGTTGCTGGGGCTCATGGTGGTGAACCGG 600  
Db 565 GTGGCACTGTTGGCTGTGGCGCCGCTGTTGCTGGGGCTCATGGTGGTGAACCGG 624  
Qy 601 CATAGCTTCCGCCAGGACTCCATGTGGTGGTGGTGAAGTGGTGGTGGATCTCTGGCG 660  
Db 625 CATAGCTTCCGCCAGGACTCCATGTGGTGGTGGTGAAGTGGTGGTGGATCTCTGGCG 684  
Qy 661 GCAGTGCAGGTGGGGGCGCTTTCGACAGACAGCCGCGAGCCCTCTGCGGGGCTCTGG 720  
Db 685 GCAGTGCAGGTGGGGGCGCTTTCGACAGACAGCCGCGAGCCCTCTGCGGGGCTCTGG 744  
Qy 721 TCCCTGTGTTCTTGTATACATCCATACAGCTCCCTCCCATCCGATCGGGCTGCC 780  
Db 745 TCCCTGTGTTCTTGTATACATCCATACAGCTCCCTCCCATCCGATCGGGCTGCC 804  
Qy 781 GTCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATCTTGGCTGGCAACTTAACCGT 840  
Db 805 GTCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATCTTGGCTGGCAACTTAACCGT 864  
Qy 841 GGTGATGCTTCTCTGGAAAGCAGCTCGGTGCCAATGTGCTGCTTCTCTGCAACCAAC 900  
|||||

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Db 865 GGTGATGCTTCTCTCGAAGCAGCTCGGTGCCAATGTGCTGTTCCTCTGTCACCAAC 924
Qy 901 GTCAATTAGCATCTGCACACACTATCCAGCAGAGGTGCTCTCAGCGCCAGGCTTTTCAGGAG 960
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 925 GTCATTGGCATCTGCACACACTATCCAGCAGAGGTGCTCTCAGCGCCAGGCTTTTCAGGAG 984
Qy 961 ACCGCGATGTACATCCAGGCGCGGCTCCACCTGCAGCATGAGAAATCGGCAGCAGGCGG 1020
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 985 ACCGCGGTTACATCCAGGCGCGGCTCCACCTGCAGCATGAGAAATCGGCAGCAGGAGCGG 1044
Qy 1021 CTGCTGCTGTCGGTATTGCCCCACGCTTGCCATGCGAGATGAAGAAGACATCAACACA 1080
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1045 CTGCTGCTGTCGGTATTGCCCCACGCTTGCCATGCGAGATGAAGAAGACATCAATGAG 1104
Qy 1081 AAAAAGAAGACATGTTCCACAAGA 1105
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1105 CACTCCTTCAACATTTCCAGATGA 1129

RESULT 4
US-10-121-911A-2
: Sequence 2, Application US/10121911A
: GENERAL INFORMATION:
: APPLICANT: Kapeller-Libermann, Rosana
: APPLICANT: Chun, Miyoung
: TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE
: FILE REFERENCE: 035800/246627
: CURRENT APPLICATION NUMBER: US/10/121.911A
: CURRENT FILING DATE: 2003-02-05
: PRIOR APPLICATION NUMBER: US 09/412,210
: PRIOR FILING DATE: 1999-10-05
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 3518
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (0)...(0)
: OTHER INFORMATION: 21529 adenylate cyclase
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (247)...(3480)
US-10-121-911A-2

Query Match 14.2%; Score 505.2; DB 6; Length 3518;
Best Local Similarity 50.0%; Pred. No. 1.7e-105;
Matches 1560; Conservative 0; Mismatches 1488; Indels 72; Gaps 9;

Qy 435 CCAGATGAACAGAGCAGCCTGCTGCTGGTGGCGGTGCTGTGCTCAGCAGCGGT 494
Db 318 CCAGCAGTACCCTGCTGCTGCTGCTGGGATGCTGCTGCTGCTGCTGCTGCTGCT 377
Qy 495 GCT----GCTGGCTTTCCAGCCGACCCGCCGCCCTCAG--CCTGCCATGTGGCACT 548
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 378 GCTCGCAGTGGCGTGGCCACGCGCAGGAGCTGACCTCAGACCCGAGCTCTCTGACCA 437
Qy 549 GTTGGCTGTGCCCGCGCTTCTGTTGGGCTCATGGTGGTGTGTAACCGGCATAGCTT 608
    || || || || || || || || || || || || || || || || || || || || || ||
Db 438 TGTGCTGTGGCGCTGGCGGCTTCTCGTCTGCTGGGCTTCGCTTCCCGGGAGACGG 497
Qy 609 CCGCAGGACTTCCATGTGGTGTGAGTACGTGCTGCTGGGCATCTTGGCGGAGTGCA 668
    || || || || || || || || || || || || || || || || || || || || || ||
Db 498 ACTGACGCTGGACGCTCCCTGTCCGGCTTGGTATGGTTCGCTGCTAGCGCTAGG 557
Qy 569 GGTGGGCGGCTTTCCGAGCAGACCCGCGGAGCCCTCTGCGGGCCCTCTGGTCCCTGT 728
    || || || || || || || || || || || || || || || || || || || || || ||
Db 558 CCAGCGCTTCTGTTACCGGGGCGGTGAGCGCCTGGGACCAAGGTGTCCTATTTCCT 617
Qy 729 GTTCTTTGTATACATACAGCTCTCCCATCCGATCGCGTGGGCTGCGCTCTCAG 788
    || || || || || || || || || || || || || || || || || || || || || ||
Db 618 CTTCGTATCTTACGGCGTATGCCATGCTGCCCTTGGGCATGCGGGACGCCGCGCTCG 677
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Qy 789 CGGCTTGGGCTCTTCCACCTTGCATTTGATCTTGGCCTGGCAA-----CTTAAAC 838
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 678 GGGCTCGCTCCTCTCACTCTCGCATCTGCTGGTCTCGGCTGTATCTTGGGCGACAGCC 737
Qy 839 GTGGTGTGCTTCTCTCTG--GAAGCAGCTCGGTGCCAATGCTGCTGTCTCTCTGCAC 896
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 738 GGACTCAGCGCTGCTGCTGCGCAGTTGGCAGAAACGCAAGTGTGCTGTCTGTCGG 797
Qy 897 CAAGCTATTAGCATCTGCACACACTATCCAGCAGAGGTGCTCTCAGCGCCAGGCTTTCA 956
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 798 GAAGCTGGCAGGAGTGTACCACAGGCGCTGATGGAGCGCCCTGCGGGCCAGGTTCCG 857
Qy 957 GGAGACCCGAGTTTACATCCAGGCGCGGCTCCACCTGCAGCATGAGAATCGGCAGCAGGA 1016
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 858 GGAGGCATCAGCTCCTGCTGCTCAGCGCGGCTGCACACCGAAGAACGACCAAGA 917
Qy 1017 CGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1076
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 918 ACACCTTCTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 977
Qy 1077 CACAA-----AAAAAGAAGACATGTTCCACAAGAT 1106
    || || || || || || || || || || || || || || || || || || || || || ||
Db 978 GGCAGGCTGCAGCAGCAGGCGTCCAGCCAGAGCAGCATTAACAATTTCCACAGCCT 1037
Qy 1107 CTACATACAGAAGCATGACAATGTACGATCCTGTTTGCAGACATTTAGGCGCTTTCACAG 1166
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1038 CTATGTCAAGAGGCCACCGAGGAGTCAGCGTCTGTATGCTTACATCGTGGGCTTTCAGCG 1097
Qy 1167 CTTGGCATCCAGTGCACCTGCGCAGGAGCTGGTTCATCACCTGAATGAGCTCTTGGCCCG 1226
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1098 GCTGGCCAGCAGGTTTCCCTTAAGGAGCTGGTCTCATGCTCAATGAGCTCTTTGGCAA 1157
Qy 1227 GTTTGACAAGCTGGCTGCGGAGATCACTGCTGAGGATCAAGATCTTGGGGGACTGTTA 1286
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1158 GTTCGACAGATTGCCAAGGAGCATGAATGCATCGGATCAAGATCTCGGGGACTGTTA 1217
Qy 1287 CTACTGTGTGAGGCTGCGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1346
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1218 CTACTGTGTCTGCTGGGCTGCACTCTCACTGCCAGACATGCCATCAACTGCGTGGCGCAT 1277
Qy 1347 GGGGTAGACATGATTGAGGCCATCTCGTGGTACGTGAGGTGACAGGTGTGAATGTGA 1406
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1278 GGGCTGGACATGTGCCGGGCCATCAGAAACTCGGGCAGCCACTGGCTGGGACATCA 1337
Qy 1407 CATGCGCTGGGCATCCACAGCGGCGGTGCATCTCGGCGTCTCTGGCTTGGGGAATG 1466
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1338 CATCGCTGTTGGCGTGCATCAGGCGAGCTGCTGTGGAGTCTATCGGCTGCAGAAAGTG 1397
Qy 1467 GCAGTTCGATGTGTGGTCCATGATGTGACCTGGCCCAACCATGGAAGCAGGAGCGG 1526
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1398 GCAGTACGAGCTTTGGTCACTGATGTGCATGGCTTAACCATGAGGCGCGGTGT 1457
Qy 1527 GGCTGGCGCATCCACATCACTCGGCAACACTGCAGTACTGAAACGGGACTACGAAGT 1586
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1458 ACCAGGCGAGTGCATACAGGGGCTACCTGGCCCTGCTGGCAGGGGCTTATGCTGT 1517
Qy 1587 GGAGCCAGGGCGTGGTGGCAAGCGCAACCGGTACTCAAGAGCAGCAGCATTTAGACTTT 1646
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1518 GGAGGCGCAGGCTGAGCATCGGACCCCTACCTTCGGGAGCTAGGGGAGCCTACCTA 1577
Qy 1647 CCTCATCTTGGGCGCCAGCAGAAACGGAAGAGGAGCATGTGCGCAAGCTGCA 1706
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1578 TCTGTCATCGATCCAGGCGCAGAGGAGGATGAAAGGCGCACTGCAGGAGGCTTGCT 1637
Qy 1707 GCGGACTCGGCGCAACTCCATGGAAGGCTGATCCCGGATGGTTCCTGATCTGCTT 1766
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1638 GTCTCTCTTGGGCGCTCAAGATGCGTCCATCACTGCTGATGACCGCTTACCTGGAGTC 1697
Qy 1767 CTCCCGGACCAAGACTTCCAGGCGCTTCCGCGAGATGGGCAATTGATGATTTCCACAAGA 1826
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1698 CTGGGGGCGCAGCGCTTTTGGCCACTGAGCCAGGACAGCCCTGTGTCCACCTC 1757
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QY 2743 GTGGAATCGACTGCCCGCTAAACTTCTCTGAACTACAGCAACAGGGGAAAAAGAG 2802
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2714 ATTGACTATTACTCGCGCTTGAGCTGCCTATGGAAGAAGAGTTCAAGAAGAGACCGAG 2773
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2803 GAGATGGAGGAGCTACAGGCATACAAACCGGAGGCTGCTGCATATACTTCTGCCCAAGAC 2862
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2774 GAGTTGAGACCATGGAAGCTGAACCGCTTCTTCTGGAAGACGCTGCCAGCCAC 2833
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2863 GTGGGGGCCCACTTCTCGCCCGGAGCGCGCAATGATGAACCTACTATCAGTCGCT 2922
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2834 GTGGCTGCCCACTTTATCG---GTGACAAGTTAAACGAGGACTGGTACCACAGTCCTAT 2890
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2923 GAGTGTGGCTGTATTTTGGCTCCCATTTGCCATCTCTCTGAGTTCTATGTGAGCTG 2982
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2891 GACTCGCTGTGTCTATGTTTGGCTCCGCTGCGGACTTCAAGTGTCTACACAGATGC 2950
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2983 GAGGCAACAATGAGGGTGCAGTGCTGCGGCTGCTCAACGAGATCATCGTGACTTT 3042
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2951 GATGTCAACAAGAAGGCTGGAGTGCCTAGCGCTGCTCAATGAGATCATTTGCCGACTC 3010
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3043 GATGAGATTATCAGGAGGAGCGGTTCCGGCAGCTGGAAGAGATCAAGACGATTGTAAGC 3102
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3011 GACGAGCTCCTACTGAAGCCCAAGTTACAGCGGCTGGAGAAGATCAAGACCATCGGACG 3070
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3103 ACCTATACATGGCTGCCTCAGGGCT-----GAAGCCAGCACCTTACGATCAG 3147
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3071 AGGTATACATGGCAGCTGCAGGGCTCAGCTCGCTCAGGGCAGCAGAACAGGAGCTGGAG 3130
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3148 GTGGGCGCTGCCACATCAGTGCCTGCTGCTGACTACGCCATGCGGCTCATGAGAGCAGATG 3207
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3131 CGGCAGCATGCCACATTTGGTGTATGTTGGAGTTTCAAGTTCAGCATCGCCCTGATGAGTAAGCTG 3190
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3208 AAGCATCATGAGCAGCTCTTCAACAATTCCAGATGAAGATGGCTGAACATGGCC 3267
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3191 GACGCATCAAGAGCATCTCTTCAACTCTTCCGCCCTCCGGCTCGGATGAACCATGGG 3250
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3268 CCAGTCTGGGAGGTGTCATCGGGCTCGGAAGCCACACAGTATGACATCTGGGGGAACACA 3327
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3251 CCGTGTATGCTGGAGTATGGGGCCCGAAACCTCAGTATGACATCTGGGGAACACT 3310
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3328 GTGAATGTCTAGTCTGATGACAGACAGGGGGTCCCGCAGCGAATCCAGGTGACACAG 3387
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3311 GTCAATGTGGCAGCGGAATGGAAGACCTGGAGAATTTGGGAAATCCAGGTTACCGAG 3370
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3388 GACCTGTACCAGTTCTAGCTGCCAAGGCTACCAGCTGGAGTGTGAGGGTGTCTCAAG 3447
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3371 GAGACCTGACCATCTCCAGGGCTCGGGTACTCTTGTGAATGCCGTGGCTGATCAAC 3430
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3448 GTGAAGGCAAGGGGAGATGACCACTTCTTCAATGGGGGCCCGCAGCAGTTAAGAG 3507
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3431 GTCAAAGCAAGGCGAGCTGAGGACTTACTTTGTCTGACGACACTGCCAAGTTTCAG 3490
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3508 GCGCCAGCCACAATTCAG 3526
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3491 GGGCTGGGGCTGAAGTGAAG 3509
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
US-10-282-942-1
; Sequence 1, Application US/10282942
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PAIN DISORDERS USING 9805
; FILE REFERENCE: MP101-240PIRM
; CURRENT APPLICATION NUMBER: US/10/282,942
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,047
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
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Db 3491 GGGCTGGGCTGAAGTGAAG 3509

RESULT 7

US-60-436-643-3039  
; Sequence 3039, Application US/60436643  
; GENERAL INFORMATION:  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Porter, Mark  
; APPLICANT: Johnson, Kory  
; APPLICANT: Castle, Arthur  
; APPLICANT: Elashoff, Michael  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Molecular Hepatotoxicology Modeling  
; FILE REFERENCE: 44921-5038-P15  
; CURRENT APPLICATION NUMBER: US/60/436,643  
; CURRENT FILING DATE: 2002-12-30  
; PRIOR APPLICATION NUMBER: US 60/222,040  
; PRIOR FILING DATE: 2000-07-31  
; PRIOR APPLICATION NUMBER: US 60/222,880  
; PRIOR FILING DATE: 2000-11-02  
; PRIOR APPLICATION NUMBER: US 60/290,029  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: US 60/290,645  
; PRIOR FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: US 60/292,336  
; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/295,798  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US 60/297,457  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,884  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 60/303,459  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: US 60/331,273  
; PRIOR FILING DATE: 2001-11-13

Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 4295  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3039  
; LENGTH: 4008  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. M80550  
US-60-436-643-3039

Query Match 12.98; Score 459; DB 7; Length 4008;

Best Local Similarity 50.88; Pred. No. 6.5e-95;

Matches 1370; Conservative 0; Mismatches 1240; Indels 87; Gaps 8;

Qy 852 CCTCTGGAAGCAGCTCGGTGCAATGTGCTGCTCTCTGCAACCAAGGTCATTAGCAT 911

Db 624 CCGTCTGGCAGATGCTGCGCAATGTGATCATTTTCATTGTGGGAACTTGGCGGAGC 683

Qy 912 CTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCGCTTTTCAGGAGACCCGCAATTA 971

Db 684 CTACCACCAAGCACCTCATGGAGCTTGCTTGCAGCAAAACCTATCGGACACGCTGAATG 743

Qy 972 CATCCAGCGCGGCTCCACCTGACAGATGAGATCGGAGAGAGCGGCTGCTGCTGTC 1031

Db 744 CATCAAGTCCCGGATCAAGCTGGAATTTGAAAAACGCGAGGAGGCTCCCTGCTCTC 803

Qy 1032 GGTATTCGCCAGCAGCTTGCATGGAGATGAAAGAGACATCA- 1075

Db 804 CTTGCTGCCAGCTCACATCGCCATGGAGATGAAAGCTGAAATCATTCAGAGGCTGCAGG 863

Qy 1076 -----ACACAAAGAAAGAGACATGTTCCACAAAGATCTACATACAGAGCA 1121

Db 864 CCCCAAGCAGGACAGATGGAACACAAACAACTTCCACATCTGTATGTCAACAGCA 923

Qy 1122 TGACAATGTACAGATCCTGTTTTCAGACATTTGAGGGTTTACCAGCCTTGGCATCCCATG 1181

Db 924 CACCAACGTGAGCATATTATACGCTGACATTTGGCTTCACCCGCTTGAAGCGATTG 983

Qy 1182 CACTGCGCAGGAGCTGGTTCATGACCCCTGAATGAGCTCTTTGCCGGTGTGCAACCTGCG 1241

Db 984 CTCCTCGGCAACTGGTCCACATGCTGAATGAACCTCTTTGGGAAGTTTGAATCAATAGC 1043

Qy 1242 TSCGAGAAATCACTCCCTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTCTCAGG 1301

Db 1044 AAGGAGAATGAATGCATGAGAATTAATTTTAGGACACTGCTATTACTGTGTTCCGG 1103

Qy 1302 GCTGCGGAGCGCGCGGCGGACCATGCCCCTGCTGTGTGTGGAGATGGGGGTAGACATGAT 1361

Db 1104 GCTCCCTATATACCTCCCTTAACCATGCCAAGAACTGTGTGAAAATGGGATGGATATGTG 1163

Qy 1362 TGAGGCCATCTCGCTGGTACCTGAGGTGACAGGTGTAATGTGACATGCGCGTGGGCAT 1421

Db 1164 CGAAGCCATAAAGAAAGTGAAGGATGCTACCGGATTTGATATCAACATGCGGTGATGAGT 1223

Qy 1422 CCACAGCGGCGCGTGCACCTGCGCGCTCTTTGGCTTTCGGGAAATGGCAGTTCGATGTGTG 1481

Db 1224 GCATTCGCGGAACTGCTCTCTGCTGTGATTTGGTCTCCAGAAAGTGGCAGTATGATGTGTG 1283

Qy 1482 GTCCAAATGATGTACCCCTGGCCAAACCATGGAAGCAGAGAGCGGGCTGGCCCGCATCCA 1541

Db 1284 GTCTCATGATGTTACTCTGCGCAACACCATGGAAGCTGGAGAGTCCCTGGCGGTGTTCATCA 1343

Qy 1542 CATCATCTGGGCAACACTGACAGTACCTGCAAGGGGACTACGAAGTGGAGCAGCGCGGTGG 1601

Db 1344 CATTTCTTCAGTCACTCTGGAGCACTTGAATGGGGCTTATAAAGTGGAGAGAGATGG 1403

Qy 1602 TGGCAAGCGCAACGCTACCTCAAGGAGCAGCACAATTCAGACTTTCCCTCATCTGGCGC 1661

Db 1404 TGAGATAAGAGACCCATATTTAAAGCAGCACTTGGTGAACACCTACTTTGTAAT----- 1457

Qy 1662 CAGCCAGAAACGGAAGAGAGAAAGGCATGCTGGCCAAAGCTGCGAGGCTGCGGGCCAA 1721

Db 1458 -----CAATCCCAAGGAGAGCAGCGAGTCCCTCAGCATCTCTTCAGACCTCGACACAC 1511

Qy 1722 CTCCATGGAAGGCTGATGCGCGCATGGTTCCTGATGCTGCTTCCTCCCGGACCAAGA 1781

Db 1512 TCTGGAGGAGCCAGATGAGAGCATCTGTCCG-----CATGACCGGTACTTGA 1562

Qy 1782 CTCGAAGSCCTTCGCCAGATGGGCATTTGATGATTTCCAGCAAGAAACACCGGGCACCACA 1841

Db 1563 GTCCTGGGAGCAGCAAGCCATTCGCACATCTGCACACAGAGATAGCATGACCACAGA 1622

Qy 1842 AGATGCCCTGAACCTGAGGATGAGGTGATGTTCTGAGCCGTGCCATCGATGCGCG 1901

Db 1623 GAATGGGAAGATTAGTACCCAGGATGTGCCAATGGGTCAACATAATTTTCAAAATCGCAC 1682

Qy 1902 CAGCATTCAGCTGCGGAAGGACCATGTGCGCGGTTTTTTTGTGCTCACCTTCCAGAGAGA 1961

Db 1683 CTTAAGAACTAAGTCACAGAAAGAGAGATTTGAAGAAACATGAATGAAGAGATGATCCA 1742

Qy 1962 GGATTTTGAAGAAAGTACTCCCGAAGGTGGATCCCGCTTCGGAGCTACGTTGCGCTG 2021

Db 1743 AGCAATTCATGGGATCAATGCACAGAACCAATGGCTCAAGTCAGAAGACATTTCAAAGAAT 1802

Qy 2022 TGCCCTGTGTGCTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCACTCCAC 2081

Db 1803 CTCCTGCTTTTCTATAACAAGAATATAGAGAAAGAAATACCGAGCTACTGCACTCCACG 1862

Qy 2082 CTTGATG---CTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTTAATCACCGTCTGAT 2138

Db 1863 ATTCAGTACTACGTGACCTGCTGCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1922

Qy 2139 CTGTGCTGTG-----TACTCCTGTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2186

Db 1923 ACTTGTATTGCCAAAGAGCTCCATCTTGGCTTCTCTCTTTCAGAGTGCATTTCTCTCTCT 1982

Qy 2187 TCTGTCCCGCAGCATGTTCCCGCTCAGGGGACATAGACCCGAGTGGCATCTTTTCGCT 2246

Db 1983 CATCTTCATCCTCTTTGCTGCTTGGTGGACAGCTTTTGCATATGACGAAAAAGGCCTC 2042  
QY 2247 CTTGCTTGTGTTTACTTCTGCCATTTGCCAATGTTTACACCTGTAAACACACACCCOCCATACG 2306  
Db 2043 CACCTCTCATGTGGCTTTTGAATCATCAGGCATCATCGCCAAACCGCCCATGGCCAG 2102  
QY 2307 GAGCTGTGACGCCGATGCTGTAATTTAAACACCTGCTGACATCAGTCCCTGCGCACCTGCA 2366  
Db 2103 GATCTCCCTCACAAATGCTCACACCGCTATCATCTAACCATGGCTGTGTTCAACATGTT 2162  
QY 2367 GCAGCTCAATTTACTTCTGGGCTGGATGCTCCCTGTGTGGGACACCATGCCACCTG 2426  
Db 2163 TTTCTGAGCACTCTGAGAGACACCCCTCCACATGCCAATACATCAATGCAACGT 2222  
QY 2427 CAGCTTTCTGAGGTGCCATCGGGAACATGCTGCTGAGTCTCTTGGCCAGCTCTGTCTT 2486  
Db 2223 TTTCTGCCGGATAAACAGCGCTGATTTCTCATGCTCGAAACTGTGTTTTCTCCCGTA 2282  
QY 2487 CTTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGCTTTGGGGCTCATCTATTT 2546  
Db 2283 CTTTATATACAGCTGCTATCTCGGGCTTGATCTCTGCTCGGTTTTCTGAGGGTGAACATA 2342  
QY 2547 GGTGCTGCTTCTGCTGGTCCCCAGCGCCATCTTTGACAACTATGACCTACTGCTTGG 2606  
Db 2343 TGAGTTAAATGTTAATCATGATGGTGGCACTCGTGGGCTACAACACCATTTACTTCCA 2402  
QY 2607 CGTCCATGCTTGGCTTTCTTCCAAATGAGACCTTTTGTGAGCTGGACTGTCCAGCTGCAGG 2666  
Db 2403 CACCCATGCC---CATGTTCTGGATGGTACAGCCAGGCTCTGTTTCAGAGACAGGCAT 2459  
QY 2667 GAGGTGGCCCTCAATATATGACCCCTGTGATTTGCTGGTGTGCTGGCTGGCGTGGTA 2726  
Db 2460 TTGGAAGACCTGAAGACCATGGGCTCCGTGTCACTCTCCATATTTCTATCAGCTGCT 2519  
QY 2727 TCTGCTATGCTCAGCAGTGAATCGACTGCCCGCTTAACTTCTCTGGAACCTACAGGC 2786  
Db 2520 GGTCTTGGGCAGACAGTGAATTTACTGTAGTTAGATCTTCTGTGGAAGACAAGTT 2579  
QY 2787 AACAGGGGAAAAAGAGATGAGGAGCTACAGGCATACAAACCGGAGGCTGTGTCATAA 2846  
Db 2580 CAAAAAGAGCGGAGAGATGAACACCATGAGAACCTAAATCGAGTGTGCTGGAGAA 2639  
QY 2847 CATCTGCCAAGAGCTGGCGCCACTTCTGGCCCGGAGCGCCCAATGATGAAT 2906  
Db 2640 CGTGTCTTGCACAGCTGGCTGAACACTTCTCGGCGAGAGGCTGAAAAATGAGGAGCT 2699  
QY 2907 CTACTATCAGTCTGTGAGTGTGGCTGTATGTTTGCCTCCATTTGCCAACTTCTCTGA 2966  
Db 2700 GTACCACCACTCTACGACTGTCTGTGTCATGTTTGCCTCCATTCGCGACTTCRAGGA 2759  
QY 2967 GTTCTATGAGCTGGAGGCAACAAATGAGGTGGCGAGTGGCTGGCGTGTCTCAACGA 3026  
Db 2760 GTTCTACACAGTTCAGATGTGAACAAGGAAGGCTTGAATGCTGCGGCTCTGGAATGA 2819  
QY 3027 GATCATGCTGACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3086  
Db 2820 GATCATGCTGACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2879  
QY 3087 CAAGAGATTTGGTAGCACTTACATGCTGCTCAGGCTGAACGCCAGCACCTACGATCA 3146  
Db 2880 CAAGACCATTTGGAGCACATACATGCGCAGCCAGGACTGAGTGCCATACCCAGCCAGGA 2939  
QY 3147 GGTGGGCT-----GCTCCCATCATCTGCCCCTGGCTGACTACGCCAT 3188  
Db 2940 GCAGGCCCAAGAACCTGAGCGTCAATATGATGATGATGATGATGATGATGATGATGATGAT 2999  
QY 3189 GCGGCTCATGAGCAGATGAGCACATCAATGAGCACTCTCTCAACAAATTTCCAGATGA 3248  
Db 3000 TGCCCTTGGTGGGAAACTGATGCCATTAATAAGCACTCTCTCAACGACTTTCAAACTGGC 3059  
QY 3249 GATTGGGCTGAACATGGGCCAGTCGTCGTCAGGTGTCTATCGGGGCTCGGAAGCCACAGTA 3308  
Db 3060 AGTGGGTATCAACCATGGGCTCTAATAGCTGGCGTCATAGGGGCTCAAAAGCCACAGTA 3119

QY 3309 TGACATCTGGGGAAACACACAGTGAATGTCTAGTCTGATGACAGACAGGGGGTCCCCGA 3368  
Db 3120 TGACATCTGGGGAAACACACTGTCAACGTGGCCAGCAGAATGACAGACCGGGGTCTCTGGA 3179  
QY 3369 CCGAATCCAGGTGACACAGGACCTGTACAGGTCTTASCTGCCAAGGGCTACCAAGCTGGA 3428  
Db 3180 CAAAATACAGGTGACTGAGGAGACAAGCCTCATCTTGCAGACGCTTGGCTACACGTGTAC 3239  
QY 3429 GTGTGAGGGGTGTCAAGGTGAAGGCAAGGGGAGATGACCACTACTTCTCTCAA 3485  
Db 3240 ATGTGAGGTATCATCAATGTGAAGGGAAGGGACCTGAAGACATATTTGTAAA 3296

RESULT 8  
US-10-305-720-1344  
; Sequence 1344, Application US/10305720  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Express  
; FILE REFERENCE: PA-0002-1 CON  
; CURRENT APPLICATION NUMBER: US/10/305,720  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: 09/016,434  
; PRIOR FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 1490  
; SOFTWARE: PERL Program  
; SEQ ID NO 1344  
; LENGTH: 2731  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: GenBank ID No: g349268  
US-10-305-720-1344

Query Match 12.7%; Score 452.4; DB 6; Length 2731;  
Best Local Similarity 52.3%; Pred. No. 1.8e-93;  
Matches 1274; Conservative 0; Mismatches 1046; Indels 114; Gaps 8;

QY 1064 AAGAAGACATCAACACAAAAAAGAACATGTTCCACAAGATCTACATACAGAAAGCATG 1123  
Db 1 AAGAGGACTTCTGAAGCCCTGAGAGGATTTTCCACAGATTTACATCCAGAGGACG 60  
QY 1124 AATATGTCAGATCTGTTTGGCAGACATTTGAGGCTTTACACAGCTTGCATGCCAGTGA 1183  
Db 61 ACAATGTGAGCATCTGTTTGTCTGACATCGTGGGTTTTCAGGGGCTTGGCATCCCAAGTGA 120  
QY 1184 CTGCGCAGGAGCTGGTCAATGACCTGAATGAGCTCTTTGCCCGTTTGCACAAAGCTGCTG 1243  
Db 121 CAGCCAGGAGCTGGTGAAGACTCTCAATGAGCTCTTTCGCAAGTTTCGATGAATAGCCA 180  
QY 1244 CGGAGATCACTGCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGC 1303  
Db 181 CGGAGAACCATCTGCGCCGCATCAAGATTTCTGGGGACTGCTACTACTGCGTGGGCC 240  
QY 1304 TGGCGGAGGCCGGCGCAGCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTG 1363  
Db 241 TCACCCAGCCCAAGACTGACCATGCCCACTGCTGTGTGGAGATGGGACTCCACATGATTG 300  
QY 1364 AGGCCATCTCGCTGGTACGTGAGGTGACAGTGTGAATGTGAACATCGGCTGGGCTGCC 1423  
Db 301 ATACCATCATCTGTGGCTGAAGCCACGAGGTGGATCTGAACATCGGCTGGGCTTGC 360  
QY 1424 ACAGCGGCGCGTGCATCTGGCGGCTCTTGGCTTTCGGAATAGCAGTTGATGTGTGGT 1483  
Db 361 ACAGCGCAGGGTCTCTGTGGTCTCTGGCTTGGCCAAAGTGGCAGTGGCAGCTGTGGT 420  
QY 1484 CCAATGATGTACCTTGGCCCAACCATGGAAGCAGGAAGCCGGGCTGGCGGCTCCACA 1543  
Db 421 CCAATGATGTGACCTTGGCCCAATGTCATGGAAGCCGCTGGCCTGCCAGGAAGTTTCATA 480  
QY 1544 TCACTCGGCGCAACACTCCAGTACCTGAAACGGGGACTACGAAGTGGAGCCAGGCCCTGGTG 1603

Db 481 TCACAAAGACGACCTAGCGTGTGTTGAATGGGACTACGAGGTAGAACC GGTTTACGGAC 540  
Qy 1604 GCAAGCCGAACGGCTAGCTCAAGGAGCAGCACATTTGAGACTTTCCTCATCTCTGGCGCCA 1663  
Db 541 ATGAGAGGAACAGTTCTTGAAGAACTCATACATTCGAACCTTTTATTTGTCGCATCCC 600  
Qy 1664 GCCAGAAACGGAAGAGAGAGAAAGGCATGCTGGCCAAAGCTGCAGCGAGCTCGGGCCAAC 1723  
Db 601 ATCCGCCAAAGATATTTCCAGGCGCTGATCTCTCAGATATAAAA- - - - -CCGSCCAAAA 654  
Qy 1724 CCATGGGAAGGCTGATCGCGGATGGGTTCCTGATCTGCTTCCTCCGGACCAAGACT 1783  
Db 655 GGATGAAGTTCAAGACTGTCTGCTACCTGTGTTGCTGAGCTCATGCATGTCGCGGAATATGT 714  
Qy 1784 CCAAGGCTTCCGCGCAGATGGCATTTGATGATTCACGAAAGCAACCGGGGCACCCAAAG 1843  
Db 715 TCAGGCGGAGATCCCTTCTCCNAATGTCATGACTCGGAGGACA- - - - - 760  
Qy 1844 ATGCCCTGAACCCCTGAGGATGAGTGGATGAGTTCTTGAGCCGTGCCATCGATCCCGCA 1903  
Db 761 - - - - -TGACAAAGCGGAGGCGATTAGAAACAGCTCGGAAAAACTCAGAAACCGCTCA 812  
Qy 1904 GCATTGATCAGCTCGGGAAGACCATGTGCGCGGTTTGTGCTCACCTTCCAGAGAGAGG 1963  
Db 813 TCTTTTCTTACCAACG- - - - -TTGCTACACACCCCGGGCACTC 852  
Qy 1964 ATTTTGAGAAAGTACTCCCGGAAGGTGGATCCCGCTTCGGAGCGCTACGTTGCCCTGTG 2023  
Db 853 GCGTCAACAGGTACATCAGCGGCTCTTAGAAGCCCGCCAGACAG- - - - -AGCTGGAGATGG 909  
Qy 2024 CCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTTAATTTTCCACACTCCACCC 2083  
Db 910 CAGACCTGAACCTTTTACCTGAAGTACAAACATGTGCAACGGGAGCAAAAGTACCACC 969  
Qy 2084 TGATGCTTGGGATTTATGCCAGCATCTCTGCTGCTGCTAACTACACGCTGCTGATCTGTG 2143  
Db 970 AGCTTCAGGAGAGATTTTACCAGCGCGGTGTGCTTACCGCTCATCTGCTGCTGCTTAT 1029  
Qy 2144 CTGTGTACTCCTGTGGTCTCTGTTCCTTAAGGCCCTGCAACGCTCTCCCGCAGCATG 2203  
Db 1030 TTGGCTTGTCTACCTTCTAATATTCACACAGAGTGGTGGTCTGCTCC- - - - - 1080  
Qy 2204 TCCGCTCAGGGCACATPAGCAGCGAGTTGGCATCTTTTCCGCTGCTGCTGTTTACTT 2263  
Db 1081 - - - - -TGCTAGTATTCTGCATCTGCTTCCGCTGCTGCTGCTGCT 1113  
Qy 2264 CTGCATTGCCAACATGTTCACTGTAAACACACACCCCATACGAGCTGTGCACCCCGGA 2323  
Db 1114 GTGTCTGTACTGCGACATCACCCGGTCCAGTGTTTTCCAGGGTGGCTGACGATTCAGA 1173  
Qy 2324 TGCTGAATTTAAACACCTGCTGACATCACTGCCTGCCACCTGCACAGCTCAATTTACTCTC 2383  
Db 1174 TTCGACTGTCTGTGATTTTCATAGTGTCTTAATCTACTAGTAGCCCAAGGTTGTG 1233  
Qy 2384 TGGCCCTGGATGTCCCTGTGTGAGGGCACCATGCGCCACCTGCGAGTTTTCCTGAGGTGT 2443  
Db 1234 TGTTGGCTGCCTTGGCTTGGGCTTGGAGTCCAAAGCCCAACAGTTCCCTGCTGCTGCTT 1293  
Qy 2444 CCATCGGGAACATGCTGCTGATCTCTTGGCCAGCTCTGCTTCTTCCATGCATCAGACGA 2503  
Db 1294 CGTCTGGGGCCAGC- - - - -GCACAGCCCTGGCCACCCCTGCCCTGGAGTCT 1340  
Qy 2504 TCGGGAAGTTGGCCATGATCTTGTCTTGGGCTTCATCTATTGGTGTGCTTCTGCTGG 2563  
Db 1341 ACACACCATGCCCTGCTGCTGCTGGTGGGACCCCTCCCGCTAGCCATATTTTCCGG 1400  
Qy 2564 GTCCCCAGCGCGCATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTT 2623  
Db 1401 GTGTCTCTTGTGCCAAAAATGATCTGCTCTCCGGGCTCACCACTGCTTACATCCTGTT 1460  
Qy 2624 CTTCCATGAGACCTTTGATGGGTGGACTGTCTCCAGCTTGAGGGAGGGTGGCCCTCAAT 2683

Db 1461 CTGGAGCTCAGCGGATACACCAGG- - - - -ACTGGGGTGGTGCCTCTCCGGGCGCAGCT 1515  
Qy 2684 ATATTACCCCTGTGATTTCTGCTGGTGTGCTGGCTGTATCTGATGCTCAGCAGG 2743  
Db 1516 ACGAGCCGATTGTGGCCATCTCTCTTCTCTGTGCGCTGGCCTGCTGCCAGCAGG 1575  
Qy 2744 TGGAACTCGACTCCCGGCTAAACTTCCCTCTCTGAAACTACAGGCAACAGGAAAAAGAGG 2803  
Db 1576 TGGACATCAGGCTGAGGCTGGACTTACCTTGGCGCGCACAGCAGAGGAGCGAGAGG 1635  
Qy 2804 AGATGGAGGACTACAGGCATACAAACCGAGGCTGCTCCATACAACTTCTGCCAAGGAGG 2863  
Db 1636 ACATGGGAAGGTGAAGCTGGACAACAGCGCATCTCTTCAACCTCTCTCGGCGCCACG 1695  
Qy 2864 TGGCGGCCACTTCTCTGCGCGGAGCGCCCAATGATGAACCTCTTACTATCAGTCTGTG 2923  
Db 1696 TCGCCAGCACTTCTCTCATGTCTCAACCTCGGAACATGAGCTTACTTACCAGTCTACT 1755  
Qy 2924 AGTGTGGCTGTATGTTTGCCTCCATTTGCTCAACTTCTCTGAGTCTTATGTGGAGCTGG 2983  
Db 1756 CCCAGGTGGGCTCATGTTTGCCTCCATCCCACTTCAATGACTTCTACATCGAGCTGG 1815  
Qy 2984 AGGCAACAATGAGGTCGCGAGTGCCTGCGGCTGCTCAACGAGATCATCTGACTGTTG 3043  
Db 1816 ACGCAACAACATGGGGTGGAGTGTCTGCGGCTTCTCAACGAGATCATCTCCCGACTTTG 1875  
Qy 3044 ATGAGATTATCAGCAGGAGCGGTTCCGCGAGCTGGAAAAAGATCAAGAGATTGTTAGCA 3103  
Db 1876 ACGAGCTCATGGAANAAGACTTTTACAAGACATAGAAAGATCAAGACCATCGGGAGCA 1935  
Qy 3104 CCTACATGGCTGCCTCAGGCTGAACGCC- - - - -AGCACCTTACGATCAGSTGGGCC 3154  
Db 1936 CCTACATGGCGCTGTGGGCTAGCGCCACCTCGGGGACCAAGGCTAAGAAGTCCATCT 1995  
Qy 3155 GCTCCACATCACTGCCCTGCTGACTAGCCATCGGCTCATGAGCAGATGAAGCACA 3214  
Db 1996 CCTCCCACTGAGCAGCTGCGGACTTTCCTTGGATGATGTTGACCTTCTGGATGAAA 2055  
Qy 3215 TCAATGAGCACTCCTTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGGCCAGTCG 3274  
Db 2056 TCAACTACCACTCTTACAACGACTTTGTCTCCGAGTTGGCATCAATCTTGGCCTGTGG 2115  
Qy 3275 TGGCAGTGTCTATCGGGCTCGGAAGCCACAGTATGACATCTGGGGGAACACAGTGAATG 3334  
Db 2116 TGGCTGGAGTGAITGGGCTCGCAGGCCAGTAGACATCTGGGGAACACAGTCAACG 2175  
Qy 3335 TCTCTAGTCTGATGACAGCACGGGGTCCCGCAGCGAATCCAGTGAACACGAGCTCT 3394  
Db 2176 TGGCCAGTCGGATGATAGCAGGGGTCCAGGGCAGATCCAGTGAAGTCC 2235  
Qy 3395 ACCAGTTCTAGCTGCCAAGGGCTACAGCTGGAGTGTGCGAGGGTGTCAAGGTGAAGG 3454  
Db 2236 ACCGCTGCTGAGAAGGTGCCCTTACCATTGTTGTCGCGAGGCAAGTCAAGTGTCAAG 2295  
Qy 3455 GCAAGGGGAGATACCACTTACTTCTCAATGG 3488  
Db 2296 GCAAAGCGAGATGTTGACATACTTCTTAGAAGG 2329

## RESULT 9

US-10-144-771-18424  
; Sequence 18424, Application US/10144771  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF  
; FILE REFERENCE: CL001321  
; CURRENT APPLICATION NUMBER: US/10/144,771  
; CURRENT FILING DATE: 2002-05-15  
; NUMBER OF SEQ ID NOS: 47235  
; SEQ ID NO 18424  
; LENGTH: 5124  
; TYPE: DNA  
; ORGANISM: HUMAN

US-10-144-771-18424

Query Match		12.2%; Score 432.4; DB 6; Length 5124;
Best Local Similarity		51.1%; Pred. No. 8.6e-89;
Matches 1434; Conservative		0; Mismatches 1221; Indels 149; Gaps 12;
QY	853	CTCTGGAAGCAGTCCGGTGCATATGCTGCTCTCTCTGCAACCAAGCATATAGCATC 912
DB	1136	CTGGGGCTGCAGCTCCTGGCCAAATGCGGTATATCTCTCTGGGTGGGAATTCACGGGTGCC 1195
QY	913	TGCACACACTATCCAGCAGAGGTGCTCTACGCCAGGCCCTTCAGGAGACCCGAGTTAC 972
DB	1196	TTCCAAAGCACCAGTGTCCAGGAGCGGTCCAGGGATCTCTTTATCTACACCGTCAATGC 1255
QY	973	ATCCAGGCCCGCTCCACCTGCAAGCATGAGAATCGGCAGCAGAGCGGCTGCTGCTGCG 1032
DB	1256	ATCCAGATCCGTGCGAAGCTTCGTGTGGAGAAGCGCCAGCAGAGAACCTGCTCTCTGCA 1315
QY	1033	GTATTTGCCCAGCAGCTTGGCATGGAGATGAAGAAGACATCA----- 1075
DB	1316	GTGCTCCAGCACACATCTCCATGGGTATGAAGCTGGCCATCATTTGAGCGCCTCAAGAG 1375
QY	1076	-----ACACAAAAAAGAGACATGTTCCACAGATCTACATACAGAGCAT 1122
DB	1376	GGTGGTACCGACACATACATGCCCCGACAACTTTTCACAGCCTCTATGTCAAGCGGCAC 1435
QY	1123	GACAATGTACAGCATCTCTGTTTGGAGACATTTAGGGGCTTACACAGCCTGGCATCCCACTGC 1182
DB	1436	CAGANTGTACGATCTTGATGATGACAGATCGTGGGCTTACAGAGGCTGGCCAGGACTGC 1495
QY	1183	ACTGGCAGGAGTGGTTCATGACCCCTGAATGAGCTCTTTTCCCGGTTTGAACAGCTGGCT 1242
DB	1496	TCCTCCAAAGAGAGCTGGTGGTGGCTCAACAGAGCTGTTTGGGAAGTGTGACCAAGATTGCT 1555
QY	1243	GCGAGAAATCACTGCCTGAGGATCAAGATCTTGGGAGCTGTTACTCTGTGTACAGGG 1302
DB	1556	AAGGCCAATGAGTGATGCGGGATCAAGATCCTGGGTGACTGTTACTACTCGGTGTACGGC 1615
QY	1303	CTCCGAGAGCCCGGCGGACCATGCCACTGCTGTGTGAGATGGGGGTAGACATGATT 1362
DB	1616	CTGCCGTGTGCTGCCACACATGCCGCAACTGTGTGAAGATGGGTCTGGACATCTGC 1675
QY	1363	GAGGCCATCTCGTGGTACGTGAGGTGACAGGTGTGAATGTGAACATGCCCGTGGGATC 1422
DB	1676	GAGGCCATTAAGCAGAGTGGCTGAGGCCACGGGCTGGACATCAGCATGCGTGTGGGCATT 1735
QY	1423	CACAGCGGCGCTGCACTCGCGCTCTCTTGGCTTGGGAAATGGCAGTTCGATGTGTGG 1482
DB	1736	CACTCCGGGAATGTGCTATGTGGGTATCGGGCTCGGTAAAGTGGCAGTATGTGTGG 1795
QY	1483	TCCAATGATGACCTTGGCCACCAATGGAAGCAGGAAGCCGGGCTGCCCGCATCCAC 1542
DB	1796	TCCCATGATGTGCTCCCTGGCCAAACAGGATGGAGCAGCTGGAGTCCCTGGCGGGTGCAC 1855
QY	1543	ATCACTGGGCAACACTGCACTGAGTGAAGCGGACTACCAAGTGGAGCGGCGGTGGT 1602
DB	1856	ATCACAGAGCAACATTTGAATCACTTGGCAAGGCATACGAGGTGGAGGATGGGCATGGG 1915
QY	1603	GGCAAGCGCAACCGTACCTCAAGGACGACATTTGAGACTTTCCATCTCTGGGGGCC 1662
DB	1916	GAGCAGGAGACCCCTATCTTGAAGAGATGAACATCGGAACCTACCTGGTGTGATCGATCCC 1975
QY	1663	AGCCAGAAACGGAAGAGGAGAGGATGCT-----GGCCAAAGCTGCACGCGACT 1713
DB	1976	CGGAGCCAGCAGCACCACCCACCCAGCCACCTCTCCAAAGCCCAAGGGGAGCGCAACT 2035
QY	1714	CGGGCCAACTTCCATGGAAGGGCTGATGCCCGGATGGGTTCCCTGATGCTGCTTCTCCCGG 1773
DB	2036	CTGAAGATGGGGCTTCAGTGGCTGTAAACCCGCTATCTGGAGTCTTGGGGGCGAGCAAGG 2095
QY	1774	ACCAAGGACTTCAAGGCTTCCGCCACA---TGGGCATTGATGATTCACCAAGACAAC 1830
DB	2096	CCCTTTTGACACCTCAACCAACCGGAGAGTGTGAGCAGAGTGAACCCCGCTCTCTCCAAT 2155

QY	1831	CGGGGCAACCAAGATGCCCT----- 1850
DB	2156	GGACGGAGGCAAGAGGCCATTCTCTCGCTGCACACCGTGCCTCTAGTAGAGTGCATCC 2215
QY	1851	-----GAACCCCTGAGGATGAGTGGATGAGTTCCTTGAGCGGTGCCATCGATGCCCGCA 1903
DB	2216	CCCAAGGGCGCTTGGAGATGACTGTGATCAGGAGATGCTGTACAGCCATTTGAGGGTCTCA 2275
QY	1904	GCATTGATCAGCTGCG-----GAAGGACCATGTCGCCCGGTTTTTGTCTCACTTCC 1954
DB	2276	CTCCACCAAGCCCTGCTGCTCCAAAGTCTGATGACTTCCACACCTTTGGTTCCTATCTCT 2335
QY	1955	AGAGAGAGGATTTTGAAGAAGTACTTCCCGGAAGTGGATCCCGCTTCGGAGCCCTACG 2014
DB	2336	TGAGAAGAGGCTTTGAGCGTGAATACCGCTGTGTGCCCATCCCGCGGCTCGCTACGACT 2395
QY	2015	TTGCTGTGCCCTGTGGTCTCTGCTTCATCTGCTTCATCCAGCTTCCTAATTTTCCAC 2074
DB	2396	TCGCCCTGTGCCAGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2455
QY	2075	ACTCCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCCCTGCTGCTGCTGCTGCTGCTGCT 2134
DB	2456	GGATGGCAACTCTGGGTGCTGCTTTGGGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2515
QY	2135	TGATCTGTGCTGTACTCTCTGCTGTGCTTCTGCTTCCCTAAAGGCCCTGCAACGCTGTGCC 2194
DB	2516	GTCTCTG-----CTTTGCTACTGAGTCTCGAGTGTCTTCCATCCCGAAGTA 2563
QY	2195	GCAGCATTTGCCCTCAGGGCAGATAGCAGCGGAGTTGGCATCTTTTCCGCTCTGCTGCTG 2254
DB	2564	CACCTCCAGGCCATCTCGAGAGCGTGGAGAGCGCAGGCCCTTGGTCAGGCTTGTCTGCTGCTG 2623
QY	2255	TGTTTACTTCTGCAATGGCCAACTGTTACCTGTGAACACACACCCCATACGGAGCTGTG 2314
DB	2624	TGCTGACTGTGGCAGCTACTGACTGTGCCCATCATTAACATGCCACTGACGCTTAACC 2683
QY	2315	CAGCCCGGATGCTGAATTTAACACCTGCTGCAATCACTGCTGCTGCTGCTGCTGCTGCTGCTG 2374
DB	2684	CAGGCCAGAGCAG-----CCTGGAGACAACAAGAACAGCCACCTGGCTGCACAGA 2734
QY	2375	ATTACTCTCTGGGCTGGATGCTCCCTGTGTGAGGACCATGTCACCTGCGAGCTGCTGCTGCTG 2434
DB	2735	ACAGAGTGGAGACCCCATGTGAGCTCCTCCCGTACTACACTGCGAGCTGCACTGCTGGGCT 2794
QY	2435	CTGAGTGTCCATCGGGAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2494
DB	2795	TCATTGCACTCTGTTTTCTCGGGATGAGCCTAGAGCTGAAGGCCATGCTGCTGACAG 2854
QY	2495	TCAGCAGCATCGGGAAGTTGGCCATGATCTTTGCTTTGGGGCTCATCTATTTGGTGTGCTG 2554
DB	2855	TGGCCTTGGTGGCTACCTGCTGCTTCAACCTCTCCCATGCTGCGACGT-CTCAGGC 2913
QY	2555	TTCTGCTGGTTCCTCCAGCGCCATCTTTGACAACTATGACCTACTGCTGCTGGCTGCTGCTG 2614
DB	2914	AACAGACTGAGACCAACGGGACACAAGAGCAGGGCTG--CTCCTGTCTGATGCACAAA 2971
QY	2615	GCTTGGCTTCTTCAATGAGACCTTTTGGGCTGGAGCTTCCAGCTGCGAGGAG----- 2669
DB	2972	GCATGCCACCCACACCTTGTCTCCGGGGCTCGGGAGACTGCCCTTCTCCCACTTATT 3031
QY	2670	-----GGTGGCCCTCAAAATATATGACCCCTGTGATTTCTGCTGGTGTGCTGGCTGGCTGT 2725
DB	3032	TAGAGAGAGACCTGAACATCATGTTAACTTCTACCTGATGCTCTTCTATGCCACCTCA 3091
QY	2726	ATCTGATGCTCAGCAGGTGAATCGACTGCCCGCCTAAACTCTCTGGAACACTACAGG 2785
DB	3092	TCTTGTGCTAGACAGATTGACTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3151
QY	2786	CAACAGGGGAAAAGAGCAGATGGAGGCTTACAGGCATACAAACCGGAGGCTGCTGCTGCTG 2845
DB	3152	TCAAAAGGAGCAGGAGGATTTGAACAATGGAGAATGTGAACCCGCTCTCTCTGAGAGA 3211









Db 724 ATGTCTACTATATGGCAGACCGCAAGCAGCGAGGCTTCTTGGAGGCGCCGACATCA 783  
Qy 973 ATCCAGGCGCGCTCCACCTGCACGATGAGAAATCGGAGCAGGAGCGGCTGCTGCTGCG 1032  
Db 784 CTGAGGTGAAGATGAATCTGGAGGACGAGCAGCAGCAGGAAACCTTATGCTTCC 843  
Qy 1033 GTATTGCCCCAGCAGCTTGC-----CATGGAGATGAAGAAGACATCAACACA 1080  
Db 844 ATCTGCCCCAAGCAGCTGGCTGAGGAGATGCTGAAGACATGAAGAAGCAGAGGCCAG 903  
Qy 1081 AAAAAGAAGACATGTTCCAAAGATCTACATACAGAGCATGACATGTCAAGCATCTG 1140  
Db 904 AAGACAGCAGCAGCTCAATATACATGATGATGATGATGATGATGATGATGATGATGAT 963  
Qy 1141 TTTGCAGACATGTAGGGCTTCAACAGCTGGCATCCAGTCCAGTCCAGTCCAGTCCAGTCC 1200  
Db 964 TTTGCAGATATTGGGGCTTTACCCAGCTGCTCTGCTTGCAGTGGCCAGGAGCTCGT 1023  
Qy 1201 ATGACCTGAATGAGCTCTTTGCGCGGTTTGACAAGCTGGCTGGGAGAAATCACTGCTG 1260  
Db 1024 AAGTTACTCAACAGAGCTCTTGCCTGGCTTTGACAAGCTGGCAGCACAATACACAGCTG 1083  
Qy 1261 AGGATCAAGATCTTGGGGAGCTGTTACTACTGTGTGTCAGGCTGCGGAGGCGCGGCC 1320  
Db 1084 AGGATCAAGATCTTGGGGAGCTGTTACTACTGTGTGTCAGGCTGCGGCTGCGGCTGCT 1143  
Qy 1321 GACCATGCCACTGCTGTGTGGAGTGGGGTAGACATGATTGAGGCCATCTCGCTGCTGA 1380  
Db 1144 GACCATGCCGTGCTCCATCTTATGGGCTTCCATGATGATGATGATGATGATGATGATG 1203  
Qy 1381 CGTAGGTGAGCTGTGAATGTGAACATGCGCGTGGGATCCACAGGCGCGGTGTCAC 1440  
Db 1204 CGGAGAGACCAAGACTGGAGTGGACATGCGTGGGAGTGGCAGAGGCACTGTCTCA 1263  
Qy 1441 TGGCGCTTCTGCTTGGGAAATGCAAGTTCGATGTGTGCTCCATGATGTGACCTG 1500  
Db 1264 GCGGCTGCTTGGGCGAGAGCGCTGGCAGTATGATGATGATGATGATGATGATGATGAT 1323  
Qy 1501 GCCAACCATGGAAGCAGGAGCGGGCTGGCGGCGATCCACATCACTCGGCGCAACACTG 1560  
Db 1324 GCAACAAGATGAGGCTGGTGGCATCCAGGCGCGTGCACATTTCCAGAGCACCATG 1383  
Qy 1561 CAGTACCTGAACGGGAGCTAGAGTGGAGCGAGCGCGTGTGGCAGCGCAACCGGTAC 1620  
Db 1384 GACTGCTTGAAGGGGAGTTGATGTGAGGCTGTGATGGGGCAGCTGCTGCGACTAC 1443  
Qy 1621 CTCAGGAGCAGCATGACATTTCTCATCTCTGGCGCC-AGCCAGAAACGAAAGA 1679  
Db 1444 CTAGATGAAGAGGCATCGAAACCTACCTCATATGCTCTCAAGCCAGAGGTGAAGAA 1503  
Qy 1680 GGAGAAAGGCATGCTGCCAAAGCTGCAGCGGACTCGGGCCCACTCCATGGAAGGCTGAT 1739  
Db 1504 ACAGCCCCAAATGGCTCAACGGCTGGCGCTGCGCAACAGGAGCGCGGCATCTCCAAA 1563  
Qy 1740 GCC-GCGATGGTTCCTGATGCTGCTTCTCCCGGACCAAGGACTCCAAAGGCTTCCGCC 1798  
Db 1564 CCCAGCTCCCTGCGCTCATCGAGACCAAGAGGCCAATGGAAGTGGCCATGCGCAGCGGC 1623  
Qy 1799 AGATGGGATTTGATTTCCAGCAAAAGCAACCGGGGCGCCCAAGATGCCCTGAAACCTG 1858  
Db 1624 TCCACATCAGAGAGGCTGAAGACAGAGGCGCCAGGCTGACACCCCTCGTTCGCCAAC 1683  
Qy 1859 AGGATGAGGTGGATGAG--TTCTGAGCGGTGCTCATGATGATGATGATGATGATGATGAT 1916  
Db 1684 CCCCAGGAGGCTGGCGCTCCAGGACCTGGCGGACCGCTGTGGTGGAGCGCTCTGAGGAT 1743  
Qy 1917 CGGAGGAGACCATGTCGCCCGGTTTTCCTGAGCGGTGCTCATGATGATGATGATGATGAT 1976  
Db 1744 GAGCACGAACCTGAACAGCTGCTTAATGAGGCGCTGCTGAGCGGAGTCCGCCAGGTG 1803  
Qy 1977 GTACTCCCGGAGGTGGATCCCGCTTCCGAGCGCTTACCTGCTGCTGCTGCTGCTGCTG 2034  
Db 1804 GTAAAGAGAGAAACACATTTCTCTCT---GACCATGAGGTTGATGGACCCAGAGATGGAA 1860

Qy 2035 TTCTGCTTCATCTGCTTATCCAGCTTCTAATTTTCCACACTCCACCTGATGCTTGGG 2094  
Db 1861 ACAGCTACTGCTGGTGGAG 1920  
Qy 2095 ATTTATGCGCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2154  
Db 1921 GTCCTCTTCTGACGGCATGCTGGAGATCACTATGACC-----CTGGCTGATG 1971  
Qy 2155 TGTGTTCTCTGTTCCCTTAAGGCCCTGCAACGCTGTCGCCGACAGATGTCGGTCAAGG 2214  
Db 1972 ACAACTATGAGACCTTGTGTTGGGAGGTTCTGCTCTGATCCTGACCATCTGCTCG 2031  
Qy 2215 GCACATGACACCGCAGTGGCATCTTTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2274  
Db 2032 ATGCTGCCATCTTTCCAGGTCATTTCCCAAGAAGCTTGTGGCTTCTCATCTTGGATT 2091  
Qy 2275 AACATGTTACCTGTAACACACACCCCATAGGAGCTGTGAGCCCGGATGCTGAATTA 2334  
Db 2092 GACCGGACCGCTGGCAAGAACACCTGGGCCATGTAGCCATCTTCAATCTGTTATG 2151  
Qy 2335 ACACCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAATTAATCTCTGCGGCTGAT 2394  
Db 2152 GCCAATGTTGGACATGCTCAGCTGTCTCAGTACTACATGGGACCTTACAACATGACA 2211  
Qy 2395 GCTCCCTGTGTGAGGACACCATGCCACCTGCAGCTTTTCTGAGGTGCTCATCGGAAAC 2454  
Db 2212 GCTGGATGGAGCTGGAGCGGCTGCATGGAGAAC---CCCAAGTACTACAACATACCTA 2268  
Qy 2455 ATGCTGCTGAGTCTTGGGCCAGCTGTCTTCTGACATCAAGCAGCATCGGAAGTTG 2514  
Db 2269 GCTGTGCTGCTCATCGCCACCATCATGCTGTGTGAGTCAAGTCAAGTCAAGTCAAG 2328  
Qy 2515 GCCATGATCTTGTCTTGGGCTCATCTATTTGTGTGCTGCTTCTGCTGGTCCCCCAGCC 2574  
Db 2329 ACGCTCATGCTGCTGCACAGGCGCGTGAATGCGCTCAACCTGCTAGCCCTGCTGCT 2388  
Qy 2575 GCCATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGCTTGGCTTCTTCCAATGAG 2634  
Db 2389 GTCCTTGTATGAATACGACCAAGCGCTTTCAGGAAAGGACAGGCTGCC----- 2438  
Qy 2635 ACCTTTGATGGGCTGGACTGTCAGCTGCAGGAGGCTGGCCCTCAATATATGACCCCT 2694  
Db 2439 -----CTGGTGGCTTCCAGTACTCCATGACT 2466  
Qy 2695 GTGATCTGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2754  
Db 2467 GTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2526  
Qy 2755 GCCCGCTTAACTTCTCTGGAACCTACAGGCAACAGGGGAAAGAGAGAGATGGAGAG 2814  
Db 2527 GCCCGAACACTGTTCTTGTGAAGATTGAGGTCCATGACCAAGAGAGAGAGAGAGAGAG 2586  
Qy 2815 CTACAGGATACACCGGAGCTGCTGCATAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 2874  
Db 2587 ATGCGCGATGGAAGAGGCTTGTGTCACCAACTGTTGCTGAGCATGTTGCGACGCCAT 2646  
Qy 2875 TTCTGGCGCGGAGCGCGCAATGATGAATCTACTATGCTGCTGCTGCTGCTGCTGCTGCT 2934  
Db 2647 TTTCTGGGCTCCAAAGAGAGATGAGGAGCTGTACAGCCAGTCTTATGACGAGATTGA 2706  
Qy 2935 GTTATGTTGCTCCATTTGCCAATCTTCTGAGTCTATGTTGGAGCTGGAGCAACAAT 2994  
Db 2707 GTCATGTTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2766  
Qy 2995 GAGGTGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3054  
Db 2767 GCGGATCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2826  
Qy 3055 AGCGAGGAGCGGTTCCGCGAGCTGGAAAGATCAAGAGGATTTGGTAGCACCTTACATGCT 3114  
Db 2827 GACATCCCAATTTCCGGTCTATCACCAGATCAAACTATTTGGCAGCACCTATATGSCA 2886

QY 3115 GCCTCAGGGCT-----GAAGCCAGC 3135  
Db GCTTCAGGAGTCACACAGATGTAACACCAATGGCTTTACAAAGCTCCAGCAAGGAGG 2946  
QY 3136 ACCTACCATCAGGTGGCCCTCCACATCAGTCCCTGCTGACTACGCGCATCGGCTC 3195  
Db AAGTCAGACAAGAGGCGCTGGCAGCACCTGGCTGACTGGCTGACTTTGGCATTAGCCATG 3006  
QY 3196 ATGAGCAGATGAAGCAGACATCAATGAGCACTCTCTTCAACAATTTCCAGATGAAGATTGGG 3255  
Db AAGGACAGCTCACAACATCAACAACCAAGTCAATCAACAATTCATGTTGCCATAGGC 3066  
QY 3256 CTGAACATGGCCCGAGTCGTGGCAGTGTCTATCGGGCTCGGAAGCCACAGATATGACATC 3315  
Db ATGAACAAGAGGGGTCTCTGGCTGGCTCATTTGGAGCCCGAAACACACACTATGACATC 3126  
QY 3316 TGGGGAAACACAGTATGCTCTAGTCTGATGGACAGCAGGGGCTCCCGACCGAATC 3375  
Db TGGGGCAATACGGTCAATGTGGCCAGCAGGATGGAATCCACAGGAGTCAATGGGCAACATC 3186  
QY 3376 CAGGTGACCACGAGCTGTACCAGTTTCTAGCTGCCAAGGGCTACCAGCTGGAGTGTGCA 3435  
Db CAGGTGTAGAGAGCGCAGGTCACTCTTCGAGAGTACGGCTTCCGCTTTGTGAGCGCA 3246  
QY 3436 GGGTGTCTAAGGTGAAGGCAAGGGGAGATGACACACCTACTTTCCTCAATGGGGGGCCC 3495  
Db GGTCCCATCTTTGTGAAGGCAAGGGGAGCTTGTGACCTTTTCTTTGAAGGGGCGGGAC 3306  
QY 3496 AG 3497  
Db 3307 AG 3308

RESULT 12  
US-10-144-771-3825  
; Sequence 3825, Application US/10144771  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craly  
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF  
; FILE REFERENCE: CL001321  
; CURRENT APPLICATION NUMBER: US/10/144,771  
; CURRENT FILING DATE: 2002-05-15  
; NUMBER OF SEQ ID NOS: 47235  
; SEQ ID NO 3825  
; LENGTH: 3458  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-144-771-3825

Query Match 11.6%; Score 410.8; DB 6; Length 3458;  
Best Local Similarity 50.4%; Pred. No. 6.5e-84;  
Matches 1380; Conservative 0; Mismatches 1227; Indels 133; Gaps 10;

QY 862 CAGCTCGTCCCAATGCTGCTTCTCTGCACCAACGTCATAGCATCTGCACAC 921  
Db CAGTTGTCAGCAACACGGGTATTGTTCTCTGTGGGACATGGTGGAGCGCTACCAAG 688  
QY 922 TATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAGACCCGCGAGTTACATCCAGGCC 981  
Db GCCCTGATGAGCGAGCATTTGGGGCCACGTTCCGGGAGGCTCTTAGCTCTCTGCATCA 748  
QY 982 CGGTTCACCTCGCAGCATGAGATGCGCAGCAGAGCGGCTGCTGCTCGGTATTGCC 1041  
Db CGCGCGGAGGTGGACACTGAGAAAAAGCACAGGACACCTCTCTGCTATCTCTTCT 808  
QY 1042 CAGCAGCTTCCCATGGAGATGAAGAGACATCAAC----- 1077  
Db GCCTACTGCGCCGAGATGAAGAGACAGATCATGGCCCGGCTGCAGGCTGGACAGCGC 868  
QY 1078 -----ACAAAAAAGAGACATGTTCCACCAAGATCTACATACAGAGCATGACAAATGTC 1131  
Db TCAGGGCCAGAGAACCAAACTTTTCACAGCCTGTATCTCAAGAGGCGCAAGGAGTG 928

QY 1132 AGCATCTCTGTTTCAGACATTTGAGGGCTTCCACGAGCCTGGCATCCAGTGCATGCGCAG 1191  
Db AGTGTGCTGTATGCTGACATCGTGGGCTTTCACGCGGCTGGCCAGCGAGTGTTCGCCGAAG 988  
QY 1192 GAGCTGGTCAATGACCCCTGAATGAGCTCTTTTCCCGGTTTTCACAGAGCTGGCTGCGGAGAAT 1251  
Db GAGCTGGTGTCTGCTGCTGAATGAGCTCTTTTGGCAAGTTCGACCAAAATGGCAAGAGCAC 1048  
QY 1252 CAGTGCCTGAGGATCAAGATCTTGGGGAGCTGTTACTACTGTGTGTCAGGSGCTCCGGAG 1311  
Db GAATGATGCGGATCAAGATCTTGGGAGACTGTTACTACTGTGTGCTCCGGGCTGCCCTC 1108  
QY 1312 GCCCGGGCCGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGATTTGAGGCCATC 1371  
Db TCCTGCTGCTGACCAAGCTATCAATTTGTCGCATGGGCTGGACATGTCCCGSGCCATC 1168  
QY 1372 TCCTGCTGCTGAGGTGACAGGTGTGAATGTGAACATGCGGCTGGGCGCATCCACAGCGG 1431  
Db AGAAATCTTCGGGTAGCACCGGCTGTGGATATCAACATGCTGTGGCGCTGCATCTCGGGC 1228  
QY 1432 CGCTGCTGCTGCGGCTTTCGCGAAATGGCAGTTTCGATGTGTGCTGCTCAATGAT 1491  
Db AGCTTCTCTGCTGAGTCAATTTGGCTACAGAAGTGGCAGTATGATGCTGCTGCCATGAT 1288  
QY 1492 GTGACCTTGCCCAACACATGGAAGAGAGAGCGGCTGCGCGCATPCCACATCACTCGG 1551  
Db GTCACATTTGGCCCAACCATATGGAAGAGAGCGGCTGTACAGGAGAGTGCACATCACAGG 1348  
QY 1552 GCAACACTGCAGTACCTGAACGGGCTAGCAAGTGGAGCGGCTGTGTGGCAAGCGC 1611  
Db GCCACGCTGGCCCTGTAGCAGGAGCTTATGCTGTGGAGAGGCGACACAGGAAACCCGA 1408  
QY 1612 AACCGCTTACCTCAAGGAGCAGCACATTTGAGACTTTCCTCATCTCTGGCGCGCAGCAAAA 1671  
Db GACCCATACCTTCGGGAGCTAGGAGAACCTACATACCTGCTGCTGCTCGGGCTGAG 1468  
QY 1672 CGGAAGAGAGAGAGAGCATGCTGGCCCAAGCTGAGCGGAGCTCGGGCCAACTCATGAGAA 1731  
Db GAGGAAGACAGAGAGGAGCGACCCGCAAAAGAGATGCTGCTCTCTGGAGGGGCGACAGATG 1528  
QY 1732 GGGCTGATGCGCGGATGGGTTCTGATGCTGCTTCCCGGAGCTTCCCGGAGCTTCCAAAG 1788  
Db CTGCGCTCACTACTGATGACTCGCTATCTGAGTCTTGGGCTGCAGCCAGCCCTTTCGCC 1588  
QY 1789 GCCTTCCGCCAGATGGGCATTTGATATTC----- 1818  
Db CACCTAAGCCACCTTGACAGTCCGCTGTCCACCTCCACTCCACTCCCGGAGAAAGCCTTC 1648  
QY 1819 -----AGCAAGACACCGGGGCAACCAAGATGCCCTGAACCTCTGA---GGAT 1863  
Db AGCCCCCAGTGGAGCCTTGGACCGAGTGCACACCCCGGGGAGCTAGATGATGAACCTGGAC 1708  
QY 1864 GAGTGGATCAGTTCTCTGACCGTGCATCGATGCCCGCAGCATTTGATGAGTGCAGGAG 1923  
Db ACTGGTGTATCTAAGTTCTTCCAGGTCTCGAACAACTCACTCTCAGAGATGAGAAGC 1768  
QY 1924 GACCATGTGCGCGGTTTTCCTCACCTTCCAGAGAGAGGATTTTGGAGAAAGTACTCC 1983  
Db CAGAGGCTGGAAGCCCAATGGTGTGTGGAGAGGTGGAAGCAGTGCAGAGGACTTC 1828  
QY 1984 CGGAAGTGGATCCCGCTTCGGAGCCTAGTTGCGCTGTCGCCCTGTGTTGCTTCTGCTTC 2043  
Db AACCTCTGACGCTGATTTTCAGAGAGAGGAGATGGAGAAACAGTATCGGCTCTCTGCA 1888  
QY 2044 ATCTGCTTTCACAGCTTCTAATTTTCCACACTCCACCTGATGCTGGGATTTATGCC 2103  
Db CTCCCGCCTTCAA-----ATACTAGCAGCCTGACCTTCTCTGTTTCTGTCTCAAC 1942  
QY 2104 AGCATCTTCTGCTGCTGCTTAATCAGCGTGTGATGCTGCTGTGATCTCTCTCTGTTG--- 2159  
Db TTCATCTATCCAAATGCTGGTGACAACCCAGGCCCGCCAGCTCTGATCATCACTACAGCATC 2002  
QY 2160 -----TTCTCTGTTCCCTAAGCCCTGCAACGTCTGTGCCGAGCATTTGTCCGCTCAC 2212

Db	3072	TGGAGTCTATCAACAGCACTCGTTCAATACTTCGGCTCGGTGGGGTGTGAACCAAG	3132
Qy	3266	GCCCAAGTCGTGGCAGAGTGTCAATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGGAACA	3326
Db	3132	GACCAAGTAGTAGCAGGGGTGATTGGGGCGCAGAAGCCACAGTACCAATCTGGGGGAACA	3191
Qy	3326	CAGTGAATGTCCTAGTTCGTATGGACAGACACGGGGTCCCCGACCCGATCCAGGTGACCA	3385
Db	3192	CAGTGAATGTGGCCAGCCGAATGGAGGACACAGCGGTTCTCGGCAAGATCCAAGTGTACTG	3251
Qy	3386	CGGACCTGTACCAAGGTTCTAGCTGCCCAAGGGGTACCAAGTGGAGTGTCCGAGGGGTGGTCA	3445
Db	3252	AGGAGACGCGGGCCCTGCAGTCCCTGGTGTACAGTGTCTATAGCAGAGCGCAATCA	3311
Qy	3446	AGGTGAAGGCAAGGGGGAGATGACCACCTACTTCTCAA	3485'
Db	3312	AGGTCAAAGGCAAGGGGAACTCTGTACCTACTTCTGAA	3351

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RESULT 13
; US-10-144-771-855
; Sequence 855, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CU001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 855
; LENGTH: 3820
; TYPE: DNA
; ORGANISM: HUMAN
; US-10-144-771-855

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Query Match	11.2%	Score 397.4	DB 6	Length 3820	
Best Local Similarity	50.7%	Pred. No. 7.8e-81			
Matches 1430	Conservative	0	Mismatches 1196	Indels 195	Gaps
Qy	728	TGTTCTTGTATACATCGCATACAGCTCTCTCCCATCCGCATCGGGCTGCGCTCTCA	787		
Db	419	TCTTCATCATCTCGTGGGTACACCATGCTCCCTTCAACATGAGGATGCCATCATCG	478		
Qy	788	CGCGCTGGGGCTCTCCACCTTGCATTGATCTGTG-----GCCTGGCAACTTAAC	837		
Db	479	CCAGGTCCTCACCTCTTCATCTCATAGATAGTGTGAGTGTCTACCTGTCTGCACAC	538		
Qy	838	C--GTGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGCTGCTCTTCTCTGCA	895		
Db	539	CAGGGCCAAAGCAGCACTGTTCTGGCAGATACTGGCCAAAGTGATCATTTTTCATCTGTG	598		
Qy	896	CCAAGCTATTTAGCATCTGCACACACTATCCAGCAGAGTGTCTCAGCGCCAGGCTTTC	955		
Db	599	GGAACTTGGCGGGAGCTTACCATAAGCACCTCATGTGAACCTTGCCCTGCAGCAAAACCTATC	658		
Qy	956	AGGAGACCCGAGTTACATCCAGGCCCGGCTCCACCTGCGAGCATGAGAAATCGCGACGAGG	1011		
Db	659	GGGACATGTAATTGCATCAAGTCCCGGATCAAGCTGGAATTTGAAAACGGCAGCAGG	718		
Qy	1016	AGCGCTGCTGCTGCGTATTGCCCCAGCAGCGTTGCCATGGAGATGAAAGAGAGATCA	1071		
Db	719	AACGACTTCTGCTTTCCTTGCTGCTGCATGCGCATGGCAATGGAATGAAGGCTGAAATCA	778		
Qy	1076	-----ACAAAAAAGAGACATCTTCCACAAGA	1101		
Db	779	TTCAAAGGCTACAGGGACCCNAACAGCAGCATAGTGGAAAACAGCAACTTCCACACC	838		
Qy	1106	TCTACATACAGAAGCATGACAATGTCAGCATCTGTTTTCAGAGACATTTAGGGCTTCACCA	1161		
Db	839	TGTATGTCACGGACACACCAAGCTGAGCATATTATATGCTGACATTTGTTGGCTTCACC	898		
Qy	1166	GCCTGGCATCCAGTGGCATGCGCAGGAGCTGGTTCATGACCCCTGAATGAGCTCTTTTGCC	1221		









